Identifier:	AAH51470 DNA Sequence 1001 BP
Release Info:	Derwent Geneseq Database Release No. 200124; Date released 26-NOV-01
Database XReference:	WPI; 2000-638353/61.
Accession Number:	AAH51470
Patent Title:	Polynucleotides comprising sequences from malate decarboxylase enzyme-related biallelic markers used for genotyping -
Patented by:	(GEST) GENSET.
Inventor:	Blumenfeld M, Bougueleret L, Chumakov I, Cohen-Akenine A
Description:	Human UGT2B4 related DNA containing a biallelic polymorphism SEQ ID 361.
Patent Number:	WO200058508-A2
Patent Publication Date:	05-OCT-2000
Modification Date:	29-AUG-2001 (first entry)
Local Filing:	24-MAR-2000; 2000WO-IB00403
Priority:	25-MAR-1999
Abstract:	Sequences AAH51110-AAH51593 represent human DNA fragments which contain biallelic markers. The sequences are related to various human genes including microsomal glutathione S-transferase II (MGSTII), malate decarboxylase enzyme (DME1/ME1), cytochrome P450, glutathione reductase/synthase (GSHR/GSHS), flavin-containing monooxygenases (FMO), gamma-glutamyltransferase 5 (GGT5), dipeptidase (DP), glucose 6-phosphate dehydrogenase (G6PDH), phosphogluconate dehydrogenase (PGDH), and uridine diphosphate glucoronosyl transferases (UGT2). Each of these sequences contains a biallelic marker/polymorphism, which is represented in the sequence as a degenerate/undefined base. The genes to which the biallelic marker containing sequences are related are involved in drug metabolism. Sequences AAH51594 - AAH51598 represent the genomic sequence of the MGSTII gene and four alternative MGSTII cDNA sequences. AAB62905-AAB62906 are MGSTII gene products. PCR primers AAH51599 and AAH51600 are used in an example for the amplification of human genomic DNA fragments. The invention includes a method of genotyping comprising determining the identity of a nucleotide at a DME- or MGSTII-related biallelic marker in a biological sample. The method is used to determine the frequency in population of an allele of a DME- or MGST-II related biallelic marker and to select an individual for inclusion in a clinical trial of a drug treatment. The method is also used to detect association between allele and phenotype, and to detect association between haplotype and phenotype. The polynucleotides are used, in hybridization assays, sequencing assays or allele specific amplification assays. The method can be used to determine whether an individual suffers or is at risk of developing asthma or is at risk of developing hepatoxicity on treatment with zileuton.
KeyWords:	Human;biallelic marker;single nucleotide polymorphism;SNP;MGSTII;microsomal glutathione S-transferase II;malate decarboxylase enzyme;DME1;ME1;cytochrome P450;glutathione reductase;GSHR;GSHS;GGT5;flavin-containing monooxygenase;FMO;gamma-glutamyltransferase 5;dipeptidase;DP;glucose 6-phosphate dehydrogenase;G6PDH;haplotype;phosphogluconate dehydrogenase;PGDH;drug metabolism;phenotype;uridine diphosphate glucoronosyl transferase;UGT2;asthma;hepatoxicity;zileuton;ds.
Organism	Homo sapiens.
Sequence Composition:	Sequence 1001 BP; 331 A; 177 C; 153 G; 300 T; 40 other;
Sequence:	>AAH51470 WO200058508-A2 PA (GEST) PR 25-MAR-1999 PF 24-MAR-2000 Human UGT2B4 related DNA containing a biallelic polymorphism SEQ ID 361. [Homo sapiens.] NNNNTNNNGTGNNNNNNNNNNNNCTNNNNANANNNNNNNANANNNNCCNNNNGAAGAAAGGC CTGGTGGCCTCTTCTATTCTGGTGCCAGTGCTGCCTCTGAGACACAACAAAGTGATGATG AGAGTTCCTCACATGCAGTTAGAAATAGCACATCAATTTAACAGTGTGATTTCAGGGCAA TAGGTGTTCCACCTAAACAATNAACCTGAAAGGTACAATTATTCAACAACTAACTATAAA

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Identifier: AAH51513 DNA Sequence 1001 BP

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Patented by: (GEST) GENSET.

Inventor: Blumenfeld M, Bougueleret L, Chumakov I, Cohen-Akenine A

Description: Human UGT2B10 related DNA containing a biallelic polymorphism SEQ ID 404.

Patent Number: WO200058508-A2

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Organism Homo sapiens.

Sequence Composition: Sequence 1001 BP; 346 A; 157 C; 147 G; 343 T; 8 other;

Sequence: >AAH51513 WO200058508-A2 PA (GEST) PR 25-MAR-1999 PF 24-MAR-2000 Human UGT2B10 related DNA containing a biallelic polymorphism SEQ ID 404. [Homo sapiens.]
CATTAGTCCAACTGGAAANTCTTGTATTAANGTTTTGCAGTCTGAAGTCACACCACCATA
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GCTGAATGCACTGAAGACAGTAATTAATGATCCTTCGTGAGTAGAACAATATTTTTCACT
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ATAGCATAAAACCCACCTATTTATGGCAAAAATTCCAAATATTTTTACTATGTTTACAGA
GTCATGAAGTCATCACCAGTGTATAAGTTTGGAACATTTTT

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(54) Title: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM

(57) Abstract

The invention provides polynucleotides including biallelic markers derived from genes involved in the biotransformation of xenobiotics such as drugs and from genomic regions flanking those genes. Primers hybridizing to regions flanking these biallelic markers are also provided. This invention also provides polynucleotides and methods suitable for genotyping a nucleic acid containing sample for one or more biallelic markers of the invention. Further, the invention provides methods to detect a statistical correlation between a biallelic marker allele and a phenotype and/or between a biallelic marker haplotype and a phenotype.

BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM

FIELD OF THE INVENTION

The present invention is in the field of pharmacogenomics, and is primarily directed to biallelic markers that are located in or in the vicinity of genes, which have an impact on the metabolism of xenobiotics such as drugs and the uses of these markers. The present invention encompasses methods of establishing associations between these markers and a phenotype such as drug response, toxicity and susceptibility to disease. The present invention also provides means to determine the genetic predisposition of individuals to such drug responses, toxicity and diseases.

BACKGROUND OF THE INVENTION

To assess the origins of individual variations in drug response, pharmacogenomics uses the genomics technologies to identify polymorphisms within genes associated with drug response. In this respect, there are three main categories of genes that may theoretically be expected to be associated with drug response, namely genes linked with the targeted disease, genes related to the drug's mode of action and genes involved in the drug's metabolism. Among these genes of pharmacogenomic importance, genes coding for drug-metabolizing enzymes have a central role.

Drug Metabolism

Drug-metabolizing enzymes are important determinants of drug disposition, safety and efficacy. The enzyme systems involved in the metabolism and the subsequent elimination from the body of environmental chemicals, food toxins and drugs are mainly localized in the liver, although every tissue examined has some metabolic activity.

In order to produce its characteristic effects, a given drug must be present in appropriate concentrations at its sites of action. The absorption, distribution, biotransformation and excretion of a drug all involve its passage across cell membranes. The lipophilic characteristics of drugs that promote their passage through biological membranes and subsequent access to their site of action reduce their elimination from the body. Renal excretion of unchanged drug plays only a modest role in the overall elimination of most therapeutic agents, since lipophilic compounds filtered through the glomerulus are largely reabsorbed through the tubular membranes. Biotransformation of drugs into more hydrophilic metabolites plays a major role in the termination of their biological activity and their elimination from the body. In general, biotransformation

reactions generate more polar, inactive metabolites that are readily excreted from the body. However in some cases, metabolites with potent biological activity or toxic properties are generated and may result in adverse side effects. Metabolic biotransformation of drugs can be classified as either Phase I functionalization reactions or Phase II biosynthetic reactions. Phase I reactions introduce or expose a functional group on the parent compound, and generally result in the loss of pharmacological activity although there are some examples of retention or enhancement of activity. Phase II conjugation reactions lead to the formation of a covalent linkage between a functional group on the parent compound with glucuronic acid, sulfate, glutathione, amino acids or acetate. These highly polar conjugates are generally inactive and are excreted rapidly in the urine and feces. Within a given cell, most drug metabolizing Phase I enzymes are located primarily in the endoplasmic reticulum, while the Phase II conjugation enzyme systems are mainly cytosolic. In some cases, drugs biotransformed through a Phase I reaction in the endoplasmic reticulum are further metabolized by conjugation in the cytosolic fraction of the same cell (Hardman J.G., Goodman, Gilman A., Limbird L.E.; *Goodman & Gilman's The Pharmacological Basis of Therapeutics*, 9^{th} edition, McGraw-Hill, N.Y., 1996).

Enzymes Involved in the Biotransformation of Xenobiotics

Besides being involved in the biotransformation of drugs, drug-metabolizing enzymes are also involved in the metabolism of xenobiotics (foreign compounds) as well as in the metabolism of endogenous compounds including steroids, vitamins and fatty acids. Foreign compounds include therapeutic agents, carcinogens, plant metabolites, environmental pollutants, foodstuffs and other dietary components as well as industrial chemicals. The biotransformation of foreign compounds (xenobiotics) is often regarded as detoxification because it usually converts compounds into more water-soluble, readily excreted substances. This tends to decrease the exposure of the organism to the compound and therefore tends to decrease toxicity. However, in some cases the reverse occurs and a metabolite is produced which is more toxic than the parent compound. For example, drug-metabolizing enzymes may activate some carcinogens, and interindividual differences in cancer susceptibilities, have been linked to polymorphisms in drug-metabolizing enzymes. There are many factors, which affect biotransformation and toxicity, such as the dose, availability of cofactors and the relative activity of the various drug-metabolizing enzymes. There may also be several competing pathways of metabolism – some leading to detoxification others to toxicity. Factors, such as genetic factors or environmental factors,

which influence the balance between these competing pathways, will also determine the eventual toxicity.

As mentioned above, the metabolic conversion of drugs and other xenobiotics is enzymatic in nature. The enzyme systems involved in the biotransformation of drugs are localized in the liver, although every tissue examined has some metabolic activity. Other organs with significant metabolic capacity include the kidneys, gastrointestinal tract, skin and lungs. Following non-parenteral administration of a drug, a significant portion of the dose may be metabolically inactivated in either the liver or intestines before it reaches the systemic circulation. This first-pass metabolism significantly limits the oral availability of highly metabolized drugs.

Cytochrome P450

The cytochrome P450 enzyme family is the major catalyst of biotransformation reactions. Since its origin, the cytochrome P450 gene family has diversified to accommodate the metabolism of a growing number of environmental chemicals, food toxins and drugs. The resulting superfamily of enzymes catalyzes a wide variety of oxidative and reductive reactions and has activity towards a chemically diverse group of substrates. Cytochrome P450 enzymes are heme-containing membrane proteins localized in the smooth endoplasmic reticulum of numerous tissues. Oxidative reactions catalyzed by the microsomal monooxygenase system require the cytochrome P450 hemoprotein, NADPH-cytochrome P450 reductase, NADPH, and molecular oxygen. Oxidative biotransformations catalyzed by cytochrome P450 monooxygenases include aromatic and side chain hydroxylation, N-, O-, S- dealkylation, N-oxidation, sulfoxidation, N-hydroxylation, deamination, dehalogenation, and desulfuration. Cytochrome P450 enzymes also catalyze a number of reductive reactions, generally under conditions of low oxygen tension. The only common structural feature of the diverse group of xenobiotics oxidized by cytochrome P450 enzymes is their high lipid solubility.

Twelve cytochrome P450 gene families have been identified in human beings, and a number of distinct cytochrome P450 enzymes often exist within a single cell. The cytochrome P450 1, 2 and 3 families (CYP1, CYP2, CYP3) encode the enzymes involved in the majority of all drug biotransformations, while the gene products of the remaining cytochrome P450 families are important in the metabolism of endogenous compounds such as steroids and fatty acids. CYP1A2 gene expression may play an important role in individual risk of environmental toxicity or cancer. CYP1A2 substrates include clinically important drugs such as imipramine, propranolol, paracetamol, clozapine, theophyline,

caffeine and acetaminophen. CYP1A2 is also involved in the conversion of heterocyclic amines and arylamines to their proximal carcinogenic and mutagenic forms, as well as in the metabolism of endogenous substances including estradiol and uroporphyrinogen III. Interindividual differences in susceptibility to arylamine- and heterocyclicamine-induced cancers have been linked to CYP1A2 polymorphism. CYP2C8 appears to be responsible for retinol and retinoic acid metabolism and actively catalyzes benzphetamine N-demethylation. CYP2C9 catalyzes the hydroxylation of tolbutamide, a hypoglycemic agent used in the treatment of type II diabetes mellitus, and one allelic variant of CYP2C9 accounts for the occurrence of poor metabolizers of tolbutamide. CYP2C9 may also have an important role in terminating the anti-coagulant activity of warfarin. Wide spread interindividual differences in the response to warfarin have been recognized. Such variability is particularly important for drugs such as warfarin which have narrow therapeutic indices (Steward D.J. et al., *Pharmacogenetics*, 7:361-367, 1997). CYP2C9 is further involved in the oxidation of tielinic acid and several non-steroidal anti-inflammatory agents. The oxidative metabolism through CYP2C9 of tilenic acid can result in the emergence of a drug induced autoimmune hepatitis. CYP3A4 is involved in the biotransformation of a majority of drugs and is expressed at significant levels extrahepatically. It is now recognized that extensive metabolism by CYP3A4 in the gastrointestinal tract is a significant factor contributing to the poor oral availability of many drugs (first-pass metabolism). Barbiturates, certain steroids and macrolide antibiotics can induce this enzyme. It appears to play a central role in the metabolism of the immunosuppressive cyclic peptide cyclosporin A as well as macrolide antibiotics, such as erythromycin.

Flavin-containing monooxygenases (FMOs)

The mammalian flavin-containing monooxygenases (FMOs) are microsomal enzymes that catalyze the NADPH-dependent oxygenation of a wide variety of drugs and other xenobiotics that possess a soft nucleophilic heteroatom, typically a nitrogen, sulfur, phosphorus or selenium atom. Of special clinical interest is the oxidation of trimethylamine in the liver by the FMO, because its deficiency causes the "Fish Odor Syndrome." Drugs oxidized by FMOs include, among others, antidepressant, antipsychotic-neuroleptic, antihypertensive drugs. FMOs have been implicated in the detoxification but also in the metabolic activation of several different environmental toxins and carcinogens.

Unlike all other known oxidases and monooxygenases, among which the well-studied cytochrome P450 monooxygenases, FMOs have the unique property of forming a stable enzyme intermediate in the absence of an oxygenatable substrate. Because the energy

for catalysis is already present in the FMO enzyme before contact with the potential substrate, the fit of the substrate does not need to be as stringent as with the other enzymes. This feature, unique to FMOs among monooxygenases, is responsible for the wide range of substrates accepted by FMOs (including tertiary and secondary alkyl- and arylamines, many hydrazines, thiocarbamides, thioamides, sulfides, disulfides, thiols, among others), and determines that any soft nucleophilic xenobiotic accessible to the active enzyme will probably be oxidized by FMO *in vivo*. Although some FMO substrates are oxidized to less active derivatives, several soft nucleophiles are metabolized to highly reactive and potentially toxic intermediates.

The FMOs represent a multigene family. Five distinct mammalian FMO isoenzymes have been identified and cloned from various animal and human tissues: FMO1, FMO2, FMO3, FMO4 and FMO5. Human FMO2 and human FMOX were cloned and sequenced by the inventors as described in PCT Publication WO 9824914. FMOX represents a new member of the FMO gene family not previously identified in mammals. Tissue specificity and activities of the different FMOs have been thoroughly characterized. FMO1 is known to be expressed in the human kidney but is absent from the liver. In man the enzyme is subject to developmental regulation. FMO2 is predominantly expressed in lung of all mammalian species tested. FMO3 was isolated from human liver, and accounts for the majority of FMO expressed in adult human liver.

Many of the FMO substrates may also be oxidized by the cytochrome P450 monooxygenases. However, the final oxidation products are usually different, and the nitrogen of a specific compound is rarely N-oxygenated by both types of monooxygenases. Today, a large number of drugs in human clinical trials contain a nitrogen, sulfur, phosphorous or some other nucleophilic functionality. Of the two major monooxygenase systems considered to be responsible for heteroatom-containing chemical and drug oxidative metabolism (CYP 450 and FMO), relatively little is known concerning the role of the FMO in human drug metabolism. Yet, given the wide range of substrates potentially oxidized by FMOs, this class of monooxygenases seems to represent a major determinant of drug safety and efficacy.

Uridine diphosphate glucoronosyl transferase (UGTs)

Glucoronidation is a major detoxification pathway of Phase II metabolism that is catalyzed by the UDP-glucuronosyl transferase family of enzymes. Glucuronidation is quantitatively the most important conjugation reaction. Members of this enzyme family catalyze the conjugation of numerous endogenous substances of widely differing structures

such as bilirubin, steroid hormones and fat-soluble vitamins. In general, xenobiotics become substrates for glucoronidation by first passing through Phase I metabolism, but many compounds do not require this step because they already possess reactive functionalities (e.g. hydroxyl, carboxyl, amino, sulfhydryl etc.) that are direct targets for glucuronosyl transferase. The human UGT genes appear to have evolved by a series of gene-duplication and gene-conversion events resulting in the emergence of a diversity of isoforms. They are divided into two families, UGT1 which is known to have bilirubin and phenol as substrates, and UGT2 which is known to have steroid, bile, and odorant as substrates, with these two families located on different chromosomes. The UGT2 family is divided into subfamilies UGT2A and UGT2B. The UGTs have different but sometimes overlapping substrate specificities. They catalyze the transfer of an activated glucuronic acid molecule to aromatic and aliphatic alcohols, carboxylic acids, amines and free sulfhydryl groups of both exogenous and endogenous compounds, to form O- N- and S-glucuronide conjugates. The increased water solubility of the glucuronide conjugates promotes their elimination in the urine or bile. In addition to high levels of expression in the liver, UGTs are also found in the kidney, intestine, brain and skin. Glucoronidation constitutes, from a general point of view, a reaction of detoxification and elimination. It generally leads to the formation of inactive metabolites and therefore, glucoronidation can dramatically modify the pharmacological activity of a drug. Moreover, UGTs play a major role in the elimination of nucleophilic metabolites of carcinogens, such as phenols and quinols of polycyclic aromatic hydrocarbons. In this way they prevent their further oxidation to electrophiles, which may react with DNA, RNA or protein. On the other hand, glucoronidation of certain compounds facilitates metabolic activation. Aromatic amines are some of the most studied examples of the role glucoronidation plays in metabolic activation of carcinogens. Glucoronidation has also been implicated in adverse drug reactions of certain carboxylic drugs, which resulted in a toxic immunological response. Glucoronidation although generally a detoxification reaction, may occasionally be involved in increasing toxicity.

Glutathione conjugation and further metabolism

Glutathione is a tripepetide (γ-glutamylcysteinylglycine, GSH) found in high concentrations in most mammalian tissues, but especially in the liver. Glutathione has several functions including roles in metabolism, transport and catalysis. Glutathione is also important for the maintenance of the thiol moieties of proteins and for the maintenance of the reduced form of other molecules such as cysteine, coenzyme A, and antioxidants such as

ascorbic acid; it is also used in the formation of deoxyribonucleic acids (Anderson M.E., *Advances in Pharmacology*, 38: 65-74, 1997). Glutathione has a major protective role in the body, as it is the major cellular antioxidant. GSH can react non-enzymatically with reactive oxygen species (ROS) and thereby protect the cell from oxidative damage. ROS have been widely implicated in the pathology of numerous diseases such as arteriosclerosis, rheumatoid arthritis, cancer, AIDS, adult respiratory distress syndrome and Parkinson's disease.

Moreover, conjugation with the tripeptide glutathione represents a major detoxification pathway for xenobiotics including drugs and carcinogens. Glutathione may react either chemically or in enzyme catalyzed reactions with a variety of compounds, which are reactive electrophilic metabolites produced in Phase I reactions. The glutathione S-transferase enzymes (GSTs) that catalyze these reactions are members of a multigene family and are expressed in virtually all tissues. Glutathione conjugates are cleaved to cysteine derivatives and subsequently are acetylated by a series of enzymes located primarily in the kidney to give N-acetylcysteine conjugates collectively referred to as mercapturic acids. Mercapturic acid derivatives are the ultimate metabolites excreted in the urine. This is a particularly important route of Phase II metabolism from the toxicological point of view, as it is often involved in the removal of reactive intermediates. Xenobiotics that act as substrates for the glutathione S-transferases (GSTs) fall into four broad categories: electropilic carbon, nitrogen, sulfur and oxygen. Examples of substrates for glutathione S-transferases include aromatic, heterocyclic, alicyclic and aliphatic epoxides; aromatic halogen and nitro compounds; alkyl halides; and unsaturated aliphatic compounds (Ballantyne, B., Marrs T. and Turner P., *General & Applied Toxicology*, Stockton Press, New York, 1993). The GSTs are also involved in the metabolism of endogenous molecules such as the leukotrienes. As mentioned above, many of the enzymes involved in xenobiotic metabolism are also involved in specific aspects of the metabolism of normal cellular biochemical constituents. Leukotrienes are important mediators and modulators of the inflammatory reaction and contribute to a number of physiological and pathological processes. Moreover, the GSTs are also capable of directly binding hydrophobic compounds such as heme, bilirubin, and steroids, which may enable them to serve as intracellular storage and transport proteins for biological substances with limited water solubility. By their catalytic activity and their capacity for binding, the GSTs provide the cell with mechanism to protect itself from the noxious effects of various xenobiotics and endogenous substances. Further, GSTs may undergo amplification in tumors and may

thereby be implicated in drug resistance in cancer chemotherapy. GSTs are mostly cytosolic although, more recently, microsomal GSTs have been identified. Human microsomal GST II (MGST II) is a member of the microsomal glutathione S-transferase family. This enzyme catalyzes the production of LTC4 (leukotriene C4) from LTA4 (leukotriene A4) and reduced glutathione. Leukotrienes are derived from arachidonic acid and related fatty acids. Metabolites of arachidonic acid have been collectively termed eicosanoids, the principal eicosanoids are prostaglandins, thromboxanes and leukotrienes (LT). Eicosanoids are among the most important chemical mediators and modulators of the inflammatory reaction and contribute to a number of physiological and pathological processes (see Hardman J.G., Goodman, Gilman A., Limbird L.E.; *Goodman & Gilman's The Pharmacological Basis of Therapeutics*, 9th edition, McGraw-Hill, N.Y., 1996). The ability to mount an inflammatory response is essential for survival in the face of environmental pathogens and injury, although in some situations and diseases the inflammatory response may be exaggerated and sustained for no apparent beneficial reason. This is the case in numerous chronic inflammatory diseases and allergic inflammation. Acute allergic inflammation is characterized by increased blood flow, extravasation of plasma and recruitment of leukocytes. These events are triggered by locally released inflammatory mediators including eicosanoids and more particularly leukotrienes. The participation of arachidonic acid metabolism in inflammatory diseases such as rheumatoid arthritis, asthma and acute allergy is well established. Pathological actions of leukotrienes are best understood in terms of their roles in immediate hypersensitivity and asthma. LTC4 and LTD4 are potent bronchoconstrictors, they act principally on smooth muscle in peripheral airways and are a 1000 times more potent than histamine both *in vitro* and *in vivo*. They also stimulate bronchial mucus secretion and cause mucosal edema. A complex mixture of chemical messengers is released when sensitized lung tissue is challenged by the appropriate antigen. Various prostaglandins and leukotrienes are prominent components of this mixture. Response to the leukotrienes probably dominates during allergic constriction of the airway. A particularly important role for the cysteinyl-leukotrienes (LTC4, LTD4, and LTE4) has been suggested in pathogenesis of asthma, which is now recognized as a chronic inflammatory condition. They are potent spasmogens causing a contraction of bronchiolar muscle and an increase in mucus secretion. An increased LTC4 formation has also been reported in leukocytes from patients with chronic myelogenous leukemia (Stenke et al., *Acta Oncologica*, 27:803-805, 1987) and in experimental glomerulonephritis (Petric et al., *Biochim. Biophys. Acta*, 1254:207-215, 1995).

Moreover, MGST II has the capacity to conjugate other compounds such as 1-chloro-2, 4 dinitrobenzene with glutathione and may be involved in a general metabolic system for detoxifying fatty acid epoxides (Jakobsson et al., *Journal of Biological Chemistry*, 271:22203-22210, 1996).

The resulting glutathione conjugate usually undergoes further metabolism, which involves first a removal of the glutamyl residue, catalyzed by γ-glutamyltransferase (GGT). In addition to catalyzing the initial step in the conversion of glutathione-conjugated compounds to mercapturic acids, GGT also converts LTC4 to LTD4. Interestingly, expression of GGT is often increased in cancerous tissues.

Renal dipeptidase is also implicated in the renal metabolism of glutathione and its conjugates including conjugated xenobiotics and endogenous molecules such as Leukotriene D4. Pharmacologically it is an important enzyme, for it is responsible for hydrolysis of some β-lactam antibiotics such as penem and carbapenem.

The effectiveness of the GSTs and therefore of detoxification by glutathione conjugation in general as well as the ability of the cell to resist to oxidative stress, are strongly influenced by the availability of reduced glutathione. Reduction of oxidized glutathione and *de novo* synthesis of glutathione, are both completely dependent on NADPH. Glutathione reductase (GSHR) maintains high levels of reduced glutathione in the cytosol in an NADPH dependent reaction. Reduced glutathione is synthesized *de novo* in the cytosol of most cells via the γ-glutamyl cycle; a series of tightly controlled, enzyme catalyzed reactions. The first and second step in the *de novo* glutathione biosynthesis are catalyzed by γ-glutamylcysteine synthetase (GLCL) and glutathione synthase (GSHS) respectively. Deficiencies in γ–glutamylcysteine synthetase and GSH synthetase are associated with hemolytic anemia and impaired central nervous system function.

Glucose 6-phosphate dehydrogenase (G6PDH), phosphogluconate dehydrogenase (PGDH) and malate dehydrogenase: generation of NADPH

NADPH (nicotinamide adenine dinucleotide phosphate) serves as an electron donor in reductive biosyntheses. In the pentose phosphate pathway, NADPH is generated when glucose 6-phosphate is oxidized to ribose 5-phosphate. G6PDH and PGDH are key enzymes of the pentose phosphate pathway and directly lead to the generation of NADPH. Another major source of NADPH is the oxidative decarboxylation of malate by malic enzyme.

NADPH may be used in anabolic processes such as fatty acid biosynthesis. One of the major functions of malic enzyme may be supplying NADPH to the cytosol for the

synthesis of fatty acids from acetyl CoA (coenzyme A). Further, the cytochrome P450 system is dependent on NADPH. As mentioned above, availability of NADPH is also critical for the reduction of glutathione. The connection between generation of NADPH and reduction of glutathione is clearer in tissues that have limited glycolytic metabolism, e.g. the lens and the erythrocyte. Thus the viability of the erythrocyte depends on glutathione, kept reduced by this pathway. Moreover, factors that influence the availability of reduced glutathione drastically alter the effectiveness of glutathione S-transferases therefore also affecting drug metabolism. Under most conditions saturating levels of NADPH are provided to the cell. However, certain conditions can stress the ability of the cell to provide NADPH and it may become rate limiting.

G6PDH and PGDH are present in most cells and tissues. They serve as the key enzymes of the pentose phosphate pathway that control the flow of carbon through the pathway and produce reducing equivalents as NADPH to meet cellular needs for reductive biosynthesis and to maintain the redox state of the cell at physiological levels. Deficiency of G6PDH and PGDH leads to decreased levels of NADPH and is associated with hemolytic anemia in response to oxidative stress. The red cells of G6PDH deficient persons are susceptible to hemolysis by dietary substances, and by drugs such as primaquine, sulfones, sulfonamides, nitrofurans, vitamin K analogs, acetophenetidin, chloramphenicol, and many others.

Genetic Polymorphisms in Drug Metabolizing Enzymes and Pharmacogenomics

Genetic, environmental, and physiological factors are involved in the regulation of drug biotransformation reactions. Results obtained from epidemiological studies and experimental animal model systems have shown a wide range of phenotypic variation in the ability of individuals to metabolize drugs and environmental chemicals. While some of this variation can be attributed to different environmental exposures, it has become clear that genetic factors also play an important role in determining the response of the individual to exogenous agents. Certain allelic forms of drug-metabolizing enzymes can render the individual either more sensitive or resistant to the toxic or therapeutic effects of exogenous drugs and chemicals. Genetic factors seem to be the major determinants of the variability of drug effects and are responsible for a number of striking quantitative and qualitative differences in pharmacological activity. Genetic differences in the ability of individuals to metabolize a drug through a given pathway are an important contributor to the large interindividual differences of drug efficacy and adverse effects within a population. There are many diverse examples of xenobiotics whose toxicity is directly dependent on the

activity of drug-metabolizing enzymes. Often impaired metabolism of a drug through a genetically polymorphic pathway has been associated with an increased incidence of adverse effects in the slow metabolizer population (Weber W.W., *Pharmacogenetics*, Oxford University Press, N.Y., 1997). Moreover, genetic differences in the regulation, expression and activity of genes coding for Phase I and Phase II drug-metabolizing enzymes can be crucial factors in defining cancer susceptibility and the toxic or carcinogenic power of environmental chemicals and xenobiotics. In addition, the majority of serious cases of drug-drug interactions are a result of the interference of the metabolic clearance of one drug by a coadministered drug. The interference usually occurs via inhibition or induction of drug-metabolizing enzymes. Interindividual differences in susceptibility to severe drug-drug interactions also involve drug-metabolizing enzyme polymorphism. In some cases the design of the drug takes into account the activity of drug-metabolizing enzymes. For example, prodrugs require activation by drug-metabolizing enzymes to exhibit their therapeutic activity. The activation and efficiency of such prodrugs depends on interindividual polymorphism in drug-metabolizing enzymes.

Individual differences in metabolism of therapeutics can lead to severe toxicity or therapeutic failure. Therapeutic management and drug development can be markedly improved by the identification of specific genetic polymorphisms that determine and predict patient susceptibility to diseases or patient responses to drugs. Assessing individual risk rather than population risk will lead to better targeted therapeutic strategies defining individual drug usage based on a benefit/risk prognosis. To assess the origins of individual variations in disease susceptibility or drug response, pharmacogenomics uses the genomic technologies to identify polymorphisms within genes, which are part of biological pathways involved in disease susceptibility, etiology, and development, or more specifically in drug response pathways responsible for a drug's efficacy, tolerance or toxicity. It can provide tools to refine the design of drug development by decreasing the incidence of adverse events in drug tolerance studies, by better defining patient subpopulations of responders and non-responders in efficacy studies and, by combining the results obtained therefrom, to further allow better enlightened individualized drug usage based on efficacy/tolerance prognosis. Pharmacogenomics can also provide tools to identify new targets for designing drugs and to optimize the use of already existing drugs, in order to either increase their response rate and/or exclude non-responders from corresponding treatment, or decrease their undesirable side effects and/or exclude from corresponding treatment patients with marked susceptibility to undesirable side effects.

Drug-metabolizing enzymes are highly relevant to pharmacogenomics because they are at the core of drug response, drug efficacy and toxicity. Drug-metabolizing enzymes also determine an individual's susceptibility to exogenous chemicals and to a number of diseases associated with exposure to toxic or carcinogenic chemicals.

The complexity of the pathways and enzymes that are involved in detoxification and metabolism of drugs has limited the precise identification of the drug-metabolizing enzymes, which play the causal role in pathologies or in drug response. Therapeutic management and drug development can be markedly improved by the identification of genetic markers derived from drug-metabolizing enzymes that predict patient susceptibility to diseases or patient responses to drugs.

Genetic Analysis of Complex Traits

Until recently, the identification of genes linked with detectable traits has relied mainly on a statistical approach called linkage analysis. Linkage analysis is based upon establishing a correlation between the transmission of genetic markers and that of a specific trait throughout generations within a family. Linkage analysis involves the study of families with multiple affected individuals and is useful in the detection of inherited traits, which are caused by a single gene, or possibly a very small number of genes. Linkage analysis has been successfully applied to map simple genetic traits that show clear Mendelian inheritance patterns and which have a high penetrance (the probability that a person with a given genotype will exhibit a trait). About 100 pathological trait-causing genes have been discovered using linkage analysis over the last 10 years.

But, most traits of medical relevance do not follow simple Mendelian monogenic inheritance and linkage studies have proven difficult when applied to complex genetic traits. Many complex traits such as height, blood pressure or cancer susceptibility have been known to run in families and are at least partially determined by genetic factors. However, the genes or combination of genes that underlie these observable characteristics or traits remain unknown in most cases. Such complex traits are often due to the combined action of multiple genes as well as environmental factors. Because of their low penetrance, such complex traits do not segregate in a clear-cut Mendelian manner as they are passed from one generation to the next. Drug efficacy, response and tolerance/toxicity can also be considered as multifactoral traits involving a genetic component in the same way as complex diseases. Linkage analysis is impractical when the trait under study is drug response due to the lack of availability of familial cases. In fact, the likelihood of having more than one individual in a family being exposed to the same drug at the same time is very low. Linkage analysis

cannot be applied to the study of such traits for which no large informative families are available. Attempts to map complex traits have been plagued by inconclusive results, demonstrating the need for more sophisticated genetic tools.

Knowledge of genetic variation in drug-metabolizing enzymes is important for understanding why some people are more susceptible to toxicity, pathology or respond differently to drugs. Ways to identify genetic polymorphism and to analyze how they impact and predict disease susceptibility and response to treatment are needed.

Whereas a number of polymorphisms and rare mutations have been identified in drug-metabolizing enzymes (see Weber W.W., *Pharmacogenetics*, Oxford University Press, New York, 1997), genetic markers for use in determining which genes contribute to multigenic or quantitative traits and suitable methods for exploiting those markers have not been found and brought to bare on the genes coding for drug-metabolizing enzymes.

SUMMARY OF THE INVENTION

The present invention is based on the discovery of a set of novel DME-related biallelic markers. See Figure 1. These markers are located in the coding regions as well as non-coding regions adjacent to genes which are involved in the metabolic conversion of drugs and other xenobiotics. The position of these markers and knowledge of the surrounding sequence has been used to design polynucleotide compositions which are useful in determining the identity of nucleotides at the marker position, as well as more complex association and haplotyping studies which are useful in determining the genetic basis for variability in drug response and adverse reactions to drugs as well as the genetic basis for disease states involving the metabolic conversion of xenobiotics such as drugs. In addition, the compositions and methods of the invention find use in the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterization of the differential efficacious responses to and side effects from pharmaceutical agents.

The present invention further stems from the isolation and characterization of the genomic sequence of the MGST-II gene including its regulatory regions and of the complete cDNA sequence encoding the MGST-II enzyme. Oligonucleotide probes and primers hybridizing specifically with a genomic sequence of MGST-II are also part of the invention. A further object of the invention consists of recombinant vectors comprising any of the nucleic acid sequences described in the present invention, and in particular of recombinant vectors comprising the promoter region of MGST-II or a sequence encoding the MGST-II enzyme, as well as cell hosts comprising said nucleic acid sequences or recombinant

vectors. The invention also encompasses methods of screening of molecules which, modulate or inhibit the expression of the MGST-II gene. The invention is also directed to biallelic markers that are located within the MGST-II genomic sequence. these biallelic markers representing useful tools in order to identify a statistically significant association between specific alleles of MGST-II gene and one or several disorders related to asthma and/or hepatotoxicity.

A first embodiment of the invention encompasses polynucleotides consisting of, consisting essentially of, or comprising a contiguous span of nucleotides of a sequence selected as an individual or in any combination from the group consisting of SEQ ID No. 1-38, 40-54, 56-463, 465-487, 490-493, the complements thereof, the sequences described in any one or more of Figures 2, 3, 4, 5, 6, 7, and 8, and the complements thereof, wherein said contiguous span is at least 6, 8, 10, 12, 15, 20, 25, 30, 35, 40, 50, 75, 100, 200, 500, or 1000 nucleotides in length, to the extent that such a length is consistent with the lengths of the particular Sequence ID. The present invention also relates to polynucleotides hybridizing under stringent or intermediate conditions to a sequence selected from the group consisting of SEQ ID No. 1-38, 40-54, 56-463, 465-487, 490-493; and the complements thereof. In addition, the polynucleotides of the invention encompass polynucleotides with any further limitation described in this disclosure, or those following, specified alone or in any combination: Said contiguous span may optionally include the DME-related biallelic marker in said sequence; Optionally either the original or the alternative allele of Figure 3 may be specified as being present at said DME-related biallelic marker; Optionally either the first or the second allele of Figure 2 or 4 may be specified as being present at said DME-related biallelic marker; Optionally, said polynucleotide may comprise, consists of, or consist essentially of a contiguous span which ranges in length from 8, 10, 12, 15, 18 or 20 to 25, 35, 40, 50, 60, 70, or 80 nucleotides, or be specified as being 12, 15, 18, 20, 25, 35, 40, or 50 nucleotides in length and including a DME-related biallelic marker of said sequence, and optionally the original allele of Figure 3 is present at said biallelic marker; Optionally, said biallelic marker may be within 6, 5, 4, 3, 2, or 1 nucleotides of the center of said polynucleotide or at the center of said polynucleotide; Optionally, the 3' end of said contiguous span may be present at the 3' end of said polynucleotide; Optionally, biallelic marker may be present at the 3' end of said polynucleotide; Optionally, the 3' end of said polynucleotide may be located within or at least 2, 4, 6, 8, 10, 12, 15, 18, 20, 25, 50, 100, 250, 500, or 1000 nucleotides upstream of a DME-related biallelic marker in said sequence, to the extent that such a distance is consistent with the lengths of the particular Sequence

ID; Optionally, the 3' end of said polynucleotide may be located 1 nucleotide upstream of a DME-related biallelic marker in said sequence; and Optionally, said polynucleotide may further comprise a label.

A second embodiment of the invention encompasses any polynucleotide of the invention attached to a solid support. In addition, the polynucleotides of the invention which are attached to a solid support encompass polynucleotides with any further limitation described in this disclosure, or those following, specified alone or in any combination: Optionally, said polynucleotides may be specified as attached individually or in groups of at least 2, 5, 8, 10, 12, 15, 20, or 25 distinct polynucleotides of the inventions to a single solid support; Optionally, polynucleotides other than those of the invention may attached to the same solid support as polynucleotides of the invention; Optionally, when multiple polynucleotides are attached to a solid support they may be attached at random locations, or in an ordered array; Optionally, said ordered array may be addressable.

A third embodiment of the invention encompasses the use of any polynucleotide for, or any polynucleotide for use in, determining the identity of one or more nucleotides at a DME-related biallelic marker. In addition, the polynucleotides of the invention for use in determining the identity of one or more nucleotides at a DME-related biallelic marker encompass polynucleotides with any further limitation described in this disclosure, or those following, specified alone or in any combination. Optionally, said DME-related biallelic marker may be in a sequence selected individually or in any combination from the group consisting of SEQ ID No. 1-38, 40-54, 56-463, 465-487, 490-493; and the complements thereof; Optionally, said polynucleotide may comprise a sequence disclosed in the present specification; Optionally, said polynucleotide may consist of, or consist essentially of any polynucleotide described in the present specification; Optionally, said determining may be performed in a hybridization assay, sequencing assay, microsequencing assay, or an enzyme-based mismatch detection assay; Optionally, said polynucleotide may be attached to a solid support, array, or addressable array; Optionally, said polynucleotide may be labeled.

A fourth embodiment of the invention encompasses the use of any polynucleotide for, or any polynucleotide for use in, amplifying a segment of nucleotides comprising a DME-related biallelic marker. In addition, the polynucleotides of the invention for use in amplifying a segment of nucleotides comprising a DME-related biallelic marker encompass polynucleotides with any further limitation described in this disclosure, or those following, specified alone or in any combination: Optionally, said DME-related biallelic marker may

be in a sequence selected individually or in any combination from the group consisting of SEQ ID 1-38, 40-54, 56-463, 465-487, 490-493; and the complements thereof; Optionally, said DME-related biallelic marker may be selected individually or in any combination from the biallelic markers described in Figure 1; Optionally, said DME-related biallelic marker may be selected from the biallelic markers found in Figures 9, 10, 11 and 12; Optionally, said DME-related biallelic marker may be selected from the following biallelic markers: 12-455-326, 12-453-429, 12-454-363, 12-441-233, 12-461-299, 12-426-154, 12-424-198, 12-716-295, 10-428-219, 12-720-80, 12-156-91, 12-140-134, 12-653-423, 10-471-84, 10-471-85, 10-470-25, 12-652-203, 12-637-219, 12-721-440, and 10-420-284; Optionally, said polynucleotide may comprise a sequence disclosed in the present specification; Optionally, said polynucleotide may consist of, or consist essentially of any polynucleotide described in the present specification; Optionally, said amplifying may be performed by a PCR or LCR. Optionally, said polynucleotide may be attached to a solid support, array, or addressable array. Optionally, said polynucleotide may be labeled.

A fifth embodiment of the invention encompasses methods of genotyping a biological sample comprising determining the identity of a nucleotide at a DME-related biallelic marker. In addition, the genotyping methods of the invention encompass methods with any further limitation described in this disclosure, or those following, specified alone or in any combination: Optionally, said DME-related biallelic marker may be in a sequence selected individually or in any combination from the group consisting of SEQ ID No. 1-38, 40-54, 56-463, 465-487, 490-493, and the complements thereof; Optionally, said DME-related biallelic marker may be selected individually or in any combination from the biallelic markers described in Figure 1; Optionally, said DME-related biallelic marker may be selected individually or in any combination from the biallelic markers described in Figure 1; Optionally, said DME-related biallelic marker may be selected from the biallelic markers found in Figures 9, 10, 11 and 12; Optionally, said DME-related biallelic marker may be selected from the following biallelic markers: 12-455-326, 12-453-429, 12-454-363, 12-441-233, 12-461-299, 12-426-154, 12-424-198, 12-716-295, 10-428-219, 12-720-80, 12-156-91, 12-140-134, 12-653-423, 10-471-84, 10-471-85, 10-470-25, 12-652-203, 12-637-219, 12-721-440, and 10-420-284; Optionally, said method further comprises determining the identity of a second nucleotide at said biallelic marker, wherein said first nucleotide and second nucleotide are not base paired (by Watson & Crick base pairing) to one another; Optionally, said biological sample is derived from a single individual or subject; Optionally, said method is performed in vitro; Optionally, said biallelic marker is

determined for both copies of said biallelic marker present in said individual's genome; Optionally, said biological sample is derived from multiple subjects or individuals; Optionally, said method further comprises amplifying a portion of said sequence comprising the biallelic marker prior to said determining step; Optionally, wherein said amplifying is performed by PCR, LCR, or replication of a recombinant vector comprising an origin of replication and said portion in a host cell; Optionally, wherein said determining is performed by a hybridization assay, sequencing assay, microsequencing assay, or an enzyme-based mismatch detection assay.

A sixth embodiment of the invention comprises methods of estimating the frequency of an allele in a population comprising genotyping individuals from said population for a DME-related biallelic marker and determining the proportional representation of said biallelic marker in said population. In addition, the methods of estimating the frequency of an allele in a population of the invention encompass methods with any further limitation described in this disclosure, or those following, specified alone or in any combination: Optionally, said DME-related biallelic marker may be in a sequence selected individually or in any combination from the group consisting of SEQ No. 1-38, 40-54, 56-463, 465-487, 490-493; and the complements thereof; Optionally, said DME-related biallelic marker may be selected from the biallelic markers described in Figure 1; Optionally, said DME-related biallelic marker may be selected individually or in any combination from the biallelic markers described in Figure 1; Optionally, said DME-related biallelic marker may be selected from the biallelic markers found in Figures 9, 10, 11 and 12; Optionally, said DME-related biallelic marker may be selected from the following biallelic markers: 12-455-326, 12-453-429, 12-454-363, 12-441-233, 12-461-299, 12-426-154, 12-424-198, 12-716-295, 10-428-219,12-720-80, 12-156-91, 12-140-134, 12-653-423, 10-471-84, 10-471-85, 10-470-25, 12-652-203, 12-637-219, 12-721-440, and 10-420-284; Optionally, determining the frequency of a biallelic marker allele in a population may be accomplished by determining the identity of the nucleotides for both copies of said biallelic marker present in the genome of each individual in said population and calculating the proportional representation of said nucleotide at said DME-related biallelic marker for the population; Optionally, determining the frequency of a biallelic marker allele in a population may be accomplished by performing a genotyping method on a pooled biological sample derived from a representative number of individuals, or each individual, in said population, and calculating the proportional amount of said nucleotide compared with the total.

A seventh embodiment of the invention comprises methods of detecting an association between an allele and a phenotype, comprising the steps of a) determining the frequency of at least one DME-related biallelic marker allele in a case (trait positive) population, b) determining the frequency of said DME-related biallelic marker allele in a control population and; c) determining whether a statistically significant association exists between said genotype and said phenotype. In addition, the methods of detecting an association between an allele and a phenotype of the invention encompass methods with any further limitation described in this disclosure, or those following, specified alone or in any combination: Optionally, said DME-related biallelic marker may be in a sequence selected individually or in any combination from the group consisting of SEQ ID No.1-38, 40-54, 56-463, 465-487, 490-493, and the complements thereof; Optionally, said DME-related biallelic marker may be selected from the biallelic markers described in Figure 1; Optionally, said control population may be a trait negative population, or a random population; Optionally, said phenotype is a response to a drug, or a side effects to a drug, or a disease involving the metabolic conversion of xenobiotics; Optionally, the identity of the nucleotides at the biallelic markers in everyone of the following sequences: SEQ ID No. 1-38, 40-54, 56-463, 465-487, 490-493 is determined in steps a) and b).

An eighth embodiment of the present invention encompasses methods of estimating the frequency of a haplotype for a set of biallelic markers in a population, comprising the steps of: a) genotyping each individual in said population for at least one DME-related biallelic marker, b) genotyping each individual in said population for a second biallelic marker by determining the identity of the nucleotides at said second biallelic marker for both copies of said second biallelic marker present in the genome; and c) applying a haplotype determination method to the identities of the nucleotides determined in steps a) and b) to obtain an estimate of said frequency. In addition, the methods of estimating the frequency of a haplotype of the invention encompass methods with any further limitation described in this disclosure, or those following, specified alone or in any combination: Optionally said haplotype determination method is selected from the group consisting of asymmetric PCR amplification, double PCR amplification of specific alleles, the Clark method, or an expectation maximization algorithm; Optionally, said second biallelic marker is a DME-related biallelic marker in a sequence selected from the group consisting of the biallelic markers of SEQ ID No. 1-38, 40-54, 56-463, 465-487, 490-493, and the complements thereof; Optionally, said DME-related biallelic markers may be selected individually or in any combination from the biallelic markers described in Figure 1;

Optionally, said DME-related biallelic marker may be selected individually or in any combination from the biallelic markers described in Figure 1; Optionally, said DME-related biallelic marker may be selected from the biallelic markers found in Figures 9, 10, 11 and 12; Optionally, said DME-related biallelic marker may be selected from the following biallelic markers: 12-455-326, 12-453-429, 12-454-363, 12-441-233, 12-461-299, 12-426-154, 12-424-198, 12-716-295, 10-428-219, 12-720-80, 12-156-91, 12-140-134, 12-653-423, 10-471-84, 10-471-85, 10-470-25, 12-652-203, 12-637-219, 12-721-440, and 10-420-284; Optionally, the identity of the nucleotides at the biallelic markers in everyone of the sequences of SEQ ID No. 1-38, 40-54, 56-463, 465-487, 490-493 is determined in steps a) and b).

A ninth embodiment of the present invention encompasses methods of detecting an association between a haplotype and a phenotype, comprising the steps of: a) estimating the frequency of at least one haplotype in a trait positive population according to a method of estimating the frequency of a haplotype of the invention; b) estimating the frequency of said haplotype in a control population according to the method of estimating the frequency of a haplotype of the invention; and c) determining whether a statistically significant association exists between said haplotype and said phenotype. In addition, the methods of detecting an association between a haplotype and a phenotype of the invention encompass methods with any further limitation described in this disclosure, or those following, specified alone or in any combination: Optionally, said DME-related biallelic marker may be in a sequence selected individually or in any combination from the group consisting of SEQ ID No. 1-38, 40-54, 56-463, 465-487, 490-493, and the complements thereof; Optionally, said DME-related biallelic markers may be selected individually or in any combination from the biallelic markers described in Figure 1; Optionally, said DME-related biallelic marker may be selected individually or in any combination from the biallelic markers described in Figure 1; Optionally, said DME-related biallelic marker may be selected from the biallelic markers found in Figures 9, 10, 11 and 12; Optionally, said DME-related biallelic marker may be selected from the following biallelic markers: 12-455-326, 12-453-429, 12-454-363, 12-441-233, 12-461-299, 12-426-154, 12-424-198, 12-716-295, 10-428-219, 12-720-80, 12-156-91, 12-140-134, 12-653-423, 10-471-84, 10-471-85, 10-470-25, 12-652-203, 12-637-219, 12-721-440, and 10-420-284; Optionally, said control population may be a trait negative population, or a random population; Optionally, said phenotype is a response to a drug, or a side effects to a drug, or a disease involving the metabolic conversion of xenobiotics; Optionally, said drug is zileuton and said side effect to said drug is

hepatoxicity; Optionally, the identity of the nucleotides at the biallelic markers in everyone of the following sequences: SEQ ID No. 1-38, 40-54, 56-463, 465-487, 490-493 is included in the estimating steps a) and b).

A tenth embodiment of the present invention is a method of administering a drug or a treatment comprising the steps of: a) obtaining a nucleic acid sample from an individual; b) determining the identity of the polymorphic base of at least one DME-related biallelic marker which is associated with a positive response to the treatment or the drug; or at least one biallelic DME-related biallelic marker which is associated with a negative response to the treatment or the drug; and c) administering the treatment or the drug to the individual if the nucleic acid sample contains said biallelic marker associated with a positive response to the treatment or the drug or if the nucleic acid sample lacks said biallelic marker associated with a negative response to the treatment or the drug. In addition, the methods of the present invention for administering a drug or a treatment encompass methods with any further limitation described in this disclosure, or those following, specified alone or in any combination: optionally, said DME-related biallelic marker may be in a sequence selected individually or in any combination from the group consisting of SEQ ID Nos. 1-38, 40-54, 56-463, 465-487, 490-493; the complements thereof; or preferably SEQ ID Nos. 3, 5, 9, 13-15, 25, 31, 33, 37, 38, 41, 323, 345, 351-353, 357, 377, 380; and the complements thereof or optionally, the administering step comprises administering the drug or the treatment to the individual if the nucleic acid sample contains said biallelic marker associated with a positive response to the treatment or the drug and the nucleic acid sample lacks said biallelic marker associated with a negative response to the treatment or the drug.

An eleventh embodiment of the present invention is a method of selecting an individual for inclusion in a clinical trial of a treatment or drug comprising the steps of: a) obtaining a nucleic acid sample from an individual; b) determining the identity of the polymorphic base of at least one DME-related biallelic marker which is associated with a positive response to the treatment or the drug, or at least one DME-related biallelic marker which is associated with a negative response to the treatment or the drug in the nucleic acid sample, and c) including the individual in the clinical trial if the nucleic acid sample contains said DME-related biallelic marker associated with a positive response to the treatment or the drug or if the nucleic acid sample lacks said biallelic marker associated with a negative response to the treatment or the drug. In addition, the methods of the present invention for selecting an individual for inclusion in a clinical trial of a treatment or drug encompass methods with any further limitation described in this disclosure, or those

following, specified alone or in any combination: Optionally, said DME-related biallelic marker may be in a sequence selected individually or in any combination from the group consisting of SEQ ID Nos. 1-38, 40-54, 56-463, 465-487, 490-493; the complements thereof; or preferably SEQ ID Nos. 3, 5, 9, 13-15, 25, 31, 33, 37, 38, 41, 323, 345, 351-353, 357, 377, 380; and the complements thereof, optionally, the including step comprises administering the drug or the treatment to the individual if the nucleic acid sample contains said biallelic marker associated with a positive response to the treatment or the drug and the nucleic acid sample lacks said biallelic marker associated with a negative response to the treatment or the drug.

Additional embodiments are set forth in the Detailed Description of the Invention and in the Examples.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is a chart containing a list of all of the DME-related biallelic markers for each gene with an indication of the gene for which the marker is in closest physical proximity, an indication of whether the markers have been validated by microsequencing (with a Y indicating that the markers have been validated by microsequencing and an N indicating that it has not), and an indication of the identity and frequency of the least common allele determined by genotyping (with a blank left to indicate that the frequency has not yet been reported for some markers).

Figure 2, 3, and 4 are charts containing lists of the DME-related biallelic markers. Each marker is described by indicating its SEQ ID, the biallelic marker ID, and the two most common alleles. Figure 2 is a chart containing a list of biallelic markers surrounded by preferred sequences. In the column labeled, "POSITION RANGE OF PREFERRED SEQUENCE" of Figure 2, regions of particularly preferred sequences are listed for each SEQ ID, which contain a DME-related biallelic marker, as well as particularly preferred regions of sequences that may not contain a DME-related biallelic marker but, which are in sufficiently close proximity to a DME-related biallelic marker to be useful as amplification or sequencing primers.

Figure 5 is a chart listing particular preferred sequences that are useful for designing some of the primers and probes of the invention. Each sequence is described by indicating its Sequence ID and the positions of the first and last nucleotides (position range) of the particular sequence in the Sequence ID.

Figure 6 is a chart listing microsequencing primers which have been used to genotype DME-related biallelic markers (indicated by an *) and other preferred

microsequencing primers for use in genotyping DME-related biallelic markers. Each of the primers which falls within the strand of nucleotides included in the Sequence Listing are described by indicating their Sequence ID number and the positions of the first and last nucleotides (position range) of the primers in the Sequence ID. Since the sequences in the Sequence Listing are single stranded and half the possible microsequencing primers are composed of nucleotide sequences from the complementary strand, the primers that are composed of nucleotides in the complementary strand are described by indicating their SEQ ID numbers and the positions of the first and last nucleotides to which they are complementary (complementary position range) in the Sequence ID.

Figure 7 is a chart listing amplification primers which have been used to amplify polynucleotides containing one or more DME-related biallelic markers. Each of the primers which falls within the strand of nucleotides included in the Sequence Listing are described by indicating their Sequence ID number and the positions of the first and last nucleotides (position range) of the primers in the Sequence ID. Since the sequences in the Sequence Listing are single stranded and half the possible amplification primers are composed of nucleotide sequences from the complementary strand, the primers that are composed of nucleotides in the complementary strand are defined by the SEQ ID numbers and the positions of the first and last nucleotides to which they are complementary (complementary position range) in the Sequence ID.

Figure 8 is a chart listing preferred probes useful in genotyping DME-related biallelic markers by hybridization assays. The probes are generally 25-mers with a DME-related biallelic marker in the center position, and described by indicating their Sequence ID number and the positions of the first and last nucleotides (position range) of the probes in the Sequence ID. The probes complementary to the sequences in each position range in each Sequence ID are also understood to be a part of this preferred list even though they are not specified separately.

Figure 9 is a chart containing a list of preferred MGST-II-related biallelic markers with an indication of the frequency of both alleles determined by genotyping. Frequencies were determined in a random US Caucasian population.

Figure 10 is a chart containing a list of preferred ME1-related biallelic markers with an indication of the frequency of both alleles determined by genotyping. Frequencies were determined in a random US Caucasian population.

Figure 11 is a chart containing a list of preferred UGT1A7-related biallelic markers with an indication of the frequency of both alleles determined by genotyping. Frequencies

were determined in a random US Caucasian population and a random French Caucasian population.

Figure 12 is a chart containing a list of preferred UGT2B4-related biallelic markers with an indication of the frequency of both alleles determined by genotyping. Frequencies were determined in a random US Caucasian population and a random French Caucasian population..

Figure 13 is a chart showing the results of a haplotype analysis study demonstrating an association between asthma and MGST-II-related biallelic marker haplotypes.

Figure 14 is a chart showing the results of a permutation test which evaluates the statistical significance of the results obtained for the haplotype analysis.

Figure 15 is a chart showing the results of a haplotype analysis study demonstrating an association between side effects upon treatment with the anti-asthmatic drug Zyflo™ (zileuton) and MGST-II related biallelic marker haplotypes.

Figure 16 is a table showing the results of a phenotypic permutation test which evaluates the statistical significance of the results obtained for the haplotype analysis in Figure 15.

Figure 17 is a block diagram of an exemplary computer system.

Figure 18 is a flow diagram illustrating one embodiment of a process 200 for comparing a new nucleotide or protein sequence with a database of sequences in order to determine the homology levels between the new sequence and the sequences in the database.

Figure 19 is a flow diagram illustrating one embodiment of a process 250 in a computer for determining whether two sequences are homologous.

Figure 20 is a flow diagram illustrating one embodiment of an identifier process 300 for detecting the presence of a feature in a sequence.

BRIEF DESCRIPTION OF THE SEQUENCES PROVIDED IN THE SEQUENCE LISTING

SEQ ID Nos. 1-484 contain the nucleotide sequence of genomic DNA fragments located in the vicinity of the candidate genes.

SEQ ID No. 485 contains the genomic sequence of the MGST-II gene comprising the 5' regulatory region (upstream untranscribed region), the exons and introns, and the 3' regulatory region (downstream untranscribed region).

SEQ ID No. 486 contains a cDNA sequence of MGST-II.

SEQ ID No. 487 contains a cDNA sequence of MGST-II corresponding to an alternative messenger RNA which is due to alternative splicing joining exon 1 to exon 3 and resulting in the absence of exon 2.

SEQ ID No. 488 contains the amino acid sequence encoded by the cDNA of SEQ ID No. 486.

SEQ ID No. 489 contains the amino acid sequence encoded by the cDNA of SEQ ID No. 487.

SEQ ID No. 490 contains a partial cDNA sequence of MGST-II sequence corresponding to a cloned partial messenger RNA.

SEQ ID No. 491 contains a partial cDNA sequence of MGST-II sequence corresponding to a cloned partial messenger RNA.

SEQ ID No. 492 contains a primer containing the additional PU 5' sequence described further in Example 1.

SEQ ID No. 493 contains a primer containing the additional RP 5' sequence described further in Example 1.

DETAILED DESCRIPTION OF THE INVENTION

Advantages of the biallelic markers of the present invention

The DME-related biallelic markers of the present invention offer a number of important advantages over other genetic markers such as RFLP (Restriction fragment length polymorphism) and VNTR (Variable Number of Tandem Repeats) markers.

The first generation of markers, were RFLPs, which are variations that modify the length of a restriction fragment. But methods used to identify and to type RFLPs are relatively wasteful of materials, effort, and time. The second generation of genetic markers were VNTRs, which can be categorized as either minisatellites or microsatellites. Minisatellites are tandemly repeated DNA sequences present in units of 5-50 repeats which are distributed along regions of the human chromosomes ranging from 0.1 to 20 kilobases in length. Since they present many possible alleles, their informative content is very high. Minisatellites are scored by performing Southern blots to identify the number of tandem repeats present in a nucleic acid sample from the individual being tested. However, there are only 10^4 potential VNTRs that can be typed by Southern blotting. Moreover, both RFLP and VNTR markers are costly and time-consuming to develop and assay in large numbers.

Single nucleotide polymorphism or biallelic markers can be used in the same manner as RFLPs and VNTRs but offer several advantages. Single nucleotide polymorphisms are densely spaced in the human genome and represent the most frequent type of variation. An

estimated number of more than 10^7 sites are scattered along the $3x10^9$ base pairs of the human genome. Therefore, single nucleotide polymorphism occur at a greater frequency and with greater uniformity than RFLP or VNTR markers which means that there is a greater probability that such a marker will be found in close proximity to a genetic locus of interest. Single nucleotide polymorphisms are less variable than VNTR markers but are mutationally more stable.

Also, the different forms of a characterized single nucleotide polymorphism, such as the biallelic markers of the present invention, are often easier to distinguish and can therefore be typed easily on a routine basis. Biallelic markers have single nucleotide based alleles and they have only two common alleles, which allows highly parallel detection and automated scoring. The biallelic markers of the present invention offer the possibility of rapid, high-throughput genotyping of a large number of individuals.

Biallelic markers are densely spaced in the genome, sufficiently informative and can be assayed in large numbers. The combined effects of these advantages make biallelic markers extremely valuable in genetic studies. Biallelic markers can be used in linkage studies in families, in allele sharing methods, in linkage disequilibrium studies in populations, in association studies of case-control populations. An important aspect of the present invention is that biallelic markers allow association studies to be performed to identify genes involved in complex traits. Association studies examine the frequency of marker alleles in unrelated case- and control-populations and are generally employed in the detection of polygenic or sporadic traits. Association studies may be conducted within the general population and are not limited to studies performed on related individuals in affected families (linkage studies). Biallelic markers in different genes can be screened in parallel for direct association with disease or response to a treatment. This multiple gene approach is a powerful tool for a variety of human genetic studies as it provides the necessary statistical power to examine the synergistic effect of multiple genetic factors on a particular phenotype, drug response, sporadic trait, or disease state with a complex genetic etiology.

Candidate genes of the present invention

Different approaches can be employed to perform association studies: genome-wide association studies, candidate region association studies and candidate gene association studies. Genome-wide association studies rely on the screening of genetic markers evenly spaced and covering the entire genome. Candidate region association studies rely on the screening of genetic markers evenly spaced covering a region identified as linked to the trait

of interest. The candidate gene approach is based on the study of genetic markers specifically derived from genes potentially involved in a biological pathway related to the trait of interest. In the present invention, genes involved in drug metabolism have been chosen as candidate genes. As mentioned above, these genes are highly relevant to pharmacogenetics because they are at the core of drug response, drug efficacy and toxicity, moreover, drug-metabolizing enzymes also determine an individuals susceptibility to exogenous chemicals and to a number of diseases associated with exposure to toxic or carcinogenic chemicals. The candidate gene analysis clearly provides a short-cut approach to the identification of genes and gene polymorphisms related to a particular trait when some information concerning the biology of the trait is available. However, it should be noted that all of the biallelic markers disclosed in the instant application can be employed as part of genome-wide association studies or as part of candidate region association studies and such uses are specifically contemplated in the present invention and claims. All of the markers are known to be in close proximity to the genes with which they are listed in Figure 1. For a portion of the markers, the precise position of the marker with respect to the various coding and non-coding elements of the genes has also been determined.

The following is a table of abbreviations for the candidate genes as they appear throughout the specification and figures:

Table 1

Candidate Gene	Abbreviation
Microsomal glutathione S-transferase II	MGST2 or MGST II
Malate decarboxylase enzyme	DME or ME1
Cytochrome P450 1A2	CYP1A2
Cytochrome P450 2C8	CYP2C8
Cytochrome P450 2C9	CYP2C9
Cytochrome P450 2C18	CYP2C18
Cytochrome P450 3A4-3A7	CYP3A4-CYP3A7
Cytochrome P450 3A7	CYP3A7
Flavin-containing monooxygenases	FMO
Glutathione reductase	GSHR
Glutathione synthase	GSHS
γ-glutamylcysteine synthetase	GLCL

γ-glutamyltransferase 5	GGT5
Dipeptidase	DP
Glucose 6-phosphate dehydrogenase	G6PDH
Phosphogluconate dehydrogenase	PGDH
Uridine diphosphate glucoronosyl transferase 1A7	UGT1A7
Uridine diphosphate glucoronosyl transferase B4	UGT2B4
Uridine diphosphate glucoronosyl transferase B7	UGT2B7
Uridine diphosphate glucoronosyl transferase B10	UGT2B10
Uridine diphosphate glucoronosyl transferase B15	UGT2B15

Definitions

As used interchangeably herein, the terms "nucleic acids," "oligonucleotides" and "polynucleotides" include RNA, DNA, or RNA/DNA hybrid sequences of more than one nucleotide in either single chain or duplex form. The term "nucleotide" as used herein as an adjective to describe molecules comprising RNA, DNA, or RNA/DNA hybrid sequences of any length in single-stranded or duplex form. The term "nucleotide" is also used herein as a noun to refer to individual nucleotides or varieties of nucleotides, meaning a molecule, or individual unit in a larger nucleic acid molecule, comprising a purine or pyrimidine, a ribose or deoxyribose sugar moiety, and a phosphate group, or phosphodiester linkage in the case of nucleotides within an oligonucleotide or polynucleotide. Although the term "nucleotide" is also used herein to encompass "modified nucleotides" which comprise at least one modifications (a) an alternative linking group, (b) an analogous form of purine, (c) an analogous form of pyrimidine, or (d) an analogous sugar, for examples of analogous linking groups, purine, pyrimidines, and sugars see for example PCT publication No. WO 95/04064. However, the polynucleotides of the invention are preferably comprised of greater than 50% conventional deoxyribose nucleotides, and most preferably greater than 90% conventional deoxyribose nucleotides. The polynucleotide sequences of the invention may be prepared by any known method, including synthetic, recombinant, *ex vivo* generation, or a combination thereof, as well as utilizing any purification methods known in the art.

Throughout the present specification, the expression "nucleotide sequence" may be employed to designate indifferently a polynucleotide or a nucleic acid. More precisely, the expression "nucleotide sequence" encompasses the nucleic material itself and is thus not

restricted to the sequence information (i.e. the succession of letters chosen among the four base letters) that biochemically characterizes a specific DNA or RNA molecule.

The term "polypeptide" refers to a polymer of amino without regard to the length of the polymer; thus, peptides, oligopeptides, and proteins are included within the definition of polypeptide. This term also does not specify or exclude prost-expression modifications of polypeptides, for example, polypeptides which include the covalent attachment of glycosyl groups, acetyl groups, phosphate groups, lipid groups and the like are expressly encompassed by the term polypeptide. Also included within the definition are polypeptides which contain one or more analogs of an amino acid (including, for example, non-naturally occurring amino acids, amino acids which only occur naturally in an unrelated biological system, modified amino acids from mammalian systems etc.), polypeptides with substituted linkages, as well as other modifications known in the art, both naturally occurring and non-naturally occurring.

The term "recombinant polypeptide" is used herein to refer to polypeptides that have been artificially designed and which comprise at least two polypeptide sequences that are not found as contiguous polypeptide sequences in their initial natural environment, or to refer to polypeptides which have been expressed from a recombinant polynucleotide.

The term "isolated" requires that the material be removed from its original environment (e. g., the natural environment if it is naturally occurring). For example, a naturally-occurring polynucleotide or polypeptide present in a living animal is not isolated, but the same polynucleotide or DNA or polypeptide, separated from some or all of the coexisting materials in the natural system, is isolated. Such polynucleotide could be part of a vector and/or such polynucleotide or polypeptide could be part of a composition, and still be isolated in that the vector or composition is not part of its natural environment.

The term "purified" is used herein to describe a polynucleotide or polynucleotide vector of the invention which has been separated from other compounds including, but not limited to other nucleic acids, carbohydrates, lipids and proteins (such as the enzymes used in the synthesis of the polynucleotide), or the separation of covalently closed polynucleotides from linear polynucleotides. A polynucleotide is substantially pure when at least about 50 %, preferably 60 to 75% of a sample exhibits a single polynucleotide sequence and conformation (linear versus covalently close). A substantially pure polynucleotide typically comprises about 50 %, preferably 60 to 90% weight/weight of a nucleic acid sample, more usually about 95%, and preferably is over about 99% pure. Polynucleotide purity or homogeneity may be indicated by a number of means well known

in the art, such as agarose or polyacrylamide gel electrophoresis of a sample, followed by visualizing a single polynucleotide band upon staining the gel. For certain purposes higher resolution can be provided by using HPLC or other means well known in the art.

The term "purified" is further used herein to describe a polypeptide of the invention which, has been separated from other compounds including, but not limited to nucleic acids, lipids, carbohydrates and other proteins. A polypeptide is substantially pure when at least about 50%, preferably 60 to 75% of a sample exhibits a single polypeptide sequence. A substantially pure polypeptide typically comprises about 50%, preferably 60 to 90% weight/weight of a protein sample, more usually about 95%, and preferably is over about 99% pure. Polypeptide purity or homogeneity is indicated by a number of means well known in the art, such as agarose or polyacrylamide gel electrophoresis of a sample, followed by visualizing a single polypeptide band upon staining the gel. For certain purposes higher resolution can be provided by using HPLC or other means well known in the art.

As used herein, the term "non-human animal" refers to any non-human vertebrate, birds and more usually mammals, preferably primates, farm animals such as swine, goats, sheep, donkeys, and horses, rabbits or rodents, more preferably rats or mice. As used herein, the term "animal" is used to refer to any vertebrate, preferable a mammal. Both the terms "animal" and "mammal" expressly embrace human subjects unless preceded with the term "non-human".

As used herein, the term "antibody" refers to a polypeptide or group of polypeptides which are comprised of at least one binding domain, where an antibody binding domain is formed from the folding of variable domains of an antibody molecule to form three-dimensional binding spaces with an internal surface shape and charge distribution complementary to the features of an antigenic determinant of an antigen., which allows an immunological reaction with the antigen. Antibodies include recombinant proteins comprising the binding domains, as wells as fragments, including Fab, Fab', $F(ab)_2$, and $F(ab')_2$ fragments.

As used herein, an "antigenic determinant" is the portion of an antigen molecule, in this case a MGST-II polypeptide, that determines the specificity of the antigen-antibody reaction. An "epitope" refers to an antigenic determinant of a polypeptide. An epitope can comprise as few as 3 amino acids in a spatial conformation which, is unique to the epitope. Generally an epitope consists of at least 6 such amino acids, and more usually at least 8-10 such amino acids. Methods for determining the amino acids which make up an epitope

include x-ray crystallography, 2-dimensional nuclear magnetic resonance, and epitope mapping e.g. the Pepscan method described by H. Mario Geysen et al. 1984. *Proc. Natl. Acad. Sci.* U.S.A. 81:3998-4002; PCT Publication No. WO 84/03564; and PCT Publication No. WO 84/03506.

The term “primer” denotes a specific oligonucleotide sequence which is complementary to a target nucleotide sequence and used to hybridize to the target nucleotide sequence. A primer serves as an initiation point for nucleotide polymerization catalyzed by either DNA polymerase, RNA polymerase or reverse transcriptase.

The term “probe” denotes a defined nucleic acid segment (or nucleotide analog segment, e.g., polynucleotide as defined herein) which can be used to identify a specific polynucleotide sequence present in samples, said nucleic acid segment comprising a nucleotide sequence complementary of the specific polynucleotide sequence to be identified.

The terms “trait” and “phenotype” are used interchangeably herein and refer to any visible, detectable or otherwise measurable property of an organism such as symptoms of, or susceptibility to a disease for example. Typically the terms “trait” or “phenotype” are used herein to refer to symptoms of, or susceptibility to a disease; or to refer to an individual’s response to a drug; or to refer to symptoms of, or susceptibility to side effects to a drug. In addition, the terms “trait” or “phenotype” may be used herein to refer to symptoms of, or susceptibility to a disease involving arachidonic acid metabolism; or to refer to an individual’s response to an agent acting on arachidonic acid metabolism; or to refer to symptoms of, or susceptibility to side effects to an agent acting on arachidonic acid metabolism.

The term “allele” is used herein to refer to variants of a nucleotide sequence. A biallelic polymorphism has two forms. Typically the first identified allele is designated as the original allele whereas other alleles are designated as alternative alleles. Diploid organisms may be homozygous or heterozygous for an allelic form.

The term "heterozygosity rate" is used herein to refer to the incidence of individuals in a population, which are heterozygous at a particular allele. In a biallelic system the heterozygosity rate is on average equal to $2P_a(1-P_a)$, where P_a is the frequency of the least common allele. In order to be useful in genetic studies a genetic marker should have an adequate level of heterozygosity to allow a reasonable probability that a randomly selected person will be heterozygous.

The term "genotype" as used herein refers the identity of the alleles present in an individual or a sample. In the context of the present invention a genotype preferably refers to the description of the biallelic marker alleles present in an individual or a sample. The term "genotyping" a sample or an individual for a biallelic marker consists of determining the specific allele or the specific nucleotide carried by an individual at a biallelic marker.

The term "mutation" as used herein refers to a difference in DNA sequence between or among different genomes or individuals which has a frequency below 1%.

The term "haplotype" refers to a combination of alleles present in an individual or a sample. In the context of the present invention a haplotype preferably refers to a combination of biallelic marker alleles found in a given individual and which may be associated with a phenotype.

The term "polymorphism" as used herein refers to the occurrence of two or more alternative genomic sequences or alleles between or among different genomes or individuals. "Polymorphic" refers to the condition in which two or more variants of a specific genomic sequence can be found in a population. A "polymorphic site" is the locus at which the variation occurs. A single nucleotide polymorphism is a single base pair change. Typically a single nucleotide polymorphism is the replacement of one nucleotide by another nucleotide at the polymorphic site. Deletion of a single nucleotide or insertion of a single nucleotide, also give rise to single nucleotide polymorphisms. In the context of the present invention "single nucleotide polymorphism" preferably refers to a single nucleotide substitution. Typically, between different genomes or between different individuals, the polymorphic site may be occupied by two different nucleotides.

The terms "biallelic polymorphism" and "biallelic marker" are used interchangeably herein to refer to a polymorphism having two alleles at a fairly high frequency in the population, preferably a single nucleotide polymorphism. A "biallelic marker allele" refers to the nucleotide variants present at a biallelic marker site. Typically the frequency of the less common allele of the biallelic markers of the present invention has been validated to be greater than 1%, preferably the frequency is greater than 10%, more preferably the frequency is at least 20% (i.e. heterozygosity rate of at least 0.32), even more preferably the frequency is at least 30% (i.e. heterozygosity rate of at least 0.42). A biallelic marker wherein the frequency of the less common allele is 30% or more is termed a "high quality biallelic marker."

The location of nucleotides in a polynucleotide with respect to the center of the polynucleotide are described herein in the following manner. When a polynucleotide has an

odd number of nucleotides, the nucleotide at an equal distance from the 3' and 5' ends of the polynucleotide is considered to be "at the center" of the polynucleotide, and any nucleotide immediately adjacent to the nucleotide at the center, or the nucleotide at the center itself is considered to be "within 1 nucleotide of the center." With an odd number of nucleotides in a polynucleotide any of the five nucleotides positions in the middle of the polynucleotide would be considered to be within 2 nucleotides of the center, and so on. When a polynucleotide has an even number of nucleotides, there would be a bond and not a nucleotide at the center of the polynucleotide. Thus, either of the two central nucleotides would be considered to be "within 1 nucleotide of the center" and any of the four nucleotides in the middle of the polynucleotide would be considered to be "within 2 nucleotides of the center", and so on. For polymorphisms which involve the substitution, insertion or deletion of 1 or more nucleotides, the polymorphism, allele or biallelic marker is "at the center" of a polynucleotide if the difference between the distance from the substituted, inserted, or deleted polynucleotides of the polymorphism and the 3' end of the polynucleotide, and the distance from the substituted, inserted, or deleted polynucleotides of the polymorphism and the 5' end of the polynucleotide is zero or one nucleotide. If this difference is 0 to 3, then the polymorphism is considered to be "within 1 nucleotide of the center." If the difference is 0 to 5, the polymorphism is considered to be "within 2 nucleotides of the center." If the difference is 0 to 7, the polymorphism is considered to be "within 3 nucleotides of the center," and so on. For polymorphisms which involve the substitution, insertion or deletion of 1 or more nucleotides, the polymorphism, allele or biallelic marker is "at the center" of a polynucleotide if the difference between the distance from the substituted, inserted, or deleted polynucleotides of the polymorphism and the 3' end of the polynucleotide, and the distance from the substituted, inserted, or deleted polynucleotides of the polymorphism and the 5' end of the polynucleotide is zero or one nucleotide. If this difference is 0 to 3, then the polymorphism is considered to be "within 1 nucleotide of the center." If the difference is 0 to 5, the polymorphism is considered to be "within 2 nucleotides of the center." If the difference is 0 to 7, the polymorphism is considered to be "within 3 nucleotides of the center," and so on.

The term "upstream" is used herein to refer to a location which, is toward the 5' end of the polynucleotide from a specific reference point.

The terms "base paired" and "Watson & Crick base paired" are used interchangeably herein to refer to nucleotides which can be hydrogen bonded to one another be virtue of their sequence identities in a manner like that found in double-helical DNA with thymine or

uracil residues linked to adenine residues by two hydrogen bonds and cytosine and guanine residues linked by three hydrogen bonds (See Stryer, L.. *Biochemistry,* 4th edition, 1995).

The terms "complementary" or "complement thereof" are used herein to refer to the sequences of polynucleotides which is capable of forming Watson & Crick base pairing with another specified polynucleotide throughout the entirety of the complementary region. This term is applied to pairs of polynucleotides based solely upon their sequences and not any particular set of conditions under which the two polynucleotides would actually bind.

A "promoter" refers to a DNA sequence recognized by the synthetic machinery of the cell required to initiate the specific transcription of a gene.

A sequence which is "operably linked" to a regulatory sequence such as a promoter means that said regulatory element is in the correct location and orientation in relation to the nucleic acid to control RNA polymerase initiation and expression of the nucleic acid of interest.

As used herein, the term "operably linked" refers to a linkage of polynucleotide elements in a functional relationship. For instance, a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the coding sequence. More precisely, two DNA molecules (such as a polynucleotide containing a promoter region and a polynucleotide encoding a desired polypeptide or polynucleotide) are said to be "operably linked" if the nature of the linkage between the two polynucleotides does not (1) result in the introduction of a frame-shift mutation or (2) interfere with the ability of the polynucleotide containing the promoter to direct the transcription of the coding polynucleotide.

The terms "disease involving the metabolic conversion of xenobiotics" refers to susceptibility to a condition or to a condition linked to any of the genes listed in Figure 1. "Disease involving the metabolic conversion of xenobiotics" further refers to a condition involving the biotransformation of drugs and other xenobiotics such as environmental chemicals, food toxins, plant metabolites, carcinogens and industrial chemicals. Such conditions include susceptibility to the toxic or carcinogenic effect of exogenous compounds. "Disease involving the metabolic conversion of xenobiotics" also refers to disorders in the metabolism of some endogenous compounds such as the metabolism of steroids, vitamins, fatty acids and eicosanoids such as leukotrienes involving any of the drug-metabolizing enzymes shown in Figure 1. "Disease involving the metabolic conversion of xenobiotics" includes. but is not limited to, disorders involving the

cytochrome P450 enzyme family, the flavin containing monooxygenases, glucoronidation, the metabolism of glutathione, the pentose pathway and the generation of NADPH.

The term "disease involving arachidonic acid metabolism" refers to a condition linked to disturbances in expression, production or cellular response to eicosanoids such as prostaglandins, thromboxanes, prostacyclins, leukotrienes or hydroperoxyeicosaetrenoic acids. A disease involving arachidonic acid metabolism further refers to a condition involving one or several enzymes of the distinct enzyme systems contributing to arachidonate metabolism including particularly the 5-lipoxygenase pathway. "Diseases involving arachidonic acid metabolism" also include chronic inflammatory diseases, acute allergic inflammation and inflammatory conditions such as pain, fever, hypersensitivity, asthma, psoriasis and arthritis. "Diseases involving arachidonic acid metabolism" also include disorders in platelet function, blood pressure, thrombosis, renal function, host defense mechanism, hemostasis, smooth muscle tone, male infertility, primary dysmenorrhea, disorders in parturition, and disorders in tissue injury repair, as well as disorders in cellular function and development. "Diseases involving arachidonic acid metabolism" also include diseases such as gastrointestinal ulceration, coronary and cerebrovascular syndromes, glomerular immune injury and cancer. Preferably the terms "disease involving arachidonic acid metabolism" refer to a disease including diseases such as cancer, prostate cancer, breast cancer, psoriasis and inflammatory diseases. Preferably the terms "disease involving arachidonic acid metabolism" refer to a disease involving the 5-lipoxygenase pathway and the biosynthesis of the leukotrienes. More preferably the terms "disease involving arachidonic acid metabolism" refer to a disease involving the synthesis of leukotriene C4 (LTC4) and refers to disturbances in expression, activity or function of the human MGST-II enzyme.

As used herein the term "DME-related biallelic marker" relates to a set of biallelic markers located in or in the vicinity of the genes disclosed in Figure 1 and further relates to biallelic markers in linkage disequilibrium with the biallelic markers disclosed in Figure 1. The term DME-related biallelic marker encompasses all of the biallelic markers disclosed in Figure 1.

The invention also concerns MGST-II-related biallelic markers. The term "MGST-II-related biallelic marker" is used interchangeably herein to relate to all biallelic markers in linkage disequilibrium with the biallelic markers of the MGST-II gene. The term MGST-II-related biallelic marker includes both the genic and non-genic biallelic markers described in Table 2.

The term "non-genic" is used herein to describe MGST-II-related biallelic markers, as well as polynucleotides and primers which occur outside the nucleotide positions shown in the human MGST-II genomic sequence of SEQ ID No. 485. The term "genic" is used herein to describe MGST-II-related biallelic markers as well as polynucleotides and primers which do occur in the nucleotide positions shown in the human MGST-II genomic sequence of SEQ ID No. 485.

The terms "agent acting on arachidonic acid metabolism" refers to a drug or a compound modulating the activity or concentration of one or several enzymes of the distinct enzyme systems contributing to arachidonate metabolism including particularly the 5-lipoxygenase pathway. "Agent acting on arachidonic acid metabolism" also refers to compounds modulating the formation and action of the eicosanoids including particularly the leukotrienes.

The terms "response to a drug " refer to drug efficacy, including but not limited to ability to metabolize a therapeutic compound, to the ability to convert a pro-drug to an active drug, and to the pharmacokinetics (absorption, distribution, elimination) and the pharmacodynamics (receptor-related) of a drug in an individual.

The terms "response to an agent acting on arachidonic acid metabolism" refer to drug efficacy, including but not limited to ability to metabolize a compound, to the ability to convert a pro-drug to an active drug, and to the pharmacokinetics (absorption, distribution, elimination) and the pharmacodynamics (receptor-related) of a drug in an individual.

The terms "side effects to a drug" refer to adverse effects of therapy resulting from extensions of the principal pharmacological action of the drug or to idiosyncratic adverse reactions resulting from an interaction of the drug with unique host factors. "Side effects to a drug" include, but are not limited to, adverse reactions such as dermatologic, hematologic or hepatologic toxicities and further includes gastric and intestinal ulceration, disturbance in platelet function, renal injury, generalized urticaria, bronchoconstriction, hypotension, and shock.

The terms "side effects to an agent acting on arachidonic acid metabolism" refer to adverse effects of therapy resulting from extensions of the principal pharmacological action of the drug or to idiosyncratic adverse reactions resulting from an interaction of the drug with unique host factors. The terms "side effects to an agent acting on arachidonic acid metabolism" include, but are not limited to, adverse reactions such as dermatologic, hematologic or hepatologic toxicities.

The term "sequence described in Figure 2" is used herein to refer to the entire collection of nucleotide sequences or any individual sequence defined in Figure 2. The SEQ ID that contains each "sequence described in Figure 2" is provided in the column labeled, "SEQ ID NO." The range of nucleotide positions within the Sequence ID of which each sequence consists is provided in the same row as the Sequence ID in a column labeled, "POSITION RANGE OF PREFERRED SEQUENCE". It should be noted that some of the Sequence ID numbers have multiple sequence ranges listed, because they contain multiple "sequences described in Figure 2." Unless otherwise noted the term "sequence described in Figure 2" is to be construed as encompassing sequences that contain either of the two alleles listed in the columns labeled, "1ST ALLELE" and "2ND ALLELE" at the position identified in field <222> of the allele feature in the appended Sequence Listing for each Sequence ID number referenced in Figure 2.

The term "sequence described in Figure 3" is used herein to refer to the entire collection of nucleotide sequences or any individual sequence defined in Figure 3. Unless otherwise noted, the "sequences described in Figure 3" consist of the entire sequence of each Sequence ID provided in the column labeled, "SEQ ID NO." Also unless otherwise noted the term "sequence described in Figure 3" is to be construed as encompassing sequences that contain either of the two alleles listed in the columns labeled, "ORIGINAL ALLELE" and "ALTERNATIVE ALLELE" at the position identified in field <222> of the allele feature in the appended Sequence Listing for each Sequence ID number referenced in Figure 3.

The term "sequence described in Figure 4" is used herein to refer to the entire collection of nucleotide sequences or any individual sequence defined in Figure 4. Unless otherwise noted, the "sequences described in Figure 4" consist of the entire sequence of each Sequence ID provided in the column labeled, "SEQ ID NO." Also unless otherwise noted the term "sequence described in Figure 4" is to be construed as encompassing sequences that contain either of the two alleles listed in the columns labeled, "1ST ALLELE" and "2ND ALLELE" at the position identified in field <222> of the allele feature in the appended Sequence Listing for each Sequence ID number referenced in Figure 4.

The term "sequence described in Figure 5" is used herein to refer to the entire collection of nucleotide sequences or any individual sequence defined in Figure 5. The SEQ ID that contains each "sequence described in Figure 5 " is provided in the column labeled, "SEQ ID NO." The range of nucleotide positions within the Sequence ID of which each sequence consists is provided in the same row as the Sequence ID in a column labeled,

"POSITION RANGE OF PREFERRED SEQUENCE". It should be noted that some of the Sequence ID numbers have multiple sequence ranges listed, because they contain multiple "sequences described in Figure 5."

The term "sequence described in Figure 6" is used herein to refer to the entire collection of nucleotide sequences or any individual sequence defined in Figure 6. The SEQ ID that contains each "sequence described in Figure 6 " is provided in the column labeled, "SEQ ID" The range of nucleotide positions within the Sequence ID of which half of the sequences consists is provided in the same row as the Sequence ID in a column labeled, "POSITION RANGE OF MICROSEQUENCING PRIMERS". The remaining half of the sequences described in Figure 6 are complementary to the range of nucleotide positions within the Sequence ID provided in the same row as the Sequence ID in a column labeled, "COMPLEMENTARY POSITION RANGE OF MICROSEQUENCING PRIMERS".

The term "sequence described in Figure 7" is used herein to refer to the entire collection of nucleotide sequences or any individual sequence defined in Figure 7. The SEQ ID that contains each "sequence described in Figure 7 " is provided in the column labeled, "SEQ ID" The range of nucleotide positions within the Sequence ID of which half of the sequences consists is provided in the same row as the Sequence ID in a column labeled, "POSITION RANGE OF AMPLIFICATION PRIMERS". The remaining half of the sequences described in Figure 7 are complementary to the range of nucleotide positions within the Sequence ID provided in the same row as the Sequence ID in a column labeled, "COMPLEMENTARY POSITION RANGE OF AMPLIFICATION PRIMERS".

The term "sequence described in Figure 8" is used herein to refer to the entire collection of nucleotide sequences or any individual sequence defined in Figure 8. The SEQ ID that contains each "sequence described in Figure 8 " is provided in the column labeled, "SEQ ID". The range of nucleotide positions within the Sequence ID of which each sequence consists is provided in the same row as the Sequence ID in a column labeled, "POSITION RANGE OF PROBES". The sequences which are complementary to the ranges listed in the column labeled, "POSITION RANGE OF PROBES" are also encompassed by the term, "sequence described in Figure 8." Unless otherwise noted the term "sequence described in Figure 8 " is to be construed as encompassing sequences that contain either of the two alleles listed in the allele feature in the sequence listing.

The terms "biallelic marker described in Figure" and "allele described in Figure" are used herein to refer to any or all alleles which are listed in the allele feature in the appended

Sequence Listing for each Sequence ID number referenced in the particular Figure being mentioned.

Variants and Fragments

The invention also relates to variants and fragments of the polynucleotides described herein, particularly of a MGST-II gene containing one or more biallelic markers according to the invention.

Variants of polynucleotides, as the term is used herein, are polynucleotides that differ from a reference polynucleotide. A variant of a polynucleotide may be a naturally occurring variant such as a naturally occurring allelic variant, or it may be a variant that is not known to occur naturally. Such non-naturally occurring variants of the polynucleotide may be made by mutagenesis techniques, including those applied to polynucleotides, cells or organisms. Generally, differences are limited so that the nucleotide sequences of the reference and the variant are closely similar overall and, in many regions, identical. Variants of polynucleotides according to the invention include, without being limited to, nucleotide sequences which are at least 95% identical , preferably at least 99% identical, more particularly at least 99.5% identical, and most preferably at least 99.8% identical to a polynucleotide selected from the group consisting of the polynucleotides of a sequence from any sequence in the Sequence Listing as well as sequences which are complementary thereto or to any polynucleotide fragment of at least 8 consecutive nucleotides of a sequence from any sequence in the Sequence Listing. Nucleotide changes present in a variant polynucleotide may be silent, which means that they do not alter the amino acids encoded by the polynucleotide. However, nucleotide changes may also result in amino acid substitutions, additions, deletions, fusions and truncations in the polypeptide encoded by the reference sequence. The substitutions, deletions or additions may involve one or more nucleotides. The variants may be altered in coding or non-coding regions or both. Alterations in the coding regions may produce conservative or non-conservative amino acid substitutions, deletions or additions. In the context of the present invention, particularly preferred embodiments are those in which the polynucleotides encode polypeptides which retain substantially the same biological function or activity as the mature MGST-II protein, or those in which the polynucleotides encode polypeptides which maintain or increase a particular biological activity, while reducing a second biological activity. A polynucleotide fragment is a polynucleotide having a sequence that is entirely the same as part but not all of a given nucleotide sequence, preferably the nucleotide sequence of a MGST-II gene, and variants thereof. The fragment can be a portion of an exon or of an intron of a MGST-II

gene. It can also be a portion of the regulatory regions of MGST-II, preferably of the promoter sequence of the MGST-II gene. Such fragments may be "free-standing", i.e. not part of or fused to other polynucleotides, or they may be comprised within a single larger polynucleotide of which they form a part or region. Indeed, several of these fragments may be present within a single larger polynucleotide.

Identity Between Nucleic Acids or Polypeptides

The terms "percentage of sequence identity" and "percentage homology" are used interchangeably herein to refer to comparisons among polynucleotides and polypeptides, and are determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide or polypeptide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity. Homology is evaluated using any of the variety of sequence comparison algorithms and programs known in the art. Such algorithms and programs include, but are by no means limited to, TBLASTN, BLASTP, FASTA, TFASTA, and CLUSTALW (Pearson and Lipman, *Proc. Natl. Acad. Sci.* 85(8):2444-2448, 1988; Altschul et al., *J. Mol. Biol.* 215(3):403-410,1990; Thompson et al., *Nucleic Acids Res.* 22(2):4673-4680, 1994; Higgins et al., *Methods Enzymol.* 266:383-402, 1996; Altschul et al., *Nature Genetics* 3:266-272, 1993). In a particularly preferred embodiment, protein and nucleic acid sequence homologies are evaluated using the Basic Local Alignment Search Tool ("BLAST") which is well known in the art (See, e.g., Karlin and Altschul,. *Proc. Natl. Acad. Sci. USA* 87:2267-2268, 1990; Altschul et al., *J. Mol. Biol.* 215(3):403-410, 1990; Altschul et al., *Nature Genetics* 3:266-272, 1993; Altschul et al., *Nuc. Acids Res.* 25:3389-3402, 1997). In particular, five specific BLAST programs are used to perform the following task:

(1) BLASTP and BLAST3 compare an amino acid query sequence against a protein sequence database;

(2) BLASTN compares a nucleotide query sequence against a nucleotide sequence database;

(3) BLASTX compares the six-frame conceptual translation products of a query nucleotide sequence (both strands) against a protein sequence database;

(4) TBLASTN compares a query protein sequence against a nucleotide sequence database translated in all six reading frames (both strands); and

(5) TBLASTX compares the six-frame translations of a nucleotide query sequence against the six-frame translations of a nucleotide sequence database.

The BLAST programs identify homologous sequences by identifying similar segments, which are referred to herein as "high-scoring segment pairs," between a query amino or nucleic acid sequence and a test sequence which is preferably obtained from a protein or nucleic acid sequence database. High-scoring segment pairs are preferably identified (i.e., aligned) by means of a scoring matrix, many of which are known in the art. Preferably, the scoring matrix used is the BLOSUM62 matrix (Gonnet et al., *Science* 256:1443-1445, 1992; Henikoff and Henikoff, *Proteins* 17:49-61, 1993). Less preferably, the PAM or PAM250 matrices may also be used (See, e.g., Schwartz and Dayhoff, eds., *Matrices for Detecting Distance Relationships: Atlas of Protein Sequence and Structure, Washington:National Biomedical Research Foundation*, 1978 The BLAST programs evaluate the statistical significance of all high-scoring segment pairs identified, and preferably selects those segments which satisfy a user-specified threshold of significance, such as a user-specified percent homology. Preferably, the statistical significance of a high-scoring segment pair is evaluated using the statistical significance formula of Karlin (see, e.g., Karlin and Altschul, 1990).

Stringent Hybridization Conditions

By way of example and not limitation, procedures using conditions of high stringency are as follows: Prehybridization of filters containing DNA is carried out for 8 h to overnight at 65°C in buffer composed of 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 μg/ml denatured salmon sperm DNA. Filters are hybridized for 48 h at 65°C, the preferred hybridization temperature, in prehybridization mixture containing 100 μg/ml denatured salmon sperm DNA and 5-20 X 10^6 cpm of ^{32}P-labeled probe. Alternatively, the hybridization step can be performed at 65°C in the presence of SSC buffer, 1 x SSC corresponding to 0.15M NaCl and 0.05 M Na citrate. Subsequently, filter washes can be done at 37°C for 1 h in a solution containing 2 x SSC, 0.01% PVP, 0.01% Ficoll, and 0.01% BSA, followed by a wash in 0.1 X SSC at 50°C for 45 min. Alternatively, filter washes can be performed in a solution containing 2 x SSC and 0.1% SDS, or 0.5 x SSC and 0.1% SDS, or 0.1 x SSC and 0.1% SDS at 68°C for 15

minute intervals. Following the wash steps, the hybridized probes are detectable by autoradiography. Other conditions of high stringency which may be used are well known in the art and as cited in Sambrook et al., 1989; and Ausubel et al., 1989. These hybridization conditions are suitable for a nucleic acid molecule of about 20 nucleotides in length. There is no need to say that the hybridization conditions described above are to be adapted according to the length of the desired nucleic acid, following techniques well known to the one skilled in the art. The suitable hybridization conditions may for example be adapted according to the teachings disclosed in the book of Hames and Higgins (*NucleicAcid Hybridization: A Practical Approach*, IRL Press, Oxford, 1985) or in Sambrook et al. (*Molecular Cloning: A Laboratory Manual*, 2nd edition, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, 1989).

I. Biallelic Markers and Polynucleotides Comprising Biallelic Markers

I.A. Polynucleotides of the Present Invention

The present invention encompasses polynucleotides for use as primers and probes in the methods of the invention. These polynucleotides may consist of, consist essentially of, or comprise a contiguous span of nucleotides of a sequence from any sequence in the Sequence Listing as well as sequences which are complementary thereto ("complements thereof"). The "contiguous span" may be at least 8, 10, 12, 15, 18, 20, 25, 35, 40, 50, 70, 80, 100, 250, 500 or 1000 nucleotides in length, to the extent that a contiguous span of these lengths is consistent with the lengths of the particular Sequence ID. It should be noted that the polynucleotides of the present invention are not limited to having the exact flanking sequences surrounding the polymorphic bases which, are enumerated in the Sequence Listing. Rather, it will be appreciated that the flanking sequences surrounding the biallelic markers, or any of the primers of probes of the invention which, are more distant from the markers, may be lengthened or shortened to any extent compatible with their intended use and the present invention specifically contemplates such sequences. It will be appreciated that the polynucleotides referred to in the Sequence Listing may be of any length compatible with their intended use. Also the flanking regions outside of the contiguous span need not be homologous to native flanking sequences which actually occur in human subjects. The addition of any nucleotide sequence, which is compatible with the nucleotides intended use is specifically contemplated. The contiguous span may optionally include the DME-related biallelic marker in said sequence. Biallelic markers generally consist of a polymorphism at one single base position. Each biallelic marker therefore corresponds to two forms of a polynucleotide sequence which, when compared with one another, present a nucleotide

modification at one position. Usually, the nucleotide modification involves the substitution of one nucleotide for another. Optionally either the original or the alternative allele of the biallelic markers disclosed in Figure 3, or the first or second allele disclosed in Figure 2 and 3 may be specified as being present at the DME-related biallelic marker. Optionally, the biallelic markers may be specified as 12-421-135, 12-442-133, 12-449-63, 12-454-242, 12-463-230, 12-462-199, 10-430-287, 12-718-432, 12-269-301, 2-13-398, 2-28-132, 2-39-27, 2-45-155, 2-4-391, 12-345-410, 10-358-353, 10-360-190, 10-365-374, 10-367-58, 12-468-424, 12-481-293, 12-499-86, 12-500-217, 12-511-101, 12-586-443, 12-593-287, 12-795-383, 10-494-332, 12-659-251, 12-912-419, 12-914-28, 12-624-307 which consist of more complex polymorphisms including insertions/deletions of at least one nucleotide. Optionally either the original or the alternative allele of these biallelic markers may be specified as being present at the DME-related biallelic marker. Preferred polynucleotides may consist of, consist essentially of, or comprise a contiguous span of nucleotides of a sequence from SEQ ID No. 436-468 well as sequences which are complementary thereto. The "contiguous span" may be at least 8, 10, 12, 15, 18, 20, 25, 35, 40, 50, 70, 80, 100, 250, 500 or 1000 nucleotides in length, to the extent that a contiguous span of these lengths is consistent with the lengths of the particular Sequence ID. The contiguous span may optionally comprise a biallelic marker selected from the group consisting of biallelic markers 12-421-135, 12-442-133, 12-449-63, 12-454-242, 12-463-230, 12-462-199, 10-430-287, 12-718-432, 12-269-301, 2-13-398, 2-28-132, 2-39-27, 2-45-155, 2-4-391, 12-345-410, 10-358-353, 10-360-190, 10-365-374, 10-367-58, 12-468-424, 12-481-293, 12-499-86, 12-500-217, 12-511-101, 12-586-443, 12-593-287, 12-795-383, 10-494-332, 12-659-251, 12-912-419, 12-914-28, 12-624-307.

The preferred polynucleotides of the invention include the sequence ranges included in any one the sequence ranges of Figures 2, and 5 to 8 individually or in groups consisting of all the possible combinations of the ranges of included in Figures 2, and 5 to 8. The preferred polynucleotides of the invention also include fragments of at least 8, 10, 12, 15, 18, 20, 25, 35, 40, 50, 70, 80, 100, 250, 500 or 1000 consecutive nucleotides of the sequence ranges included in any one of the sequence ranges of Figures 2, and 5 to 8 to the extent that fragments of these lengths are consistent with the lengths of the particular sequence range. The preferred polynucleotides of the invention also include fragments of at least 8, 10, 12, 15, 18, 20, 25, 35, 40, 50, 70, 80, 100, 250, 500 or 1000 consecutive nucleotides of the sequence complementary to the sequence ranges included in any one of the sequence ranges

of Figures 2, and 5 to 8 to the extent that fragments of these lengths are consistent with the lengths of the particular sequence range.

Preferred polynucleotides of the invention include isolated, purified or recombinant polynucleotides comprising a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of a sequence selected from the group consisting of the sequences of SEQ ID Nos. 2-3, 5-30, 437-441, 472, 485-487, and 490-493 and the complements thereof.

Particularly preferred polynucleotides of the invention include isolated, purified or recombinant polynucleotides comprising a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 485, wherein said contiguous span comprises at least 1, 2, 3, 4, 5 or 10 of the following nucleotide positions of SEQ ID No. 485: 1 to 7667, 7726 to 20264, 20365 to 36918, 36991 to 45180, 45263 to 45741, and 45980 to 49327, and the complements thereof. Other particularly preferred polynucleotides of the present invention include isolated, purified or recombinant polynucleotides comprising a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 486, wherein said contiguous span comprises at least 1, 2, 3, 4, 5 or 10 of nucleotide positions 1 to 198 of SEQ ID No. 486 and the complements thereof. Other particularly preferred polynucleotides of the present invention include isolated, purified or recombinant polynucleotides comprising a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 487, wherein said contiguous span comprises at least 1, 2, 3, 4, 5 or 10 of nucleotide positions 1 to 198 of SEQ ID No. 487 and the complements thereof. Other particularly preferred polynucleotides of the present invention include isolated, purified or recombinant polynucleotides comprising a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 490, wherein said contiguous span comprises at least 1, 2, 3, 4, 5 or 10 of nucleotide positions 1 to 198 of SEQ ID No. 490 and the complements thereof. Other preferred polynucleotides of the present invention include polynucleotides comprising, consisting of, or consisting essentially of a nucleotide sequence of SEQ ID No. 491.

Particularly preferred polynucleotides of the present invention include purified, isolated or recombinant polynucleotides comprising a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of a sequence selected from the group consisting of SEQ ID SEQ ID Nos. 3, 5, 9, 13-15, 25, 31, 33, 37,

38, 41, 323, 345, 351-353, 357, 377, and 380, or the complements thereof, wherein said span includes a MGST-II-related biallelic marker. Optionally either allele of the biallelic markers described above in the definition of MGST-II-related biallelic marker is specified as being present at the MGST-II-related biallelic marker.

Additional preferred polynucleotides of the invention include isolated, purified or recombinant polynucleotide comprising a contiguous span of at least 12 nucleotides of SEQ ID No. 485 or the complementary sequence thereof, wherein said contiguous span comprises a nucleotide selected from the group consisting of a T at position 36971, a C at position 45214 or a T at position 45741 of SEQ ID No. 485. Additional preferred polynucleotides of the invention include isolated, purified or recombinant polynucleotides comprising a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides from a sequence of SEQ ID No. 486, wherein said contiguous span comprises a T at position 426, a C at position 478 or a T at position 526 of SEQ ID No. 486; or the complement thereof. Additional preferred polynucleotides of the invention include isolated, purified or recombinant polynucleotides comprising a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides from a sequence of SEQ ID No. 487, wherein said contiguous span comprises a T at position 325, a C at position 378 or a T at position 426 of SEQ ID No. 487; or the complements thereof.

Table 2 contains a list of preferred MGST-II-related biallelic markers. Each marker is described by indicating its Marker ID, the position of the marker in the SEQ ID and the two most common alleles.

Table 2

BIALLELIC MARKER ID	ALLELES	POSITION OF BIALLELIC MARKER IN SEQ ID
	Non-genic biallelic markers	
12-424-192	A/G	SEQ ID No. 2, position 501
12-424-198	G/T	SEQ ID No. 3, position 501
12-426-154	G/A	SEQ ID No. 5, position 461
12-429-198	C/T	SEQ ID No. 6, position 501
12-430-80	C/T	SEQ ID No. 7, position 501
12-433-215	A/G	SEQ ID No. 8, position 501
12-441-233	A/G	SEQ ID No. 9, position 501
12-441-343	G/A	SEQ ID No. 10, position 501
12-442-221	T/C	SEQ ID No. 11, position 501
12-447-58	G/C	SEQ ID No. 12, position 501
12-449-300	T/C	SEQ ID No. 472, position 501
12-453-429	C/T	SEQ ID No. 13, position 501
12-454-363	A/G	SEQ ID No. 14, position 501

12-455-326	T/C	SEQ ID No. 15, position 501
12-455-383	G/A	SEQ ID No. 16, position 501
12-456-269	A/G	SEQ ID No. 17, position 501
12-456-380	G/T	SEQ ID No. 18, position 501
12-457-204	A/G	SEQ ID No. 19, position 501
12-457-206	C/T	SEQ ID No. 20, position 501
12-458-196	A/T	SEQ ID No. 21, position 501
12-458-438	T/C	SEQ ID No. 22, position 501
12-460-274	A/G	SEQ ID No. 23, position 501
12-461-124	A/C	SEQ ID No. 24, position 501
12-461-299	C/T	SEQ ID No. 25, position 501
12-461-465	C/T	SEQ ID No. 26, position 501
12-462-280	C/T	SEQ ID No. 27, position 501
12-464-66	G/T	SEQ ID No. 28, position 501
12-465-234	G/T	SEQ ID No. 30, position 501
12-465-26	C/T	SEQ ID No. 29, position 501
12-442-133	Deletion G	SEQ ID No. 437, position 501
12-449-63	Insertion AT	SEQ ID No. 438, position 501
10-454-242	Deletion AT	SEQ ID No. 439, position 501
12-463-230	Deletion CAT	SEQ ID No. 440, position 501
12-426-199	Deletion	SEQ ID No. 441, position 501
Genic Biallelic markers		
Biallelic Markers in Genomic sequence (SEQ ID No. 485)		
10-286-289	G/C	7564
10-286-345	A/T	7619
10-286-375	A/G	7649
12-425-57	G/A	17258
12-421-135	insertion of a T	21590
12-421-140	A/G	21595
10-523-232	C/T	36971
10-289-201	C/T	45214
10-290-37	C/T	45741
10-290-326	A/G	46029
10-290-328	G/T	46032
Biallelic Markers in MGST-II cDNA (SEQ ID No. 486)		
10-286-289	G/C	98
10-286-345	A/T	153
10-286-375	A/G	183
10-289-201	C/T	478
10-290-37	C/T	526
Biallelic Markers in MGST-II cDNA (SEQ ID No. 487)		
10-286-289	G/C	98
10-286-345	A/T	153
10-286-375	A/G	183
10-289-201	C/T	378
10-290-37	C/T	426

The invention also relates to polynucleotides that hybridize, under conditions of high or intermediate stringency, to a polynucleotide of a sequence from any sequence in the Sequence Listing as well as sequences, which are complementary thereto. Preferably such

polynucleotides are at least 20, 25, 35, 40, 50, 70, 80, 100, 250, 500 or 1000 nucleotides in length, to the extent that a polynucleotide of these lengths is consistent with the lengths of the particular Sequence ID. Preferred polynucleotides comprise a DME-related biallelic marker. Optionally either the original or the alternative allele of the biallelic markers disclosed in Figure 3 may be specified as being present at the DME-related biallelic marker. Conditions of high and intermediate stringency are further described in III.C.4 "Methods of Genotyping DNA Samples for Biallelic Markers-Hybridization assay methods."

The present invention further embodies isolated, purified, and recombinant polynucleotides which encode MGST-II polypeptides comprising a contiguous span of at least 6 amino acids, preferably at least 8 to 10 amino acids, more preferably at least 12, 15, 20, 25, 30, 40, 50, or 100 amino acids of SEQ ID No. 488. The present invention further embodies isolated, purified, and recombinant polynucleotides which encode the variant MGST-II polypeptides of SEQ ID Nos. 488 and 489. The present invention further embodies isolated, purified, and recombinant polynucleotides which encode a variant MGST-II polypeptide comprising a contiguous span of at least 6 amino acids, preferably at least 8 to 10 amino acids, more preferably at least 12, 15, 20, 25, 30, 40, 50, or 100 amino acids of SEQ ID No. 489. The present invention further embodies isolated, purified, and recombinant polynucleotides which encode polypeptides comprising a contiguous span of at least 6 amino acids, preferably at least 8 to 10 amino acids, more preferably at least 12, 15, 20, 25, 30, 40, 50, or 100 amino acids of SEQ ID No. 488 wherein said contiguous span comprises a His residue at amino acid position 93. The present invention further embodies isolated, purified, and recombinant polynucleotides which encode polypeptides comprising a contiguous span of at least 6 amino acids, preferably at least 8 to 10 amino acids, more preferably at least 12, 15, 20, 25, 30, 40, 50, or 100 amino acids of amino acid positions 1-108 of SEQ ID No. 488.

The primers of the present invention may be designed from the disclosed sequences for any method known in the art. A preferred set of primers is fashioned such that the 3' end of the contiguous span of identity with the sequences of the Sequence Listing is present at the 3' end of the primer. Such a configuration allows the 3' end of the primer to hybridize to a selected nucleic acid sequence and dramatically increases the efficiency of the primer for amplification or sequencing reactions. In a preferred set of primers the contiguous span is found in one of the sequences described in Figure 5. Allele specific primers may be designed such that a biallelic marker is at the 3' end of the contiguous span and the contiguous span is present at the 3' end of the primer. Such allele specific primers tend to

selectively prime an amplification or sequencing reaction so long as they are used with a nucleic acid sample that contains one of the two alleles present at a biallelic marker. The 3' end of primer of the invention may be located within or at least 2, 4, 6, 8, 10, 12, 15, 18, 20, 25, 50, 100, 250, 500, or 1000, to the extent that this distance is consistent with the particular Sequence ID, nucleotides upstream of a DME-related biallelic marker in said sequence or at any other location which is appropriate for their intended use in sequencing, amplification or the location of novel sequences or markers. A list of preferred amplification primers is disclosed in Figure 7. Primers with their 3' ends located 1 nucleotide upstream of a DME-related biallelic marker have a special utility as microsequencing assays. Preferred microsequencing primers are described in Figure 6.

The probes of the present invention may be designed from the disclosed sequences for any method known in the art, particularly methods which allow for testing if a particular sequence or marker disclosed herein is present. A preferred set of probes may be designed for use in the hybridization assays of the invention in any manner known in the art such that they selectively bind to one allele of a biallelic marker, but not the other under any particular set of assay conditions. Preferred hybridization probes may consists of, consist essentially of, or comprise a contiguous span which ranges in length from 8, 10, 12, 15, 18 or 20 to 25, 35, 40, 50, 60, 70, or 80 nucleotides, or be specified as being 12, 15, 18, 20, 25, 35, 40, or 50 nucleotides in length and including a DME-related biallelic marker of said sequence. Optionally the original allele or alternative allele disclosed in Figure 3 and 4 may be specified as being present at the biallelic marker site. Optionally, said biallelic marker may be within 6, 5, 4, 3, 2, or 1 nucleotides of the center of the hybridization probe or at the center of said probe. A particularly preferred set of hybridization probes is disclosed in Figure 8 or a sequence complementary thereto.

Any of the polynucleotides of the present invention can be labeled, if desired, by incorporating a label detectable by spectroscopic, photochemical, biochemical, immunochemical, or chemical means. For example, useful labels include radioactive substances, fluorescent dyes or biotin. Preferably, polynucleotides are labeled at their 3' and 5' ends. A label can also be used to capture the primer, so as to facilitate the immobilization of either the primer or a primer extension product, such as amplified DNA, on a solid support. A capture label is attached to the primers or probes and can be a specific binding member which forms a binding pair with the solid's phase reagent's specific binding member (e.g. biotin and streptavidin). Therefore depending upon the type of label carried by a polynucleotide or a probe, it may be employed to capture or to detect the target

DNA. Further, it will be understood that the polynucleotides, primers or probes provided herein, may, themselves, serve as the capture label. For example, in the case where a solid phase reagent's binding member is a nucleic acid sequence, it may be selected such that it binds a complementary portion of a primer or probe to thereby immobilize the primer or probe to the solid phase. In cases where a polynucleotide probe itself serves as the binding member, those skilled in the art will recognize that the probe will contain a sequence or "tail" that is not complementary to the target. In the case where a polynucleotide primer itself serves as the capture label, at least a portion of the primer will be free to hybridize with a nucleic acid on a solid phase. DNA Labeling techniques are well known to the skilled technician.

Any of the polynucleotides, primers and probes of the present invention can be conveniently immobilized on a solid support. Solid supports are known to those skilled in the art and include the walls of wells of a reaction tray, test tubes, polystyrene beads, magnetic beads, nitrocellulose strips, membranes, microparticles such as latex particles, sheep (or other animal) red blood cells, duracytes® and others. The solid support is not critical and can be selected by one skilled in the art. Thus, latex particles, microparticles, magnetic or non-magnetic beads, membranes, plastic tubes, walls of microtiter wells, glass or silicon chips, sheep (or other suitable animal's) red blood cells and duracytes are all suitable examples. Suitable methods for immobilizing nucleic acids on solid phases include ionic, hydrophobic, covalent interactions and the like. A solid support, as used herein, refers to any material which is insoluble, or can be made insoluble by a subsequent reaction. The solid support can be chosen for its intrinsic ability to attract and immobilize the capture reagent. Alternatively, the solid phase can retain an additional receptor which has the ability to attract and immobilize the capture reagent. The additional receptor can include a charged substance that is oppositely charged with respect to the capture reagent itself or to a charged substance conjugated to the capture reagent. As yet another alternative, the receptor molecule can be any specific binding member which is immobilized upon (attached to) the solid support and which has the ability to immobilize the capture reagent through a specific binding reaction. The receptor molecule enables the indirect binding of the capture reagent to a solid support material before the performance of the assay or during the performance of the assay. The solid phase thus can be a plastic, derivatized plastic, magnetic or non-magnetic metal, glass or silicon surface of a test tube, microtiter well, sheet, bead, microparticle, chip, sheep (or other suitable animal's) red blood cells, duracytes® and other configurations known to those of ordinary skill in the art. The

polynucleotides of the invention can be attached to or immobilized on a solid support individually or in groups of at least 2, 5, 8, 10, 12, 15, 20, or 25 distinct polynucleotides of the inventions to a single solid support. In addition, polynucleotides other than those of the invention may attached to the same solid support as one or more polynucleotides of the invention.

Any polynucleotide provided herein may be attached in overlapping areas or at random locations on the solid support. Alternatively the polynucleotides of the invention may be attached in an ordered array wherein each polynucleotide is attached to a distinct region of the solid support which does not overlap with the attachment site of any other polynucleotide. Preferably, such an ordered array of polynucleotides is designed to be "addressable" where the distinct locations are recorded and can be accessed as part of an assay procedure. Addressable polynucleotide arrays typically comprise a plurality of different oligonucleotide probes that are coupled to a surface of a substrate in different known locations. The knowledge of the precise location of each polynucleotides location makes these "addressable" arrays particularly useful in hybridization assays. Any addressable array technology known in the art can be employed with the polynucleotides of the invention. One particular embodiment of these polynucleotide arrays is known as the Genechips™, and has been generally described in US Patent 5,143,854; PCT publications WO 90/15070 and 92/10092. These arrays may generally be produced using mechanical synthesis methods or light directed synthesis methods, which incorporate a combination of photolithographic methods and solid phase oligonucleotide synthesis (Fodor et al., Science, 251:767-777, 1991). The immobilization of arrays of oligonucleotides on solid supports has been rendered possible by the development of a technology generally identified as "Very Large Scale Immobilized Polymer Synthesis" (VLSIPS™) in which, typically, probes are immobilized in a high density array on a solid surface of a chip. Examples of VLSIPS™ technologies are provided in US Patents 5,143,854 and 5,412,087 and in PCT Publications WO 90/15070, WO 92/10092 and WO 95/11995, which describe methods for forming oligonucleotide arrays through techniques such as light-directed synthesis techniques. In designing strategies aimed at providing arrays of nucleotides immobilized on solid supports, further presentation strategies were developed to order and display the oligonucleotide arrays on the chips in an attempt to maximize hybridization patterns and sequence information. Examples of such presentation strategies are disclosed in PCT Publications WO 94/12305, WO 94/11530, WO 97/29212 and WO 97/31256.

Oligonucleotide arrays may comprise at least one of the sequences selected from the group consisting of SEQ ID No. 1-38, 40-54, 56-463, 465-487, 490-493; and the sequences complementary thereto or a fragment thereof of at least 8, 10, 12, 15, 18, 20, 25, 35, 40, 50, 70, 80, 100, 250, 500 or 1000 consecutive nucleotides, to the extent that fragments of these lengths is consistent with the lengths of the particular Sequence ID, for determining whether a sample contains one or more alleles of the biallelic markers of the present invention. Oligonucleotide arrays may also comprise at least one of the sequences selected from the group consisting of SEQ ID No. 1-38, 40-54, 56-463, 465-487, 490-493; and the sequences complementary thereto or a fragment thereof of at least 8, 10, 12, 15, 18, 20, 25, 35, 40, 50, 70, 80, 100, 250, 500 or 1000 consecutive nucleotides, to the extent that fragments of these lengths is consistent with the lengths of the particular Sequence ID, for amplifying one or more alleles of the biallelic markers of Figure 1. In other embodiments, arrays may also comprise at least one of the sequences selected from the group consisting of SEQ ID No. 1-38, 40-54, 56-463, 465-487, 490-493; and the sequences complementary thereto or a fragment thereof of at least 8, 10, 12, 15, 18, 20, 25, 35, 40, 50, 70, 80, 100, 250, 500 or 1000 consecutive nucleotides, to the extent that fragments of these lengths is consistent with the lengths of the particular Sequence ID, for conducting microsequencing analyses to determine whether a sample contains one or more alleles of the biallelic markers of the invention. In still further embodiments, the oligonucleotide array may comprise at least one of the sequences selecting from the group consisting of SEQ ID No. 1-38, 40-54, 56-463, 465-487, 490-493; and the sequences complementary thereto or a fragment thereof of at least 8, 10, 12, 15, 18, 20, 25, 35, 40, 50, 70, 80, 100, 250, 500 or 1000 nucleotides in length, to the extent that fragments of these lengths is consistent with the lengths of the particular Sequence ID, for determining whether a sample contains one or more alleles of the biallelic markers of the present invention.

The present invention also encompasses diagnostic kits comprising one or more polynucleotides of the invention, optionally with a portion or all of the necessary reagents and instructions for genotyping a test subject by determining the identity of a nucleotide at a DME-related biallelic marker. The polynucleotides of a kit may optionally be attached to a solid support, or be part of an array or addressable array of polynucleotides. The kit may provide for the determination of the identity of the nucleotide at a marker position by any method known in the art including, but not limited to, a sequencing assay method, a microsequencing assay method, a hybridization assay method, or an allele specific amplification method. Optionally such a kit may include instructions for scoring the results

of the determination with respect to the test subjects' risk of contracting a diseases involving the metabolic conversion of xenobiotics, or likely response to a drug, or chances of suffering from side effects to a drug, including hepatoxicity.

I.B. Genomic Sequences of the MGST-II Gene and Biallelic Markers

The present invention encompasses the genomic sequence of the MGST-II gene of SEQ ID No. 485. The MGST-II genomic sequences comprise exons and introns. Particularly preferred genomic sequences of the MGST-II gene of the invention include isolated, purified or recombinant polynucleotides comprising a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 485, wherein said contiguous span comprises at least 1, 2, 3, 4, 5 or 10 of the following nucleotide positions of SEQ ID No. 485: 1 to 7667, 7726 to 20264, 20365 to 36918, 36991 to 45180, 45263 to 45741, and 45980 to 49327, and the complements thereof. The nucleic acids defining the MGST-II intronic polynucleotides may be used as oligonucleotide primers or probes in order to detect the presence of a copy of the MGST-II gene in a test sample, or alternatively in order to amplify a target nucleotide sequence within the MGST-II sequences.

The present invention further provides MGST-II intron and exon polynucleotide sequences including biallelic markers. Particularly preferred polynucleotides of the present invention include purified, isolated or recombinant polynucleotides comprising a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of a sequence of SEQ ID No. 485; or the complements thereof; wherein said span includes a MGST-II-related biallelic marker. Preferred polynucleotides comprise at least one biallelic marker selected from the group consisting of biallelic markers 10-286-289, 10-287-116, 10-286-375, 12-425-57, 12-421-135, 12-421-140, 10-523-232, 10-289-201, 10-290-37, 10-290-326 and 10-290-328. The present invention also provides polynucleotides which, may be used as primers and probes in order to amplify fragments carrying biallelic markers or in order to detect biallelic marker alleles.

Regulatory sequences

The genomic sequence of the MGST-II gene contains regulatory sequences both in the non-coding 5'- flanking region and in the non-coding 3'- flanking region that border the MGST-II transcribed region containing the 5 exons of this gene. 5'-regulatory sequences of the MGST-II gene comprise the polynucleotide sequences located between the nucleotide in position 1 and the nucleotide in position 7466 of the nucleotide sequence of SEQ ID No. 485. 3'-regulatory sequences of the MGST-II gene comprise the polynucleotide sequences

located between the nucleotide in position 45980 and the nucleotide in position 49327 of the nucleotide sequence of SEQ ID No. 485. Particularly preferred regulatory polynucleotides of the present invention include isolated, purified or recombinant polynucleotides comprising a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 485, wherein said contiguous span comprises at least 1, 2, 3, 4, 5 or 10 of the following nucleotide positions of SEQ ID No. 485: 1 to 7466 and 45966 to 49312; and the complements thereof.

The promoter activity of the regulatory regions contained in the MGST-II genomic sequence of polynucleotide sequence of SEQ ID No. 485 can be assessed by any method known in the art. Methods for identifying the polynucleotide fragments of SEQ ID No. 485 involved in the regulation of the expression of the MGST-II gene are well-known to those skilled in the art (see Sambrook et al., Molecular Cloning A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1989). An example of a typical method, that can be used, involves a recombinant vector carrying a reporter gene and genomic sequences from the MGST-II genomic sequence of SEQ ID No. 485. Briefly, the expression of the reporter gene (for example beta galactosidase or chloramphenicol acetyl transferase) is detected when placed under the control of a biologically active polynucleotide fragment. Genomic sequences located upstream of the first exon of the MGST-II gene may be cloned into any suitable promoter reporter vector, such as the pSEAP-Basic, pSEAP-Enhancer, pβgal-Basic, pβgal-Enhancer, or pEGFP-1 Promoter Reporter vectors available from Clontech, or pGL2-basic or pGL3-basic promoterless luciferase reporter gene vector from Promega. Each of these promoter reporter vectors include multiple cloning sites positioned upstream of a reporter gene encoding a readily assayable protein such as secreted alkaline phosphatase, luciferase, beta galactosidase, or green fluorescent protein. The sequences upstream the first MGST-II exon are inserted into the cloning sites upstream of the reporter gene in both orientations and introduced into an appropriate host cell. The level of reporter protein is assayed and compared to the level obtained with a vector lacking an insert in the cloning site. The presence of an elevated expression level in the vector containing the insert with respect to the control vector indicates the presence of a promoter in the insert.

Promoter sequences within the 5' non-coding regions of the MGST-II gene may be further defined by constructing nested 5' and/or 3' deletions using conventional techniques such as Exonuclease III or appropriate restriction endonuclease digestion. The resulting deletion fragments can be inserted into the promoter reporter vector to determine whether

the deletion has reduced or obliterated promoter activity, such as described, for example, by Coles et al. (*Hum. Mol. Genet.*, 7:791-800, 1998). In this way, the boundaries of the promoters may be defined. If desired, potential individual regulatory sites within the promoter may be identified using site directed mutagenesis or linker scanning to obliterate potential transcription factor binding sites within the promoter individually or in combination. The effects of these mutations on transcription levels may be determined by inserting the mutations into cloning sites in promoter reporter vectors. This type of assays are well known to those skilled in the art and are further described in WO 97/17359, US 5 374 544, EP 582 796, US 5 698 389, US 5 643 746, US 5 502 176, and US 5 266 488.

The activity and the specificity of the promoter of the MGST-II gene can further be assessed by monitoring the expression level of a detectable polynucleotide operably linked to the MGST-II promoter in different types of cells and tissues. The detectable polynucleotide may be either a polynucleotide that specifically hybridizes with a predefined oligonucleotide probe, or a polynucleotide encoding a detectable protein, including a MGST-II polypeptide or a fragment or a variant thereof. This type of assay is well known to those skilled in the art and is described in US 5 502 176 and US 5 266 488 for example.

Polynucleotides carrying the regulatory elements located both at the 5' end and at the 3' end of the MGST-II coding region may be advantageously used to control the transcriptional and translational activity of an heterologous polynucleotide of interest, said polynucleotide being heterologous as regards to the MGST-II regulatory region.

Thus, the present invention also concerns a purified, isolated, and recombinant nucleic acid comprising a polynucleotide which, is selected from the group consisting of, the polynucleotide sequences located between the nucleotide in position 1 and the nucleotide in position 7466 of the nucleotide sequence of SEQ ID No. 485; or a sequence complementary thereto or a biologically active fragment thereof.

By a "biologically active" fragment of SEQ ID No. 485 according to the present invention is intended a polynucleotide comprising or alternatively consisting of a fragment of said polynucleotide which is functional as a regulatory region for expressing a recombinant polypeptide or a recombinant polynucleotide in a recombinant cell host.

For the purpose of the invention, a nucleic acid or polynucleotide is "functional" as a regulatory region for expressing a recombinant polypeptide or a recombinant polynucleotide if said regulatory polynucleotide contains nucleotide sequences which contain transcriptional and translational regulatory information, and such sequences are "operably

linked" to nucleotide sequences which encode the desired polypeptide or the desired polynucleotide.

The regulatory polynucleotides according to the invention may be advantageously part of a recombinant expression vector that may be used to express a coding sequence in a desired host cell or host organism.

I.C. MGST-II cDNA Comprising Biallelic Markers and Variant MGST-II cDNA

The present invention provides a MGST-II cDNA of SEQ ID No. 486. The Open Reading Frame encoding the MGST-II protein spans from the nucleotide in position 202 to the nucleotide in position 642 of the polynucleotide sequence of SEQ ID No. 486. The cDNA of SEQ ID No. 486 also includes a 5'-UTR region and a 3'-UTR region.

Particularly preferred cDNA polynucleotides of the present invention include purified, isolated or recombinant polynucleotides comprising a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of a sequence of SEQ ID No. 486, or the complements thereof, wherein said span includes a MGST-II-related biallelic marker. Preferred cDNA fragments comprise a biallelic marker selected from the group consisting of 10-286-289 (position 98), 10-286-345 (position 153), 10-286-375 (position 183), 10-523-232 (position 426), 10-289-201 (position 478) and 10-290-37 (position 526). Additional preferred polynucleotides of the invention include isolated, purified or recombinant polynucleotides comprising a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides from a sequence of SEQ ID No. 486, wherein said contiguous span comprises a T at position 426, a C at position 478 or a T at position 526 of SEQ ID No. 486; or the complement thereof. Most biallelic polymorphism represent silent nucleotide substitutions but biallelic marker 10-289-201 is associated with an amino acid change in the corresponding MGST-II polypeptide (TYR replaced by ARG in position 93 of the polypeptide). Moreover, one biallelic marker allele of marker 10-290-37 is associated with a stop codon and the corresponding variant cDNA encodes a truncated MGST-II polypeptide including amino acids 1 to 108.

The present invention further provides a variant MGST-II cDNA of SEQ ID No. 487. corresponding to an alternative splicing form which results in the deletion of exon 2. This alternative splicing of MGST-II yields the variant MGST-II polypeptide of SEQ ID No. 489. MGST-II polypeptides of the present invention are further described below. Preferred cDNAs of the invention include isolated, purified or recombinant polynucleotides comprising a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90,

100, 150, 200, 500, or 1000 nucleotides from a sequence of SEQ ID No. 487; or the complements thereof. Additional preferred polynucleotides of the invention include isolated, purified or recombinant polynucleotides comprising a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides from a sequence of SEQ ID No. 487, wherein said contiguous span comprises a T at position 325, a C at position 378 or a T at position 426 of SEQ ID No. 487; or the complements thereof. The new exon 1/exon 3 junction sequence of the splice variant MGST-II cDNA, more particularly the nucleotide sequence comprised between the nucleotide in position 106 and the nucleotide in position 374 of the nucleic acid of SEQ ID No. 486 corresponds to the nucleotide sequence of an EST that has been obtained from a human cDNA library. Polynucleotides comprising this EST of a sequence from SEQ ID No. 490 are also part of the invention.

The above disclosed polynucleotides that contain the coding sequence of the MGST-II gene and of MGST-II variants may be expressed in a desired host cell or a desired host organism, when this polynucleotide is placed under the control of suitable expression signals. The expression signals may be either the expression signals contained in the regulatory regions in the MGST-II gene of the invention or in contrast the signals may be exogenous regulatory nucleic sequences. Such a polynucleotide, when placed under the suitable expression signals, may also be inserted in a vector for its expression and/or amplification.

Another preferred cDNA fragment comprises the 5'-UTR region (regulatory) beginning at position 1 and ending at position 201 of SEQ ID Nos. 486 and 487 . Preferably said 5'-UTR region comprises a biallelic marker selected from the group consisting of biallelic markers 10-286-289, 10-286-345 and 10-286-375. Particularly preferred 5'-UTR polynucleotides of the present invention include isolated, purified or recombinant polynucleotides comprising a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500, or 1000 nucleotides of SEQ ID No. 486, wherein said contiguous span comprises at least 1, 2, 3, 4, 5 or 10 of nucleotide positions 1 to 198 of SEQ ID No. 486; and the complements thereof. The 5'-end sequence of the MGST-II cDNA, more particularly the nucleotide sequence comprised between the nucleotide in position 1 and the nucleotide in position 357 of the nucleic acid of SEQ ID No. 486 corresponds to the nucleotide sequence of a 5'-EST that has been obtained from a human cDNA library. Polynucleotides comprising this 5'-EST of a sequence from SEQ ID No. 490 are also part of the invention.

The polynucleotide disclosed above that contains the coding sequence of the MGST-II gene of the invention may be expressed in a desired host cell or a desired host organism, when this polynucleotide is placed under the control of suitable expression signals. The expression signals may be either the expression signals contained in the regulatory regions in the MGST-II gene of the invention or may be exogenous regulatory nucleic sequences. Such a polynucleotide, when placed under the suitable expression signals, may also be inserted in a vector for its expression.

A further object of the invention consists of an isolated polynucleotide comprising:
a) a nucleic acid comprising a regulatory nucleotide sequence from a sequence of SEQ ID No. 485;
b) a polynucleotide encoding a desired polypeptide or a nucleic acid of interest, operably linked to the nucleic acid defined in (a) above;
c) Optionally, a nucleic acid comprising a 5'- UTR regulatory polynucleotide, preferably a 5'-UTR regulatory polynucleotide sequence of a sequence of SEQ ID No. 486.

The polypeptide encoded by the nucleic acid described above may be of various nature or origin, encompassing proteins of prokaryotic or eukaryotic origin. Among the polypeptides expressed under the control of a MGST-II regulatory region, there may be cited bacterial, fungal or viral antigens. Also encompassed are eukaryotic proteins such as intracellular proteins, for example "house keeping" proteins, membrane-bound proteins, for example receptors, and secreted proteins, for example cytokines. In a specific embodiment, the desired polypeptide may be the MGST-II protein, especially the proteins of the amino acid sequence of SEQ ID Nos. 488 and 489.

The desired nucleic acids encoded by the above described polynucleotide, usually a RNA molecule, may be complementary to a desired coding polynucleotide, for example to the MGST-II coding sequence, and thus useful as an antisense polynucleotide.

Such a polynucleotide may be included in a recombinant expression vector in order to express the desired polypeptide or the desired nucleic acid in host cell or in a host organism.

I.D. Polynucleotide Constructs, Recombinant Vectors, Host Cells and Transgenic Animals

Polynucleotide Constructs

The terms "polynucleotide construct" and "recombinant polynucleotide" are used interchangeably herein to refer to linear or circular, purified or isolated polynucleotides that

have been artificially designed and which comprise at least two nucleotide sequences that are not found as contiguous nucleotide sequences in their initial natural environment.

DNA constructs for expressing the MGST-II gene in recombinant host cells and in transgenic animals

In order to study the physiological and phenotype consequences of a lack of synthesis of the MGST-II protein, both at the cellular level and at the multicellular organism level, in particular as regards to disorders related to abnormal cell proliferation, notably cancers, the invention also encompasses DNA constructs and recombinant vectors enabling a conditional expression of a specific allele of the MGST-II genomic sequence or cDNA

A first preferred DNA construct is based on the tetracycline resistance operon *tet* from *E. coli* transposon Tn110 for controlling the MGST-II gene expression, such as described by Gossen et al. (*Science*, 268:1766-1769, 1995). Such a DNA construct contains seven *tet* operator sequences from Tn10 (*tet*op) that are fused to either a minimal promoter or a 5'-regulatory sequence of the MGST-II gene, said minimal promoter or said MGST-II regulatory sequence being operably linked to a polynucleotide of interest that codes either for a sense or an antisense oligonucleotide or for a polypeptide, including a MGST-II polypeptide or a peptide fragment thereof. This DNA construct is functional as a conditional expression system for the nucleotide sequence of interest when the same cell also comprises a nucleotide sequence coding for either the wild type (tTA) or the mutant (rTA) repressor fused to the activating domain of viral protein VP16 of herpes simplex virus, placed under the control of a promoter, such as the HCMVIE1 enhancer/promoter or the MMTV-LTR. Indeed, a preferred DNA construct of the invention will comprise both the polynucleotide containing the *tet* operator sequences and the polynucleotide containing a sequence coding for the tTA or the rTA repressor. In the specific embodiment wherein the conditional expression DNA construct contains the sequence encoding the mutant tetracycline repressor rTA, the expression of the polynucleotide of interest is silent in the absence of tetracycline and induced in its presence.

DNA constructs allowing homologous recombination: replacement vectors

A second preferred DNA construct will comprise, from 5'-end to 3'-end : (a) a first nucleotide sequence that is comprised in the MGST-II genomic sequence; (b) a nucleotide sequence comprising a positive selection marker, such as the marker for neomycine resistance (*neo*); and (c) a second nucleotide sequence that is comprised in the MGST-II genomic sequence, and is located on the genome downstream the first MGST-II nucleotide sequence (a).

In a preferred embodiment, this DNA construct also comprises a negative selection marker located upstream the nucleotide sequence (a) or downstream the nucleotide sequence (c). Preferably, the negative selection marker consists of the thymidine kinase (*tk*) gene (Thomas et al., *Cell*, 44:419-428, 1986), the hygromycine beta gene (Te Riele et al., *Nature*, 348:649-651, 1990), the *hprt* gene (Van der Lugt et al., *Gene*, 105:263-267, 1991; Reid et al., *Proc. Natl. Acad. Sci. USA*, 87:4299-4303, 1990) or the Diphteria toxin A fragment (*Dt-A*) gene (Nada et al., *Cell*, 73:1125-1135, 1993; Yagi et al., *Proc. Natl; Acad. Sci. USA*, 87:9918-9922, 1990). Preferably, the positive selection marker is located within a MGST-II exon sequence so as to interrupt the sequence encoding a MGST-II protein. These replacement vectors are further described by Mansour et al. (*Nature*, 336:348-352, 1988) and Koller et al. (*Ann. Rev. Immunol.*, 10:705-730, 1992). The first and second nucleotide sequences (a) and (c) may be indifferently located within a MGST-II regulatory sequence, an intronic sequence, an exon sequence or a sequence containing both regulatory and/or intronic and/or exon sequences. The size of the nucleotide sequences (a) and (c) is ranging from 1 to 50 kb, preferably from 1 to 10 kb, more preferably from 2 to 6 kb and most preferably from 2 to 4 kb.

DNA constructs allowing homologous recombination: Cre-loxP system

These new DNA constructs make use of the site specific recombination system of the P1 phage. The P1 phage possesses a recombinase called Cre which, interacts specifically with a 34 base pairs *lox*P site. The *lox*P site is composed of two palindromic sequences of 13 bp separated by a 8 bp conserved sequence (Hoess et al., *Nucleic Acids Res.*, 14:2287-2300, 1986). The recombination by the Cre enzyme between two *lox*P sites having an identical orientation leads to the deletion of the DNA fragment.

The Cre-*lox*P system used in combination with a homologous recombination technique has been first described by Gu et al. (*Cell*, 73:1155-1164, 1993). Briefly, a nucleotide sequence of interest to be inserted in a targeted location of the genome harbors at least two *lox*P sites in the same orientation and located at the respective ends of a nucleotide sequence to be excised from the recombinant genome. The excision event requires the presence of the recombinase (Cre) enzyme within the nucleus of the recombinant cell host. The recombinase enzyme may be brought at the desired time either by (a) incubating the recombinant cell hosts in a culture medium containing this enzyme, by injecting the Cre enzyme directly into the desired cell, such as described by Araki et al. (*Proc. Natl; Acad. Sci. USA*, 92: 160-164, 1995), or by lipofection of the enzyme into the cells, such as described by Baubonis et al. (*Nucleic Acids Res.*, 21:2025-2029, 1993); (b) transfecting the

cell host with a vector comprising the *Cre* coding sequence operably linked to a promoter functional in the recombinant cell host, which promoter being optionally inducible, said vector being introduced in the recombinant cell host, such as described by Gu et al. (*Cell*, 73:1155-1164, 1993) and Sauer et al. (*Proc. Natl; Acad. Sci. USA*, 85:5166-5170, 1988); (c) introducing in the genome of the cell host a polynucleotide comprising the *Cre* coding sequence operably linked to a promoter functional in the recombinant cell host, which promoter is optionally inducible, and said polynucleotide being inserted in the genome of the cell host either by a random insertion event or an homologous recombination event, such as described by Gu et al. (*Science*, 265:103-106, 1994).

In the specific embodiment wherein the vector containing the sequence to be inserted in the MGST-II gene by homologous recombination is constructed in such a way that selectable markers are flanked by *lox*P sites of the same orientation, it is possible, by treatment by the Cre enzyme, to eliminate the selectable markers while leaving the MGST-II sequences of interest that have been inserted by an homologous recombination event. Again, two selectable markers are needed: a positive selection marker to select for the recombination event and a negative selection marker to select for the homologous recombination event. Vectors and methods using the Cre-*lox*P system are further described by Zou et al. (*Curr. Biol.*, 4:1099-1103, 1994).

Thus, a third preferred DNA construct of the invention comprises, from 5'-end to 3'-end: (a) a first nucleotide sequence that is comprised in the MGST-II genomic sequence; (b) a nucleotide sequence comprising a polynucleotide encoding a positive selection marker, said nucleotide sequence comprising additionally two sequences defining a site recognized by a recombinase, such as a *lox*P site, the two sites being placed in the same orientation; and (c) a second nucleotide sequence that is comprised in the MGST-II genomic sequence, and is located on the genome downstream of the first MGST-II nucleotide sequence (a).

The sequences defining a site recognized by a recombinase, such as a *lox*P site, are preferably located within the nucleotide sequence (b) at suitable locations bordering the nucleotide sequence for which the conditional excision is sought. In one specific embodiment, two *lox*P sites are located at each side of the positive selection marker sequence, in order to allow its excision at a desired time after the occurrence of the homologous recombination event.

In a preferred embodiment of a method using the third DNA construct described above, the excision of the polynucleotide fragment bordered by the two sites recognized by a recombinase, preferably two *lox*P sites, is performed at a desired time. due to the presence

within the genome of the recombinant cell host of a sequence encoding the Cre enzyme operably linked to a promoter sequence, preferably an inducible promoter, more preferably a tissue-specific promoter sequence and most preferably a promoter sequence which is both inducible and tissue-specific, such as described by Gu et al. (*Science*, 265:103-106, 1994).

The presence of the Cre enzyme within the genome of the recombinant cell host may result of the breeding of two transgenic animals, the first transgenic animal bearing the MGST-II-derived sequence of interest containing the *lox*P sites as described above and the second transgenic animal bearing the *Cre* coding sequence operably linked to a suitable promoter sequence, such as described by Gu et al. (*Science*, 265:103-106, 1994).

Spatio-temporal control of the Cre enzyme expression may also be achieved with an adenovirus based vector that contains the Cre gene thus allowing infection of cells, or *in vivo* infection of organs, for delivery of the Cre enzyme, such as described by Anton et al. (*J. Virol.*, 69:4600-4606, 1995) and Kanegae et al. (*Nucleic Acids Res.*, 23:3816-3821, 1995).

The DNA constructs described above may be used to introduce a desired nucleotide sequence of the invention, preferably a MGST-II genomic sequence or a MGST-II cDNA sequence, and most preferably an altered copy of a MGST-II genomic or cDNA sequence, within a predetermined location of the targeted genome, leading either to the generation of an altered copy of a targeted gene (knock-out homologous recombination) or to the replacement of a copy of the targeted gene by another copy sufficiently homologous to allow an homologous recombination event to occur (knock-in homologous recombination).

Recombinant Vectors

The term "vector" is used herein to designate either a circular or a linear DNA or RNA molecule, which is either double-stranded or single-stranded, and which comprise at least one polynucleotide of interest that is sought to be transferred in a cell host or in a unicellular or multicellular host organism.

The present invention encompasses a family of recombinant vectors that comprise a regulatory polynucleotide derived from the MGST-II genomic sequence, or a coding polynucleotide from the MGST-II genomic sequence. Consequently, the present invention further deals with a recombinant vector comprising either a regulatory polynucleotide comprised in the nucleic acid of SEQ ID Nos. 485 and 486 or a polynucleotide comprising the MGST-II coding sequence or both.

In a first preferred embodiment, a recombinant vector of the invention is used to amplify the inserted polynucleotide derived from a MGST-II genomic sequence selected

from the group consisting of the nucleic acids of SEQ ID No. 485 or a MGST-II cDNA, for example the cDNA of SEQ ID Nos. 486 and 487 in a suitable host cell, this polynucleotide being amplified each time the recombinant vector replicates. Generally, a recombinant vector of the invention may comprise any of the polynucleotides described herein, including regulatory sequences and coding sequences, as well as any MGST-II primer or probe as defined above.

A second preferred embodiment of the recombinant vectors according to the invention consists of expression vectors comprising either a regulatory polynucleotide or a coding nucleic acid of the invention, or both. Within certain embodiments, expression vectors are employed to express the MGST-II polypeptide which can be then purified and, for example be used in ligand screening assays or as an immunogen in order to raise specific antibodies directed against the MGST-II protein. In other embodiments, the expression vectors are used for constructing transgenic animals and also for gene therapy. Expression requires that appropriate signals are provided in the vectors, said signals including various regulatory elements, such as enhancers/promoters from both viral and mammalian sources that drive expression of the genes of interest in host cells. Dominant drug selection markers for establishing permanent, stable cell clones expressing the products are generally included in the expression vectors of the invention, as they are elements that link expression of the drug selection markers to expression of the polypeptide.

More particularly, the present invention relates to expression vectors which include nucleic acids encoding a MGST-II protein, preferably the MGST-II protein of the amino acid sequence of SEQ ID Nos. 488 and 489, under the control of a regulatory sequence selected among theMGST-II regulatory polynucleotides of SEQ ID Nos. 485 and 486, or alternatively under the control of an exogenous regulatory sequence. Consequently, preferred expression vectors of the invention are selected from the group consisting of : (a) the MGST-II regulatory sequence comprised therein drives the expression of a coding polynucleotide operably linked thereto; (b) the MGST-II coding sequence is operably linked to regulation sequences allowing its expression in a suitable cell host and/or host organism. Additionally, the recombinant expression vector described above may also comprise a nucleic acid comprising a 5'-regulatory polynucleotide or a 3'-regulatory polynucleotide, preferably a 5'-regulatory polynucleotide or a 3'-regulatory polynucleotide of the MGST-II gene. The MGST-II 5'-regulatory polynucleotide may also comprise the 5'-UTR sequence contained in the nucleotide sequence of SEQ ID Nos. 486 and 487; or a biologically active fragment or variant thereof. The invention also pertains to a recombinant expression vector

useful for the expression of the MGST-II coding sequence, wherein said vector comprises any of the MGST-II cDNAs or cDNA variants described above; or fragments thereof.

Some of the elements which, can be found in the vectors of the present invention are described in further detail in the following sections.

1. General features of the expression vectors of the invention

A recombinant vector according to the invention comprises, but is not limited to, a YAC (Yeast Artificial Chromosome), a BAC (Bacterial Artificial Chromosome), a phage, a phagemid, a cosmid, a plasmid or even a linear DNA molecule which may consist of a chromosomal, non-chromosomal, semi-synthetic and synthetic DNA. Such a recombinant vector can comprise a transcriptional unit comprising an assembly of :

(1) a genetic element or elements having a regulatory role in gene expression, for example promoters or enhancers. Enhancers are cis-acting elements of DNA, usually from about 10 to 300 bp in length that act on the promoter to increase the transcription.

(2) a structural or coding sequence which is transcribed into mRNA and eventually translated into a polypeptide, said structural or coding sequence being operably linked to the regulatory elements described in (1); and

(3) appropriate transcription initiation and termination sequences. Structural units intended for use in yeast or eukaryotic expression systems preferably include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, when a recombinant protein is expressed without a leader or transport sequence, it may include a N-terminal residue. This residue may or may not be subsequently cleaved from the expressed recombinant protein to provide a final product.

Generally, recombinant expression vectors will include origins of replication, selectable markers permitting transformation of the host cell, and a promoter derived from a highly expressed gene to direct transcription of a downstream structural sequence. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably a leader sequence capable of directing secretion of the translated protein into the periplasmic space or the extracellular medium. In a specific embodiment wherein the vector is adapted for transfecting and expressing desired sequences in mammalian host cells, preferred vectors will comprise an origin of replication in the desired host, a suitable promoter and enhancer, and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5'-flanking non-transcribed sequences. DNA sequences derived

from the SV40 viral genome, for example SV40 origin, early promoter, enhancer, splice and polyadenylation sites may be used to provide the required non-transcribed genetic elements.

The *in vivo* expression of a MGST-II polypeptide of SEQ ID Nos. 488 and 489 may be useful in order to correct a genetic defect related to the expression of the native gene in a host organism or to the production of a biologically inactive MGST-II protein.

Consequently, the present invention also deals with recombinant expression vectors mainly designed for the *in vivo* production of the MGST-II polypeptide of SEQ ID Nos. 488 and 489 or fragments or variants thereof by the introduction of the appropriate genetic material in the organism of the patient to be treated. This genetic material may be introduced *in vitro* in a cell that has been previously extracted from the organism, the modified cell being subsequently reintroduced in the said organism, directly *in vivo* into the appropriate tissue.

2. Regulatory elements

Promoters:

The suitable promoter regions used in the expression vectors according to the present invention are chosen taking into account the cell host in which the heterologous gene has to be expressed. The particular promoter employed to control the expression of a nucleic acid sequence of interest is not believed to be important, so long as it is capable of directing the expression of the nucleic acid in the targeted cell. Thus, where a human cell is targeted, it is preferable to position the nucleic acid coding region adjacent to and under the control of a promoter that is capable of being expressed in a human cell, such as, for example, a human or a viral promoter.

A suitable promoter may be heterologous with respect to the nucleic acid for which it controls the expression or alternatively can be endogenous to the native polynucleotide containing the coding sequence to be expressed. Additionally, the promoter is generally heterologous with respect to the recombinant vector sequences within which the construct promoter/coding sequence has been inserted.

Promoter regions can be selected from any desired gene using, for example, CAT (chloramphenicol transferase) vectors and more preferably pKK232-8 and pCM7 vectors.

Preferred bacterial promoters are the LacI, LacZ, the T3 or T7 bacteriophage RNA polymerase promoters, the gpt, lambda PR, PL and trp promoters (EP 0036776), the polyhedrin promoter, or the p10 protein promoter from baculovirus (Kit Novagen) (Smith et al., 1983; O'Reilly et al., 1992), the lambda PR promoter or also the trc promoter.

Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-L. Selection of a convenient vector and promoter is well within the level of ordinary skill in the art.

The choice of a promoter is well within the ability of a person skilled in the field of genetic egineering. For example, one may refer to the book of Sambrook et al. (*Molecular Cloning: A Laboratory Manual*, 2nd edition, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, 1989).

Other regulatory elements:

Where a cDNA insert is employed, one will typically desire to include a polyadenylation signal to effect proper polyadenylation of the gene transcript. The nature of the polyadenylation signal is not believed to be crucial to the successful practice of the invention, and any such sequence may be employed such as human growth hormone and SV40 polyadenylation signals. Also contemplated as an element of the expression cassette is a terminator. These elements can serve to enhance message levels and to minimize read through from the cassette into other sequences.

The vector containing the appropriate DNA sequence as described above, more preferably MGST-II gene regulatory polynucleotide, a polynucleotide encoding the MGST-II polypeptides of SEQ ID Nos. 488 and 489 or both of them, can be utilized to transform an appropriate host to allow the expression of the desired polypeptide or polynucleotide.

3. Selectable markers

Such markers would confer an identifiable change to the cell permitting easy identification of cells containing the expression construct. The selectable marker genes for selection of transformed host cells are preferably dihydrofolate reductase or neomycin resistance for eukaryotic cell culture, TRP1 for *S. cerevisiae* or tetracycline, rifampicin or ampicillin resistance in *E. coli*, or levan saccharase for mycobacteria, this latter marker being a negative selection marker.

4. Preferred vectors

Bacterial vectors:

As a representative but non-limiting example, useful expression vectors for bacterial use can comprise a selectable marker and a bacterial origin of replication derived from commercially available plasmids comprising genetic elements of pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia, Uppsala, Sweden), and GEM1 (Promega Biotec, Madison, WI, USA). Large numbers of other suitable vectors are known to those of skill in the art, and commercially available, such as the following

bacterial vectors : pQE70, pQE60, pQE-9 (Qiagen), pbs, pD10, phagescript, psiX174, pbluescript SK, pbsks, pNH8A, pNH16A, pNH18A, pNH46A (Stratagene); ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia); pWLNEO, pSV2CAT, pOG44, pXT1, pSG (Stratagene); pSVK3, pBPV, pMSG, pSVL (Pharmacia); pQE-30 (QIAexpress).

Bacteriophage vectors

The P1 bacteriophage vector may contain large inserts ranging from about 80 to about 100 kb. The construction of P1 bacteriophage vectors such as p158 or p158/neo8 have been described by Sternberg (*Mamm. Genome*, 5:397-404, 1994). Recombinant P1 clones comprising MGST-II nucleotide sequences may be designed for inserting large polynucleotides of more than 40 kb (Linton et al., *J. Clin. Invest.*, 92:3029-3037, 1993). To generate P1 DNA for transgenic experiments, a preferred protocol is the protocol described by McCormick et al. (*Genet. Anal. Tech. Appl.*, 11:158-164, 1994). Briefly, *E. coli* (preferably strain NS3529) harboring the P1 plasmid are grown overnight in a suitable broth medium containing 25 µg/ml of kanamycin. The P1 DNA is prepared from the *E. coli* by alkaline lysis using the Qiagen Plasmid Maxi kit (Qiagen, Chatsworth, CA, USA), according to the manufacturer's instructions. The P1 DNA is purified from the bacterial lysate on two Qiagen-tip 500 columns, using the washing and elution buffers contained in the kit. A phenol/chloroform extraction is then performed before precipitating the DNA with 70% ethanol. After solubilizing the DNA in TE (10 mM Tris-HCl, pH 7.4, 1 mM EDTA), the concentration of the DNA is assessed by spectrophotometry.

When the goal is to express a P1 clone comprising MGST-II nucleotide sequences in a transgenic animal, typically in transgenic mice, it is desirable to remove vector sequences from the P1 DNA fragment, for example by cleaving the P1 DNA at rare-cutting sites within the P1 polylinker (*Sfi*I, *Not*I or *Sal*I). The P1 insert is then purified from vector sequences on a pulsed-field agarose gel, using methods similar using methods similar to those originally reported for the isolation of DNA from YACs (Schedl et al., 1993a; Peterson et al., 1993). At this stage, the resulting purified insert DNA can be concentrated, if necessary, on a Millipore Ultrafree-MC Filter Unit (Millipore, Bedford, MA, USA – 30,000 molecular weight limit) and then dialyzed against microinjection buffer (10 mM Tris-HCl, pH 7.4; 250 µM EDTA) containing 100 mM NaCl, 30 µM spermine, 70 µM spermidine on a microdyalisis membrane (type VS, 0.025 µM from Millipore). The intactness of the purified P1 DNA insert is assessed by electrophoresis on 1% agarose (Sea Kem GTG; FMC Bio-products) pulse-field gel and staining with ethidium bromide.

Baculovirus vectors:

A suitable vector for the expression of the MGST-II polypeptides of SEQ ID Nos. 488 and 489 is a baculovirus vector that can be propagated in insect cells and in insect cell lines. A specific suitable host vector system is the pVL1392/1393 baculovirus transfer vector (Pharmingen) that is used to transfect the SF9 cell line (ATCC N°CRL 1711) which is derived from *Spodoptera frugiperda*.

Other suitable vectors for the expression of the MGST-II polypeptides of SEQ ID Nos. 488 and 489 in a baculovirus expression system include those described by Chai et al. (*Biotech. Appl. Biochem.*, 18:259-273, 1993), Vlasak et al. (*Eur. J. Biochem.*, 135: 123-126, 1983) and Lenhard et al. (*Gene*, 169: 187-190, 1996).

Viral vectors

Retrovirus vectors and adeno-associated virus vectors are generally understood to be the recombinant gene delivery systems of choice for the transfer of exogenous polynucleotides *in vivo*, particularly to mammals, including humans. These vectors provide efficient delivery of genes into cells, and the transferred nucleic acids are stably integrated into the chromosomal DNA of the host.

Particularly preferred retroviruses for the preparation or construction of retroviral *in vitro* or *in vitro* gene delivery vehicles of the present invention include retroviruses selected from the group consisting of Mink-Cell Focus Inducing Virus, Murine Sarcoma Virus, Reticuloendotheliosis virus and Rous Sarcoma virus. Particularly preferred Murine Leukemia Viruses include the 4070A and the 1504A viruses, Abelson (ATCC No VR-999), Friend (ATCC No VR-245), Gross (ATCC No. VR-590), Rauscher (ATCC No VR-998) and Moloney Murine Leukemia Virus (ATCC No VR-190; PCT Application No WO 94/24298). Particularly preferred Rous Sarcoma Viruses include Bryan high titer (ATCC Nos. VR-334, VR-657, VR-726, VR-659 and VR-728). Other preferred retroviral vectors are those described in Roth et al. (*Nature Medicine*, 2:985-991, 1996), PCT Application No. WO 93/25234 and PCT Application No. WO 94/ 06920.

Yet another viral vector system that is contemplated by the invention consists in the adeno-associated virus (AAV). The adeno-associated virus is a naturally occurring defective virus that requires another virus, such as an adenovirus or a herpes virus, as a helper virus for efficient replication and a productive life cycle (Muzyczka et al., *Current Topics in Microbiol. Immunol.*, 158:97-129, 1992). It is also one of the few viruses that may integrate its DNA into non-dividing cells, and exhibits a high frequency of stable integration (McLaughlin et al., *Am. J. Hum. Genet.*, 59: 561-569, 1989). One advantageous feature of

AAV derives from its reduced efficacy for transducing primary cells relative to transformed cells.

BAC vectors:

The bacterial artificial chromosome (BAC) cloning system (Shizuya et al., 1992) has been developed to stably maintain large fragments of genomic DNA (100-300 kb) in *E. coli*. A preferred BAC vector consists of pBeloBAC11 vector that has been described by Kim et al. (*Genomics*, 34:213-218,1996). BAC libraries are prepared with this vector using size-selected genomic DNA that has been partially digested using enzymes that permit ligation into either the *Bam* HI or *Hind*III sites in the vector. Flanking these cloning sites are T7 and SP6 RNA polymerase transcription initiation sites that can be used to generate end probes by either RNA transcription or PCR methods. After the construction of a BAC library in *E. coli*, BAC DNA is purified from the host cell as a supercoiled circle. Converting these circular molecules into a linear form precedes both size determination and introduction of the BACs into recipient cells. The cloning site is flanked by two *Not* I sites, permitting cloned segments to be excised from the vector by *Not* I digestion. Alternatively, the DNA insert contained in the pBeloBAC11 vector may be linearized by treatment of the BAC vector with the commercially available enzyme lambda terminase that leads to the cleavage at the unique *cos*N site, but this cleavage method results in a full length BAC clone containing both the insert DNA and the BAC sequences.

5. Delivery of the recombinant vectors

In order to effect expression of the polynucleotides and polynucleotide constructs of the invention, these constructs must be delivered into a cell. This delivery may be accomplished *in vitro*, as in laboratory procedures for transforming cell lines, or *in vivo* or *ex vivo*, as in the treatment of certain diseases states. One mechanism is viral infection where the expression construct is encapsidated in an infectious viral particle. Several non-viral methods for the transfer of polynucleotides into cultured mammalian cells are also contemplated by the present invention, and include, without being limited to, calcium phosphate precipitation (Chen et al., *Proc. Natl. Acad. Sci. USA*, 94:10756-10761, 1987), DEAE-dextran (Gopal, *Mol. Cell. Biol.*, 5:1188-1190, 1985), electroporation (Tur-Kaspa et al., *Mol. Cell. Biol.*, 6:716-7181986), direct microinjection (Harland et al., 1985), DNA-loaded liposomes (Nicolau et al., 1982; Fraley et al., 1979), and receptor-mediate transfection (Wu and Wu, 1987; 1988). Some of these techniques may be successfully adapted for *in vivo* or *ex vivo* use.

Once the expression polynucleotide has been delivered into the cell, it may be stably integrated into the genome of the recipient cell. This integration may be in the cognate location and orientation via homologous recombination (gene replacement) or it may be integrated in a random, non-specific location (gene augmentation). In yet further embodiments, the nucleic acid may be stably maintained in the cell as a separate, episomal segment of DNA. Such nucleic acid segments or "episomes" encode sequences sufficient to permit maintenance and replication independent of or in synchronization with the host cell cycle.

One specific embodiment for a method for delivering a protein or peptide to the interior of a cell of a vertebrate *in vivo* comprises the step of introducing a preparation comprising a physiologically acceptable carrier and a naked polynucleotide operatively coding for the polypeptide of interest into the interstitial space of a tissue comprising the cell, whereby the naked polynucleotide is taken up into the interior of the cell and has a physiological effect. This is particularly applicable for transfer *in vitro* but it may be applied to *in vivo* as well.

Compositions for use *in vitro* and *in vivo* comprising a "naked" polynucleotide are described in PCT application No. WO 90/11092 (Vical Inc.) and also in PCT application No. WO 95/11307.

In still another embodiment of the invention, the transfer of a naked polynucleotide of the invention, including a polynucleotide construct of the invention, into cells may be proceeded with a particle bombardment (biolistic), said particles being DNA-coated microprojectiles accelerated to a high velocity allowing them to pierce cell membranes and enter cells without killing them, such as described by Klein et al. (*Nature* 327:70-73, 1987).

In a further embodiment, the polynucleotide of the invention may be entrapped in a liposome (Ghosh and Bacchawat, *Targeting of liposomes to hepatocytes, In: Liver Diseases, Targeted diagnosis and therapy using specific rceptors and ligands,* Marcel Dekeker, New York, 87-104, 1991; Wong et al., *Gene* 10:87-94, 1980; Nicolau et al., *Biochim. Biophys. Acta.* 721:185-190, 1982).

In a specific embodiment, the invention provides a composition for the *in vivo* production of the MGST-II protein or polypeptide described herein. It comprises a naked polynucleotide operatively coding for this polypeptide, in solution in a physiologically acceptable carrier, and suitable for introduction into a tissue to cause cells of the tissue to express the said protein or polypeptide.

The amount of vector to be injected to the desired host organism varies according to the site of injection. As an indicative dose, it will be injected between 0.1 and 100 μg of the vector in an animal body, preferably a mammal body, for example a mouse body.

In another embodiment of the invention, the vector may be introduced *in vitro* in a host cell, preferably in a host cell previously harvested from the animal to be treated and more preferably a somatic cell such as a muscle cell. In a subsequent step, the cell that has been transformed with the vector coding for the desired MGST-II polypeptide or the desired fragment thereof is reintroduced into the animal body in order to deliver the recombinant protein within the body either locally or systemically.

Host Cells

Another embodiment of the invention consists of a host cell that has been transformed or transfected with one of the polynucleotides described therein, and more precisely a polynucleotide either comprising a MGST-II regulatory polynucleotide or the coding sequence of the MGST-II polypeptide having the amino acid sequence of SEQ ID Nos. 488 and 489. The embodiment includes host cells that are transformed (prokaryotic cells) or that are transfected (eukaryotic cells) with a recombinant vector such as one of those described above. Generally, a recombinant host cell of the invention comprises any one of the polynucleotides or the recombinant vectors described therein.

A preferred recombinant host cell according to the invention comprises a polynucleotide selected from the following group of polynucleotides :

a) a purified or isolated nucleic acid encoding a MGST-II polypeptide, or a polypeptide fragment or variant thereof.

b) a purified or isolated nucleic comprising at least 8, preferably at least 15, more preferably at least 25, consecutive nucleotides of the nucleotide sequence SEQ ID No. 485, a nucleotide sequence complementary thereto, or a variant thereof.

c) a purified or isolated nucleic acid comprising at least 8 consecutive nucleotides, preferably at least 15, more preferably at least 25 of the nucleotide sequence SEQ ID Nos. 486 and 487, a nucleotide sequence complementary thereto or a variant thereof.

d) a purified or isolated nucleic acid comprising an exon of the MGST-II gene, a sequence complementary thereto or a fragment or a variant thereof.

e) a purified or isolated nucleic acid comprising a combination of at least two exons of the MGST-II gene, or the sequences complementary thereto wherein the polynucleotides are arranged within the nucleic acid, from the 5' end to the 3'end of said nucleic acid, in the same order than in SEQ ID No. 485.

f) a purified or isolated nucleic acid comprising the nucleotide sequence SEQ ID No. 485 or the sequences complementary thereto or a biologically active fragment thereof.

g) a purified or isolated nucleic acid comprising the nucleotide sequence SEQ ID No. 486, or the sequence complementary thereto or a biologically active fragment thereof.

h) a polynucleotide consisting of:

(1) a nucleic acid comprising a regulatory polynucleotide of SEQ ID No. 485 or the sequences complementary thereto or a biologically active fragment thereof

(2) a polynucleotide encoding a desired polypeptide or nucleic acid.

(3) Optionally, a nucleic acid comprising a regulatory polynucleotide of SEQ ID No. 485, or the sequence complementary thereto or a biologically active fragment thereof.

i) a DNA construct as described previously in the present specification.

Another preferred recombinant cell host according to the present invention is characterized in that its genome or genetic background (including chromosome, plasmids) is modified by the nucleic acid coding for the MGST-II polypeptide of SEQ ID Nos. 488 and 489 or fragments or variants thereof.

Preferred host cells used as recipients for the expression vectors of the invention are the following:

a) Prokaryotic host cells: *Escherichia coli* strains (I.E. DH5-α strain), *Bacillus subtilis*, *Salmonella typhimurium*, and strains from species like *Pseudomonas*, *Streptomyces* and *Staphylococcus*..

b) Eukaryotic host cells: HeLa cells (ATCC N°CCL2; N°CCL2.1; N°CCL2.2), Cv 1 cells (ATCC N°CCL70), COS cells (ATCC N°CRL1650; N°CRL1651), Sf-9 cells (ATCC N°CRL1711), C127 cells (ATCC N° CRL-1804), 3T3 (ATCC N° CRL-6361), CHO (ATCC N° CCL-61), human kidney 293.(ATCC N° 45504; N° CRL-1573) and BHK (ECACC N° 84100501; N° 84111301)

c) Other mammalian host cells:

The MGST-II gene expression in mammalian, and typically human, cells may be rendered defective, or alternatively it may be proceeded with the insertion of a MGST-II genomic or cDNA sequence with the replacement of the MGST-II gene counterpart in the genome of an animal cell by a MGST-II polynucleotide according to the invention. These genetic alterations may be generated by homologous recombination events using specific DNA constructs that have been previously described.

One kind of cell hosts that may be used are mammal zygotes, such as murine zygotes. For example, murine zygotes may undergo microinjection with a purified DNA

molecule of interest, for example a purified DNA molecule that has previously been adjusted to a concentration range from 1 ng/ml (for BAC inserts) 3 ng/μl (for P1 bacteriophage inserts) in 10 mM Tris-HCl, pH 7.4, 250 μM EDTA containing 100 mM NaCl, 30 μM spermine, and70 μM spermidine. When the DNA to be microinjected has a large size, polyamines and high salt concentrations can be used in order to avoid mechanical breakage of this DNA, as described by Schedl et al (*Nucleic Acids Res.* 21:4783-4787, 1993).

Anyone of the polynucleotides of the invention, including the DNA constructs described herein, may be introduced in an embryonic stem (ES) cell line, preferably a mouse ES cell line. ES cell lines are derived from pluripotent, uncommitted cells of the inner cell mass of pre-implantation blastocysts. Preferred ES cell lines are the following: ES-E14TG2a (ATCC n° CRL-1821), ES-D3 (ATCC n° CRL1934 and n° CRL-11632), YS001 (ATCC n° CRL-11776), 36.5 (ATCC n° CRL-11116). To maintain ES cells in an uncommitted state, they are cultured in the presence of growth inhibited feeder cells which, provide the appropriate signals to preserve this embryonic phenotype and serve as a matrix for ES cell adherence. Preferred feeder cells consist of primary embryonic fibroblasts that are established from tissue of day 13- day 14 embryos of virtually any mouse strain, that are maintained in culture, such as described by Abbondanzo et al. (*Methods in Enzymology*, Academic Press, NewYork, 803-823, 1993) and are inhibited in growth by irradiation, such as described by Robertson ("Embryo-Derived StemCell Lines," *E.J. Robertson Ed..Teratocarcinomas and Embrionic Stem Cells: A Practical Approach*. IRL Press, Oxford, 71, 1987), or by the presence of an inhibitory concentration of LIF, such as described by Pease and Williams (*Exp. Cell. Res.* 190:09-211, 1990).

The constructs in the host cells can be used in a conventional manner to produce the gene product encoded by the recombinant sequence.

Following transformation of a suitable host and growth of the host to an appropriate cell density, the selected promoter is induced by appropriate means, such as temperature shift or chemical induction, and cells are cultivated for an additional period.

Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

Microbial cells employed in the expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents. Such methods are well known by one skilled in the art.

Transgenic animals

The terms "transgenic animals" or "host animals" are used herein designate animals that have their genome genetically and artificially manipulated so as to include one of the nucleic acids according to the invention. Preferred animals are non-human mammals and include those belonging to a genus selected from *Mus* (e.g. mice), *Rattus* (e.g. rats) and *Oryctogalus* (e.g. rabbits) which have their genome artificially and genetically altered by the insertion of a nucleic acid according to the invention.

The transgenic animals of the invention all include within a plurality of their cells a cloned recombinant or synthetic DNA sequence, more specifically one of the purified or isolated nucleic acids comprising a MGST-II coding sequence, a MGST-II regulatory polynucleotide or a DNA sequence encoding an antisense polynucleotide such as described in the present specification.

Preferred transgenic animals according to the invention contains in their somatic cells and/or in their germ line cells a polynucleotide selected from the following group of polynucleotides :

a) a purified or isolated nucleic acid encoding a MGST-II polypeptide, or a polypeptide fragment or variant thereof.

b) a purified or isolated nucleic comprising at least 8, preferably at least 15, more preferably at least 25, consecutive nucleotides of the nucleotide sequence SEQ ID No. 485, a nucleotide sequence complementary thereto.

c) a purified or isolated nucleic acid comprising at least 8 consecutive nucleotides, preferably at least 15, more preferably at least 25 of the nucleotide sequence SEQ ID Nos. 486 and 487, a nucleotide sequence complementary thereto.

d) a purified or isolated nucleic acid comprising an exon of the MGST-II gene, a sequence complementary thereto or a fragment or a variant thereof.

e) a purified or isolated nucleic acid comprising a combination of at least two exons of the MGST-II gene, or the sequences complementary thereto wherein the polynucleotides are arranged within the nucleic acid, from the 5' end to the 3'end of said nucleic acid, in the same order than in SEQ ID No. 485.

f) a purified or isolated nucleic acid comprising the nucleotide sequence SEQ ID No. 485 or the sequences complementary thereto or a biologically active fragment thereof.

g) a purified or isolated nucleic acid comprising the nucleotide sequence SEQ ID No. 486, or the sequence complementary thereto or a biologically active fragment thereof.

h) a polynucleotide consisting of :

(1) a nucleic acid comprising a regulatory polynucleotide of SEQ ID No. 485 or the sequences complementary thereto or a biologically active fragment thereof

(2) a polynucleotide encoding a desired polypeptide or nucleic acid.

(3) Optionally, a nucleic acid comprising a regulatory polynucleotide of SEQ ID No. 486, or the sequence complementary thereto or a biologically active fragment thereof.

i) a DNA construct as described previously in the present specification.

The transgenic animals of the invention thus contain specific sequences of exogenous genetic material such as the nucleotide sequences described above in detail.

In a first preferred embodiment, these transgenic animals may be good experimental models in order to study the diverse pathologies related to cell differentiation, in particular concerning the transgenic animals within the genome of which has been inserted one or several copies of a polynucleotide encoding a native MGST-II protein, or alternatively a mutant MGST-II protein.

In a second preferred embodiment, these transgenic animals may express a desired polypeptide of interest under the control of the regulatory polynucleotides of the MGST-II gene, leading to good yields in the synthesis of this protein of interest, and eventually a tissue specific expression of this protein of interest.

The design of the transgenic animals of the invention may be made according to the conventional techniques well known from the one skilled in the art. For more details regarding the production of transgenic animals, and specifically transgenic mice, it may be referred to US Patents Nos. 4,873,191, issued October10, 1989, 5,464,764 issued November 7, 1995 and 5,789,215, issued August 4, 1998, these documents being herein incorporated by reference to disclose methods producing transgenic mice.

Transgenic animals of the present invention are produced by the application of procedures which result in an animal with a genome that has incorporated exogenous genetic material. The procedure involves obtaining the genetic material, or a portion thereof, which encodes either a MGST-II coding sequence, a MGST-II regulatory polynucleotide or a DNA sequence encoding a MGST-II antisense polynucleotide such as described in the present specification.

A recombinant polynucleotide of the invention is inserted into an embryonic or ES stem cell line. The insertion is preferably made using electroporation, such as described by Thomas et al. (*Cell* 51:503-512, 1987). The cells subjected to electroporation are screened (e.g. by selection via selectable markers, by PCR or by Southern blot analysis) to find positive cells which have integrated the exogenous recombinant polynucleotide into their

genome, preferably via an homologous recombination event. An illustrative positive-negative selection procedure that may be used according to the invention is described by Mansour et al. (*Nature* 336:348-352, 1988).

Then, the positive cells are isolated, cloned and injected into 3.5 days old blastocysts from mice, such as described by Bradley ("Production and Analysis of Chimaeric Mice," *E.J. Robertson (Ed.), Teratocarcinomas and embryonic stem cells: A practical approach* IRL Press, Oxford, 113, 1987). The blastocysts are then inserted into a female host animal and allowed to grow to term.

Alternatively, the positive ES cells are brought into contact with embryos at the 2.5 days old 8-16 cell stage (morulae) such as described by Wood et al. (*Proc. Natl. Acad. Sci. U.S.A.* 90:4582-4585, 1993) or by Nagy et al. (*Proc. Natl. Acad. Sci. USA.* 90: 8424-8428, 1993), the ES cells being internalized to colonize extensively the blastocyst including the cells which will give rise to the germ line.

The offspring of the female host are tested to determine which animals are transgenic e.g. include the inserted exogenous DNA sequence and which are wild-type.

Thus, the present invention also concerns a transgenic animal containing a nucleic acid, a recombinant expression vector or a recombinant host cell according to the invention.

A further object of the invention consists of recombinant host cells obtained from a transgenic animal described herein.

Recombinant cell lines may be established *in vitro* from cells obtained from any tissue of a transgenic animal according to the invention, for example by transfection of primary cell cultures with vectors expressing *onc*-genes such as SV40 large T antigen, as described by Chou (*Mol. Endocrinol.* 3:1511-1514, 1989) and Shay et al. (*Biochem. Biophys. Acta.* 1072:1-7, 1991).

I.E. MGST-II Polypeptides

The term "MGST-II polypeptides" is used herein to embrace all of the proteins and polypeptides of the present invention. Also forming part of the invention are polypeptides encoded by the polynucleotides of the invention, as well as fusion polypeptides comprising such polypeptides. The invention embodies MGST-II proteins from humans, including isolated or purified MGST-II proteins consisting, consisting essentially, or comprising the sequence of SEQ ID Nos. 488 and 489. It should be noted the MGST-II proteins of the invention are based on the naturally-occurring variants of the amino acid sequence of human MGST-II.

In a first embodiment, the present invention provides a variant MGST-II protein; wherein the Tyr residue of amino acid position 93 has been replaced with a His residue. Variant proteins and the fragments thereof which contain amino acid position 93 are collectively referred to herein as "93-His variants." More particularly, the present invention embodies isolated, purified, and recombinant polypeptides comprising a contiguous span of at least 6 amino acids, preferably at least 8 to 10 amino acids, more preferably at least 12, 15, 20, 25, 30, 40, 50, or 100 amino acids of SEQ ID No. 488, wherein said contiguous span comprises a His residue at amino acid position 93. In this amino acid substitution the original residue (Tyr) is replaced by a non-equivalent amino acid (His) presenting different chemical properties.

The present invention further provides another naturally-occurring variant of the MGST-II protein that consists or consists essentially of amino acids 1-109 of SEQ ID No. 488. This variant MGST-II polypeptide corresponds to one allele of biallelic marker 10-290-37.

Another naturally-occurring variant of the MGST-II protein of the present invention is encoded by a cDNA obtained by alternative splicing. MGST-II cDNAs and cDNA variants are further described above. This variant polypeptide of a sequence from SEQ ID No. 489 is identical to the MGST-II protein of SEQ ID No. 488 from amino acid position 1 to amino acid position 19 but comprises 11 additional amino acids. The present invention embodies isolated, purified, and recombinant polypeptides comprising, consisting of or consisting essentially of an amino acid sequence from SEQ ID No. 489. Moreover, the present invention embodies isolated, purified, and recombinant polypeptides comprising a contiguous span of at least 6 amino acids, preferably at least 8 to 10 amino acids, more preferably at least 12, 15, 20, 25, or 30 amino acids of SEQ ID No. 489, wherein said contiguous span comprises a least one of amino acid positions 20 to 30 of SEQ ID No. 489.

All the variant MGST-II polypeptides described above most probably show alterations in the activity, specificity and function of the MGST-II enzyme. In preferred embodiments the polypeptides of the present invention comprise the site of a mutation or functional mutation, including a deletion, substitution or truncation in the amino acid sequence in the MGST-II protein.

MGST-II proteins are preferably isolated from human or mammalian tissue samples or expressed from human or mammalian genes. The MGST-II polypeptides of the invention can be made using routine expression methods known in the art. The polynucleotide encoding the desired polypeptide, is ligated into an expression vector suitable for any

convenient host. Both eukaryotic and prokaryotic host systems are used in forming recombinant polypeptides. The polypeptide is then isolated from lysed cells or from the culture medium and purified to the extent needed for its intended use. Purification is by any technique known in the art, for example, differential extraction, salt fractionation, chromatography, centrifugation, and the like. See, for example, Methods in Enzymology for a variety of methods for purifying proteins.

In addition, shorter protein fragments are produced by chemical synthesis. Alternatively the proteins of the invention are extracted from cells or tissues of humans or non-human animals. Methods for purifying proteins are known in the art, and include the use of detergents or chaotropic agents to disrupt particles followed by differential extraction and separation of the polypeptides by ion exchange chromatography, affinity chromatography, sedimentation according to density, and gel electrophoresis.

Any MGST-II cDNA of the invention is used to express MGST-II proteins and polypeptides. The nucleic acid encoding the MGST-II protein or polypeptide to be expressed is operably linked to a promoter in an expression vector using conventional cloning technology. The MGST-II insert in the expression vector may comprise the full coding sequence for the MGST-II protein or a portion thereof. For example, the MGST-II derived insert may encode a polypeptide comprising a contiguous span of at least 6 amino acids, preferably at least 8 to 10 amino acids, more preferably at least 12, 15, 20, 25, 30, 40, 50, or 100 amino acids of SEQ ID No. 488, wherein said contiguous span comprises a His residue at amino acid position 93. The MGST-II derived insert may further encode a polypeptide comprising, consisting of or consisting essentially of an amino acid sequence from amino acid positions 1-108 of SEQ ID No. 488. The MGST-II derived insert may further encode a polypeptide comprising, consisting of or consisting essentially of an amino acid sequence from SEQ ID No. 489. The MGST-II derived insert may also encode a polypeptide comprising a contiguous span of at least 6 amino acids, preferably at least 8 to 10 amino acids, more preferably at least 12, 15, 20, 25,or 30 amino acids of SEQ ID No. 489, wherein said contiguous span comprises a least one of amino acid positions 20 to 30 of SEQ ID No. 489.

The expression vector is any of the mammalian, yeast, insect or bacterial expression systems known in the art. Commercially available vectors and expression systems are available from a variety of suppliers including Genetics Institute (Cambridge, MA), Stratagene (La Jolla, California), Promega (Madison, Wisconsin), and Invitrogen (San Diego, California). If desired, to enhance expression and facilitate proper protein folding, the codon context and

codon pairing of the sequence is optimized for the particular expression organism in which the expression vector is introduced, as explained by Hatfield, et al., U.S. Patent No. 5,082,767.

In one embodiment, the entire coding sequence of the MGST-II cDNA through the poly A signal of the cDNA is operably linked to a promoter in the expression vector. Alternatively, if the nucleic acid encoding a portion of the MGST-II protein lacks a methionine to serve as the initiation site, an initiating methionine can be introduced next to the first codon of the nucleic acid using conventional techniques. Similarly, if the insert from the MGST-II cDNA lacks a poly A signal, this sequence can be added to the construct by, for example, splicing out the Poly A signal from pSG5 (Stratagene) using BglI and SalI restriction endonuclease enzymes and incorporating it into the mammalian expression vector pXT1 (Stratagene). pXT1 contains the LTRs and a portion of the gag gene from Moloney Murine Leukemia Virus. The position of the LTRs in the construct allow efficient stable transfection. The vector includes the Herpes Simplex Thymidine Kinase promoter and the selectable neomycin gene. The nucleic acid encoding the MGST-II protein or a portion thereof is obtained by PCR from a bacterial vector containing a MGST-II cDNA of the present invention using oligonucleotide primers complementary to the MGST-II cDNA or portion thereof and containing restriction endonuclease sequences for Pst I incorporated into the 5'primer and BglII at the 5' end of the corresponding cDNA 3' primer, taking care to ensure that the sequence encoding the MGST-II protein or a portion thereof is positioned properly with respect to the poly A signal. The purified fragment obtained from the resulting PCR reaction is digested with PstI, blunt ended with an exonuclease, digested with Bgl II, purified and ligated to pXT1, now containing a poly A signal and digested with BglII.

The ligated product is transfected into mouse NIH 3T3 cells using Lipofectin (Life Technologies, Inc., Grand Island, New York) under conditions outlined in the product specification. Positive transfectants are selected after growing the transfected cells in 600ug/ml G418 (Sigma, St. Louis, Missouri).

Alternatively, the nucleic acids encoding the MGST-II protein or a portion thereof is cloned into pED6dpc2 (Genetics Institute, Cambridge, MA). The resulting pED6dpc2 constructs is transfected into a suitable host cell. such as COS 1 cells. Methotrexate resistant cells are selected and expanded.

The above procedures may also be used to express a mutant MGST-II protein responsible for a detectable phenotype or a portion thereof.

The expressed proteins are purified using conventional purification techniques such as ammonium sulfate precipitation or chromatographic separation based on size or charge. The

protein encoded by the nucleic acid insert may also be purified using standard immunochromatography techniques. In such procedures, a solution containing the expressed MGST-II protein or portion thereof, such as a cell extract, is applied to a column having antibodies against the MGST-II protein or portion thereof is attached to the chromatography matrix. The expressed protein is allowed to bind the immunochromatography column. Thereafter, the column is washed to remove non-specifically bound proteins. The specifically bound expressed protein is then released from the column and recovered using standard techniques.

To confirm expression of the MGST-II protein or a portion thereof, the proteins expressed from host cells containing an expression vector containing an insert encoding the MGST-II protein or a portion thereof can be compared to the proteins expressed in host cells containing the expression vector without an insert. The presence of a band in samples from cells containing the expression vector with an insert which is absent in samples from cells containing the expression vector without an insert indicates that the MGST-II protein or a portion thereof is being expressed. Generally, the band will have the mobility expected for the MGST-II protein or portion thereof. However, the band may have a mobility different than that expected as a result of modifications such as glycosylation, ubiquitination, or enzymatic cleavage.

Antibodies capable of specifically recognizing the expressed MGST-II protein or a portion thereof, are described below.

If antibody production is not possible, the nucleic acids encoding the MGST-II protein or a portion thereof is incorporated into expression vectors designed for use in purification schemes employing chimeric polypeptides. In such strategies the nucleic acid encoding the MGST-II protein or a portion thereof is inserted in frame with the gene encoding the other half of the chimera. The other half of the chimera is β-globin or a nickel binding polypeptide encoding sequence. A chromatography matrix having antibody to β-globin or nickel attached thereto is then used to purify the chimeric protein. Protease cleavage sites is engineered between the β-globin gene or the nickel binding polypeptide and the MGST-II protein or portion thereof. Thus, the two polypeptides of the chimera are separated from one another by protease digestion.

One useful expression vector for generating β-globin chimerics is pSG5 (Stratagene), which encodes rabbit β-globin. Intron II of the rabbit β-globin gene facilitates splicing of the expressed transcript, and the polyadenylation signal incorporated into the construct increases the level of expression. These techniques are well known to those skilled in the art of

molecular biology. Standard methods are published in methods texts such as Davis et al., (Basic Methods in Molecular Biology, L.G. Davis, M.D. Dibner, and J.F. Battey, ed., Elsevier Press, NY, 1986) and many of the methods are available from Stratagene, Life Technologies, Inc., or Promega. Polypeptide may additionally be produced from the construct using in vitro translation systems such as the In vitro Express^{TM} Translation Kit (Stratagene).

I.F. Production of Antibodies Against MGST-II Polypeptides

Any MGST-II polypeptide or whole protein may be used to generate antibodies capable of specifically binding to expressed MGST-II protein or fragments thereof or variants thereof. Preferably the antibody compositions of the invention are capable of specifically binding to the 93-His variant of the MGST-II protein. Alternatively the antibody compositions of the present invention are capable of specifically binding the variant MGST-II polypeptide of SEQ ID No. 489. A preferred embodiment of the invention encompasses isolated or purified antibody compositions capable of selectively binding, or which are capable of binding to an epitope-containing fragment of a polypeptide of the invention, wherein said epitope comprises at least one amino acid position selected from the group consisting of His residue at amino acid position 93 of SEQ ID No. 488 and of amino acid positions 20-30 of SEQ ID No. 489. For an antibody composition to specifically bind to these MGST-II variants it must demonstrate at least a 5%, 10%, 15%, 20%, 25%, 50%, or 100% greater binding affinity for full length MGST-II variants in an ELISA, RIA, or other antibody-based binding assay than to full length MGST-II protein described in SEQ ID No. 488. Affinity of the antibody composition for the epitope can further be determined by preparing competitive binding curves, as described, for example, by Fisher, D. (Chap. 42 in: Manual of Clinical Immunology, 2d Ed. (Rose and Friedman,Eds.) *Amer. Soc. For Microbiol.*, Washington, D.C., 1980).

The present invention also contemplates the use of variant MGST-II polypeptides in the manufacture of antibodies. In a preferred embodiment such polypeptides are useful in the manufacture of antibodies to detect the presence and absence of the 93-His variant and of the MGST-II variant of SEQ ID No. 489.

Non-human animals or mammals, whether wild-type or transgenic, which express a different species of MGST-II than the one to which antibody binding is desired, and animals which do not express MGST-II (i.e. an MGST-II knock out animal as described in herein) are particularly useful for preparing antibodies. MGST-II knock out animals will recognize all or most of the exposed regions of MGST-II as foreign antigens, and therefore produce antibodies with a wider array of MGST-II epitopes. Moreover, smaller polypeptides with

only 10 to 30 amino acids may be useful in obtaining specific binding to the 93-His variant and to the MGST-II variant of SEQ ID No. 489. In addition, the humoral immune system of animals which produce a species of MGST-II that resembles the antigenic sequence will preferentially recognize the differences between the animal's native MGST-II species and the antigen sequence, and produce antibodies to these unique sites in the antigen sequence. Such a technique will be particularly useful in obtaining antibodies that specifically bind to the 93-His variant and to the MGST-II variant of SEQ ID No. 489. The preparation of antibody compositions is further described in Example 6.

Antibody preparations prepared according to the present invention are useful in quantitative immunoassays which determine concentrations of antigen-bearing substances in biological samples; they are also used semi-quantitatively or qualitatively to identify the presence of antigen in a biological sample. The antibodies may also be used in therapeutic compositions for killing cells expressing the protein or reducing the levels of the protein in the body. The antibodies of the invention may be labeled, either by a radioactive, a fluorescent or an enzymatic label. Consequently, the invention is also directed to a method for detecting specifically the presence of a variant MGST-II polypeptide according to the invention in a biological sample, said method comprising the following steps : a) bringing into contact the biological sample with a polyclonal or monoclonal antibody that specifically binds a variant MGST-II polypeptide or to a peptide fragment or variant thereof; and b) detecting the antigen-antibody complex formed. The invention also concerns a diagnostic kit for detecting *in vitro* the presence of a variant MGST-II polypeptide according to the present invention in a biological sample, wherein said kit comprises: a) a polyclonal or monoclonal antibody that specifically binds a variant MGST-II polypeptide or to a peptide fragment or variant thereof, optionally labeled; b) a reagent allowing the detection of the antigen-antibody complexes formed, said reagent carrying optionally a label, or being able to be recognized itself by a labeled reagent, more particularly in the case when the above-mentioned monoclonal or polyclonal antibody is not labeled by itself.

II. Methods for *De Novo* Identification of Biallelic Markers

Large fragments of human DNA, carrying genes of interest involved in the biotransformation of xenobiotics such as therapeutic drugs; were cloned, sequenced and screened for biallelic markers. Biallelic markers within the candidate genes themselves as well as markers located on the same genomic fragment were identified. It will be clear to one of skill in the art that large fragments of human genomic DNA may be obtained from any appropriate source and may be cloned into a number of suitable vectors.

In a preferred embodiment of the invention, BAC (Bacterial Artificial Chromosomes) vectors were used to construct DNA libraries covering the entire human genome. Specific amplification primers were designed for each candidate gene and the BAC library was screened by PCR until there was at least one positive BAC clone per candidate gene. Genomic sequence, screened for biallelic markers, was generated by sequencing ends of BAC subclones. Details of a preferred embodiment are provided in Example 1. As a preferred alternative to sequencing the ends of an adequate number of BAC subclones, high throughput deletion-based sequencing vectors, which allow the generation of a high quality sequence information covering fragments of about 6kb, may be used. Having sequence fragments longer than 2.5 or 3kb enhances the chances of identifying biallelic markers therein. Methods of constructing and sequencing a nested set of deletions are disclosed in the related U.S. Patent Application entitled "High Throughput DNA Sequencing Vector" (Serial No. 09/058,746).

In another embodiment of the invention, genomic sequences of candidate genes were available in public databases allowing direct screening for biallelic markers.

Any of a variety of methods can be used to screen a genomic fragment for single nucleotide polymorphisms such as differential hybridization with oligonucleotide probes, detection of changes in the mobility measured by gel electrophoresis or direct sequencing of the amplified nucleic acid. A preferred method for identifying biallelic markers involves comparative sequencing of genomic DNA fragments from an appropriate number of unrelated individuals.

In a first embodiment, DNA samples from unrelated individuals are pooled together, following which the genomic DNA of interest is amplified and sequenced. The nucleotide sequences thus obtained are then analyzed to identify significant polymorphisms. One of the major advantages of this method resides in the fact that the pooling of the DNA samples substantially reduces the number of DNA amplification reactions and sequencing reactions, which must be carried out. Moreover, this method is sufficiently sensitive so that a biallelic marker obtained thereby usually demonstrates a sufficient frequency of its less common allele to be useful in conducting association studies. Usually, the frequency of the least common allele of a biallelic marker identified by this method is at least 10%.

In a second embodiment, the DNA samples are not pooled and are therefore amplified and sequenced individually. This method is usually preferred when biallelic markers need to be identified in order to perform association studies within candidate genes. Preferably, highly relevant gene regions such as promoter regions or exon regions may be

screened for biallelic markers. A biallelic marker obtained using this method may show a lower degree of informativeness for conducting association studies, e.g. if the frequency of its less frequent allele may be less than about 10%. Such a biallelic marker will however be sufficiently informative to conduct association studies and it will further be appreciated that including less informative biallelic markers in the genetic analysis studies of the present invention, may allow in some cases the direct identification of causal mutations, which may, depending on their penetrance, be rare mutations.

The following is a description of the various parameters of a preferred method used by the inventors for the identification of the biallelic markers of the present invention.

II.A. Genomic DNA Samples

The genomic DNA samples from which the biallelic markers of the present invention are generated are preferably obtained from unrelated individuals corresponding to a heterogeneous population of known ethnic background. The number of individuals from whom DNA samples are obtained can vary substantially, preferably from about 10 to about 1000, more preferably from about 50 to about 200 individuals. Usually, DNA samples are collected from at least about 100 individuals in order to have sufficient polymorphic diversity in a given population to identify as many markers as possible and to generate statistically significant results.

As for the source of the genomic DNA to be subjected to analysis, any test sample can be foreseen without any particular limitation. These test samples include biological samples, which can be tested by the methods of the present invention described herein, and include human and animal body fluids such as whole blood, serum, plasma, cerebrospinal fluid, urine, lymph fluids, and various external secretions of the respiratory, intestinal and genitourinary tracts, tears, saliva, milk, white blood cells, myelomas and the like; biological fluids such as cell culture supernatants; fixed tissue specimens including tumor and non-tumor tissue and lymph node tissues; bone marrow aspirates and fixed cell specimens. The preferred source of genomic DNA used in the present invention is from peripheral venous blood of each donor. Techniques to prepare genomic DNA from biological samples are well known to the skilled technician. Details of a preferred embodiment are provided in Example 1. The person skilled in the art can choose to amplify pooled or unpooled DNA samples.

II.B. DNA Amplification

The identification of biallelic markers in a sample of genomic DNA may be facilitated through the use of DNA amplification methods. DNA samples can be pooled or

unpooled for the amplification step. DNA amplification techniques are well known to those skilled in the art. Various methods to amplify DNA fragments carrying biallelic markers are further described hereinafter in III.B. The PCR technology is the preferred amplification technique used to identify new biallelic markers.

In a first embodiment, biallelic markers are identified using genomic sequence information generated by the inventors. Genomic DNA fragments, such as the inserts of the BAC clones described above, are sequenced and used to design primers for the amplification of 500 bp fragments. These 500 bp fragments are amplified from genomic DNA and are scanned for biallelic markers. Primers may be designed using the OSP software (Hillier L. and Green P., 1991). All primers may contain, upstream of the specific target bases, a common oligonucleotide tail that serves as a sequencing primer. Those skilled in the art are familiar with primer extensions, which can be used for these purposes.

In another embodiment of the invention, genomic sequences of candidate genes are available in public databases allowing direct screening for biallelic markers. Preferred primers, useful for the amplification of genomic sequences encoding the candidate genes, focus on promoters, exons and splice sites of the genes. A biallelic marker present in these functional regions of the gene have a higher probability to be a causal mutation.

Preferred primers include those disclosed in Figure 7.

II.C. Sequencing of Amplified Genomic DNA and Identification of Single Nucleotide Polymorphisms

The amplification products generated as described above, are then sequenced using any method known and available to the skilled technician. Methods for sequencing DNA using either the dideoxy-mediated method (Sanger method) or the Maxam-Gilbert method are widely known to those of ordinary skill in the art. Such methods are for example disclosed in Maniatis et al. (Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Second Edition, 1989). Alternative approaches include hybridization to high-density DNA probe arrays as described in Chee et al. (*Science* 274, 610, 1996).

Preferably, the amplified DNA is subjected to automated dideoxy terminator sequencing reactions using a dye-primer cycle sequencing protocol. The products of the sequencing reactions are run on sequencing gels and the sequences are determined using gel image analysis. The polymorphism search is based on the presence of superimposed peaks in the electrophoresis pattern resulting from different bases occurring at the same position. Because each dideoxy terminator is labeled with a different fluorescent molecule, the two peaks corresponding to a biallelic site present distinct colors corresponding to two different

nucleotides at the same position on the sequence. However, the presence of two peaks can be an artifact due to background noise. To exclude such an artifact, the two DNA strands are sequenced and a comparison between the peaks is carried out. In order to be registered as a polymorphic sequence, the polymorphism has to be detected on both strands.

The above procedure permits those amplification products, which contain biallelic markers to be identified. The detection limit for the frequency of biallelic polymorphisms detected by sequencing pools of 100 individuals is approximately 0.1 for the minor allele, as verified by sequencing pools of known allelic frequencies. However, more than 90% of the biallelic polymorphisms detected by the pooling method have a frequency for the minor allele higher than 0.25. Therefore, the biallelic markers selected by this method have a frequency of at least 0.1 for the minor allele and less than 0.9 for the major allele. Preferably at least 0.2 for the minor allele and less than 0.8 for the major allele, more preferably at least 0.3 for the minor allele and less than 0.7 for the major allele, thus a heterozygosity rate higher than 0.18, preferably higher than 0.32, more preferably higher than 0.42.

In another embodiment, biallelic markers are detected by sequencing individual DNA samples, the frequency of the minor allele of such a biallelic marker may be less than 0.1.

The markers carried by the same fragment of genomic DNA, such as the insert in a BAC clone, need not necessarily be ordered with respect to one another within the genomic fragment to conduct association studies. However, in some embodiments of the present invention, the order of biallelic markers carried by the same fragment of genomic DNA are determined.

II.D. Validation of the Biallelic Markers of the Present Invention

The polymorphisms are evaluated for their usefulness as genetic markers by validating that both alleles are present in a population. Validation of the biallelic markers is accomplished by genotyping a group of individuals by a method of the invention and demonstrating that both alleles are present. Microsequencing is a preferred method of genotyping alleles. The validation by genotyping step may be performed on individual samples derived from each individual in the group or by genotyping a pooled sample derived from more than one individual. The group can be as small as one individual if that individual is heterozygous for the allele in question. Preferably the group contains at least three individuals, more preferably the group contains five or six individuals, so that a single validation test will be more likely to result in the validation of more of the biallelic markers

that are being tested. It should be noted, however, that when the validation test is performed on a small group it may result in a false negative result if as a result of sampling error none of the individuals tested carries one of the two alleles. Thus, the validation process is less useful in demonstrating that a particular initial result is an artifact, than it is at demonstrating that there is a *bona fide* biallelic marker at a particular position in a sequence. For an indication of whether a particular biallelic marker has been validated see Figure 1. All of the genotyping, haplotyping, association, and interaction study methods of the invention may optionally be performed solely with validated biallelic markers.

II.E. Evaluation of the Frequency of the Biallelic Markers of the Present Invention

The validated biallelic markers are further evaluated for their usefulness as genetic markers by determining the frequency of the least common allele at the biallelic marker site. The determination of the least common allele is accomplished by genotyping a group of individuals by a method of the invention and demonstrating that both alleles are present. This determination of frequency by genotyping step may be performed on individual samples derived from each individual in the group or by genotyping a pooled sample derived from more than one individual. The group must be large enough to be representative of the population as a whole. Preferably the group contains at least 20 individuals, more preferably the group contains at least 50 individuals, most preferably the group contains at least 100 individuals. Of course the larger the group the greater the accuracy of the frequency determination because of reduced sampling error. For an indication of the frequency for the less common allele of a particular biallelic marker of the invention see Figure 1. A biallelic marker wherein the frequency of the less common allele is 30% or more is termed a "high quality biallelic marker." All of the genotyping, haplotyping, association, and interaction study methods of the invention may optionally be performed solely with high quality biallelic markers.

III. Methods of Genotyping an Individual for Biallelic Markers

Methods are provided to genotype a biological sample for one or more biallelic markers of the present invention, all of which may be performed *in vitro*. Such methods of genotyping comprise determining the identity of a nucleotide at a DME-related biallelic marker by any method known in the art. These methods find use in genotyping case-control populations in association studies as well as individuals in the context of detection of alleles of biallelic markers which, are known to be associated with a given trait, in which case both copies of the biallelic marker present in individual's genome are determined so that an individual may be classified as homozygous or heterozygous for a particular allele.

These genotyping methods can be performed nucleic acid samples derived from a single individual or pooled DNA samples.

Genotyping can be performed using similar methods as those described above for the identification of the biallelic markers, or using other genotyping methods such as those further described below. In preferred embodiments, the comparison of sequences of amplified genomic fragments from different individuals is used to identify new biallelic markers whereas microsequencing is used for genotyping known biallelic markers in diagnostic and association study applications.

III.A. Source of DNA for Genotyping

Any source of nucleic acids, in purified or non-purified form, can be utilized as the starting nucleic acid, provided it contains or is suspected of containing the specific nucleic acid sequence desired. DNA or RNA may be extracted from cells, tissues, body fluids and the like as described above in II.A. "Genomic DNA Samples." While nucleic acids for use in the genotyping methods of the invention can be derived from any mammalian source, the test subjects and individuals from which nucleic acid samples are taken are generally understood to be human.

III.B. Amplification of DNA Fragments Comprising Biallelic Markers

Methods and polynucleotides are provided to amplify a segment of nucleotides comprising one or more biallelic marker of the present invention. It will be appreciated that amplification of DNA fragments comprising biallelic markers may be used in various methods and for various purposes and is not restricted to genotyping. Nevertheless, many genotyping methods, although not all, require the previous amplification of the DNA region carrying the biallelic marker of interest. Such methods specifically increase the concentration or total number of sequences that span the biallelic marker or include that site and sequences located either distal or proximal to it. Diagnostic assays may also rely on amplification of DNA segments carrying a biallelic marker of the present invention.

Amplification of DNA may be achieved by any method known in the art. The established PCR (polymerase chain reaction) method or by developments thereof or alternatives. Amplification methods which can be utilized herein include but are not limited to Ligase Chain Reaction (LCR) as described in EP A 320 308 and EP A 439 182, Gap LCR (Wolcott, M.J., Clin. Mcrobiol. Rev. 5:370-386), the so-called "NASBA" or "3SR" technique described in Guatelli J.C. et al. (*Proc. Natl. Acad. Sci. USA* 87:1874-1878, 1990) and in Compton J. (*Nature* 350:91-92, 1991), Q-beta amplification as described in European Patent Application no 4544610, strand displacement amplification as described in

Walker et al. (*Clin. Chem.* 42:9-13, 1996) and EP A 684 315 and, target mediated amplification as described in PCT Publication WO 9322461.

LCR and Gap LCR are exponential amplification techniques, both depend on DNA ligase to join adjacent primers annealed to a DNA molecule. In Ligase Chain Reaction (LCR), probe pairs are used which include two primary (first and second) and two secondary (third and fourth) probes, all of which are employed in molar excess to target. The first probe hybridizes to a first segment of the target strand and the second probe hybridizes to a second segment of the target strand, the first and second segments being contiguous so that the primary probes abut one another in 5' phosphate-3'hydroxyl relationship, and so that a ligase can covalently fuse or ligate the two probes into a fused product. In addition, a third (secondary) probe can hybridize to a portion of the first probe and a fourth (secondary) probe can hybridize to a portion of the second probe in a similar abutting fashion. Of course, if the target is initially double stranded, the secondary probes also will hybridize to the target complement in the first instance. Once the ligated strand of primary probes is separated from the target strand, it will hybridize with the third and fourth probes which can be ligated to form a complementary, secondary ligated product. It is important to realize that the ligated products are functionally equivalent to either the target or its complement. By repeated cycles of hybridization and ligation, amplification of the target sequence is achieved. A method for multiplex LCR has also been described (WO 9320227). Gap LCR (GLCR) is a version of LCR where the probes are not adjacent but are separated by 2 to 3 bases.

For amplification of mRNAs, it is within the scope of the present invention to reverse transcribe mRNA into cDNA followed by polymerase chain reaction (RT-PCR); or, to use a single enzyme for both steps as described in U.S. Patent No. 5,322,770 or, to use Asymmetric Gap LCR (RT-AGLCR) as described by Marshall R.L. et al. (*PCR Methods and Applications* 4:80-84, 1994). AGLCR is a modification of GLCR that allows the amplification of RNA.

Some of these amplification methods are particularly suited for the detection of single nucleotide polymorphisms and allow the simultaneous amplification of a target sequence and the identification of the polymorphic nucleotide as it is further described in IIIC.

The PCR technology is the preferred amplification technique used in the present invention. A variety of PCR techniques are familiar to those skilled in the art. For a review of PCR technology, see Molecular Cloning to Genetic Engineering White. B.A. Ed. in *Methods*

in Molecular Biology 67: Humana Press, Totowa (1997) and the publication entitled "PCR Methods and Applications" (1991, Cold Spring Harbor Laboratory Press). In each of these PCR procedures, PCR primers on either side of the nucleic acid sequences to be amplified are added to a suitably prepared nucleic acid sample along with dNTPs and a thermostable polymerase such as Taq polymerase, Pfu polymerase, or Vent polymerase. The nucleic acid in the sample is denatured and the PCR primers are specifically hybridized to complementary nucleic acid sequences in the sample. The hybridized primers are extended. Thereafter, another cycle of denaturation, hybridization, and extension is initiated. The cycles are repeated multiple times to produce an amplified fragment containing the nucleic acid sequence between the primer sites. PCR has further been described in several patents including US Patents 4,683,195, 4,683,202 and 4,965,188.

The identification of biallelic markers as described above allows the design of appropriate oligonucleotides, which can be used as primers to amplify DNA fragments comprising the biallelic markers of the present invention. Amplification can be performed using the primers initially used to discover new biallelic markers which are described herein or any set of primers allowing the amplification of a DNA fragment comprising a biallelic marker of the present invention. Primers can be prepared by any suitable method. As for example, direct chemical synthesis by a method such as the phosphodiester method of Narang S.A. et al. (*Methods Enzymol.* 68:90-98, 1979), the phosphodiester method of Brown E.L. et al. (*Methods Enzymol.* 68:109-151, 1979), the diethylphosphoramidite method of Beaucage et al. (*Tetrahedron Lett.* 22:1859-1862, 1981) and the solid support method described in EP 0 707 592.

In some embodiments the present invention provides primers for amplifying a DNA fragment containing one or more biallelic markers of the present invention. Preferred amplification primers are listed in Figure 7. It will be appreciated that the primers listed are merely exemplary and that any other set of primers which produce amplification products containing one or more biallelic markers of the present invention.

The primers are selected to be substantially complementary to the different strands of each specific sequence to be amplified. The length of the primers of the present invention can range from 8 to 100 nucleotides, preferably from 8 to 50, 8 to 30 or more preferably 8 to 25 nucleotides. Shorter primers tend to lack specificity for a target nucleic acid sequence and generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. Longer primers are expensive to produce and can sometimes self-hybridize to form hairpin structures. The formation of stable hybrids depends on the

melting temperature (Tm) of the DNA. The Tm depends on the length of the primer, the ionic strength of the solution and the G+C content. The higher the G+C content of the primer, the higher is the melting temperature because G:C pairs are held by three H bonds whereas A:T pairs have only two. The G+C content of the amplification primers of the present invention preferably ranges between 10 and 75 %, more preferably between 35 and 60 %, and most preferably between 40 and 55 %. The appropriate length for primers under a particular set of assay conditions may be empirically determined by one of skill in the art.

The spacing of the primers determines the length of the segment to be amplified. In the context of the present invention amplified segments carrying biallelic markers can range in size from at least about 25 bp to 35 kbp. Amplification fragments from 25-3000 bp are typical, fragments from 50-1000 bp are preferred and fragments from 100-600 bp are highly preferred. It will be appreciated that amplification primers for the biallelic markers may be any sequence which allow the specific amplification of any DNA fragment carrying the markers. Amplification primers may be labeled or immobilized on a solid support as described in I.

III.C. Methods of Genotyping DNA samples for Biallelic Markers

Any method known in the art can be used to identify the nucleotide present at a biallelic marker site. Since the biallelic marker allele to be detected has been identified and specified in the present invention, detection will prove simple for one of ordinary skill in the art by employing any of a number of techniques. Many genotyping methods require the previous amplification of the DNA region carrying the biallelic marker of interest. While the amplification of target or signal is often preferred at present, ultrasensitive detection methods which do not require amplification are also encompassed by the present genotyping methods. Methods well-known to those skilled in the art that can be used to detect biallelic polymorphisms include methods such as, conventional dot blot analyzes, single strand conformational polymorphism analysis (SSCP) described by Orita et al. (*Proc. Natl. Acad. Sci. U.S.A* 86:27776-2770, 1989), denaturing gradient gel electrophoresis (DGGE), heteroduplex analysis, mismatch cleavage detection, and other conventional techniques as described in Sheffield, V.C. et al. (*Proc. Natl. Acad. Sci. USA* 49:699-706, 1991), White et al. (*Genomics* 12:301-306, 1992), Grompe, M. et al. (*Proc. Natl. Acad. Sci. USA* 86:5855-5892, 1989) and Grompe, M. (*Nature Genetics* 5:111-117, 1993). Another method for determining the identity of the nucleotide present at a particular polymorphic site employs a specialized exonuclease-resistant nucleotide derivative as described in US patent 4,656,127.

Preferred methods involve directly determining the identity of the nucleotide present at a biallelic marker site by sequencing assay, enzyme-based mismatch detection assay, or hybridization assay. The following is a description of some preferred methods. A highly preferred method is the microsequencing technique. The term "sequencing assay" is used herein to refer to polymerase extension of duplex primer/template complexes and includes both traditional sequencing and microsequencing.

1) Sequencing assays

The nucleotide present at a polymorphic site can be determined by sequencing methods. In a preferred embodiment, DNA samples are subjected to PCR amplification before sequencing as described above. DNA sequencing methods are described in IIC.

Preferably, the amplified DNA is subjected to automated dideoxy terminator sequencing reactions using a dye-primer cycle sequencing protocol. Sequence analysis allows the identification of the base present at the biallelic marker site.

2) Microsequencing assays

In microsequencing methods, a nucleotide at the polymorphic site that is unique to one of the alleles in a target DNA is detected by a single nucleotide primer extension reaction. This method involves appropriate microsequencing primers which, hybridize just upstream of a polymorphic base of interest in the target nucleic acid. A polymerase is used to specifically extend the 3' end of the primer with one single ddNTP (chain terminator) complementary to the selected nucleotide at the polymorphic site. Next the identity of the incorporated nucleotide is determined in any suitable way.

Typically, microsequencing reactions are carried out using fluorescent ddNTPs and the extended microsequencing primers are analyzed by electrophoresis on ABI 377 sequencing machines to determine the identity of the incorporated nucleotide as described in EP 412 883. Alternatively capillary electrophoresis can be used in order to process a higher number of assays simultaneously. An example of a typical microsequencing procedure that can be used in the context of the present invention is provided in Example 2.

Different approaches can be used to detect the nucleotide added to the microsequencing primer. A homogeneous phase detection method based on fluorescence resonance energy transfer has been described by Chen and Kwok (*Nucleic Acids Research* 25:347-353 1997) and Chen et al. (*Proc. Natl. Acad. Sci. USA* 94/20 10756-10761,1997). In this method amplified genomic DNA fragments containing polymorphic sites are incubated with a 5'-fluorescein–labeled primer in the presence of allelic dye-labeled dideoxyribonucleoside triphosphates and a modified Taq polymerase. The dye-labeled

primer is extended one base by the dye-terminator specific for the allele present on the template. At the end of the genotyping reaction, the fluorescence intensities of the two dyes in the reaction mixture are analyzed directly without separation or purification. All these steps can be performed in the same tube and the fluorescence changes can be monitored in real time. Alternatively, the extended primer may be analyzed by MALDI-TOF Mass Spectrometry. The base at the polymorphic site is identified by the mass added onto the microsequencing primer (see Haff L.A. and Smirnov I.P., *Genome Research*, 7:378-388, 1997).

Microsequencing may be achieved by the established microsequencing method or by developments or derivatives thereof. Alternative methods include several solid-phase microsequencing techniques. The basic microsequencing protocol is the same as described previously, except that the method is conducted as a heterogenous phase assay, in which the primer or the target molecule is immobilized or captured onto a solid support. To simplify the primer separation and the terminal nucleotide addition analysis, oligonucleotides are attached to solid supports or are modified in such ways that permit affinity separation as well as polymerase extension. The 5' ends and internal nucleotides of synthetic oligonucleotides can be modified in a number of different ways to permit different affinity separation approaches, e.g., biotinylation. If a single affinity group is used on the oligonucleotides, the oligonucleotides can be separated from the incorporated terminator regent. This eliminates the need of physical or size separation. More than one oligonucleotide can be separated from the terminator reagent and analyzed simultaneously if more than one affinity group is used. This permits the analysis of several nucleic acid species or more nucleic acid sequence information per extension reaction. The affinity group need not be on the priming oligonucleotide but could alternatively be present on the template. For example, immobilization can be carried out via an interaction between biotinylated DNA and streptavidin-coated microtitration wells or avidin-coated polystyrene particles. In the same manner oligonucleotides or templates may be attached to a solid support in a high-density format. In such solid phase microsequencing reactions, incorporated ddNTPs can be radiolabeled (Syvänen, *Clinica Chimica Acta* 226:225-236, 1994) or linked to fluorescein (Livak and Hainer, *Human Mutation* 3:379-385,1994). The detection of radiolabeled ddNTPs can be achieved through scintillation-based techniques. The detection of fluorescein-linked ddNTPs can be based on the binding of antifluorescein antibody conjugated with alkaline phosphatase, followed by incubation with a chromogenic substrate (such as *p*-nitrophenyl phosphate). Other possible reporter-detection pairs include:

ddNTP linked to dinitrophenyl (DNP) and anti-DNP alkaline phosphatase conjugate (Harju et al., *Clin. Chem.* 39/11 2282-2287, 1993) or biotinylated ddNTP and horseradish peroxidase-conjugated streptavidin with *o*-phenylenediamine as a substrate (WO 92/15712). As yet another alternative solid-phase microsequencing procedure, Nyren et al. (*Analytical Biochemistry* 208:171-175, 1993) described a method relying on the detection of DNA polymerase activity by an enzymatic luminometric inorganic pyrophosphate detection assay (ELIDA).

Pastinen et al. (*Genome research* 7:606-614, 1997), describe a method for multiplex detection of single nucleotide polymorphism in which the solid phase minisequencing principle is applied to an oligonucleotide array format. High-density arrays of DNA probes attached to a solid support (DNA chips) are further described in III.C.5.

In one aspect the present invention provides polynucleotides and methods to genotype one or more biallelic markers of the present invention by performing a microsequencing assay. Preferred microsequencing primers include those being featured Figure 6. It will be appreciated that the microsequencing primers listed in Figure 6 are merely exemplary and that, any primer having a 3' end immediately adjacent to a polymorphic nucleotide may be used. Similarly, it will be appreciated that microsequencing analysis may be performed for any biallelic marker or any combination of biallelic markers of the present invention. One aspect of the present invention is a solid support which includes one or more microsequencing primers listed in Figure 6, or fragments comprising at least 8, at least 12, at least 15, or at least 20 consecutive nucleotides thereof and having a 3' terminus immediately upstream of the corresponding biallelic marker, for determining the identity of a nucleotide at biallelic marker site.

3) Mismatch detection assays based on polymerases and ligases

In one aspect the present invention provides polynucleotides and methods to determine the allele of one or more biallelic markers of the present invention in a biological sample, by mismatch detection assays based on polymerases and/or ligases. These assays are based on the specificity of polymerases and ligases. Polymerization reactions places particularly stringent requirements on correct base pairing of the 3' end of the amplification primer and the joining of two oligonucleotides hybridized to a target DNA sequence is quite sensitive to mismatches close to the ligation site, especially at the 3' end. The terms "enzyme based mismatch detection assay" are used herein to refer to any method of determining the allele of a biallelic marker based on the specificity of ligases and polymerases. Preferred methods are described below. Methods, primers and various

parameters to amplify DNA fragments comprising biallelic markers of the present invention are further described above in III.B.

Allele specific amplification

Discrimination between the two alleles of a biallelic marker can also be achieved by allele specific amplification, a selective strategy, whereby one of the alleles is amplified without amplification of the other allele. This is accomplished by placing a polymorphic base at the 3' end of one of the amplification primers. Because the extension forms from the 3'end of the primer, a mismatch at or near this position has an inhibitory effect on amplification. Therefore, under appropriate amplification conditions, these primers only direct amplification on their complementary allele. Designing the appropriate allele-specific primer and the corresponding assay conditions are well with the ordinary skill in the art.

Ligation/amplification based methods

The "Oligonucleotide Ligation Assay" (OLA) uses two oligonucleotides which are designed to be capable of hybridizing to abutting sequences of a single strand of a target molecules. One of the oligonucleotides is biotinylated, and the other is detectably labeled. If the precise complementary sequence is found in a target molecule, the oligonucleotides will hybridize such that their termini abut, and create a ligation substrate that can be captured and detected. OLA is capable of detecting biallelic markers and may be advantageously combined with PCR as described by Nickerson D.A. et al. (*Proc. Natl. Acad. Sci. U.S.A.* 87:8923-8927, 1990). In this method, PCR is used to achieve the exponential amplification of target DNA, which is then detected using OLA.

Other methods which are particularly suited for the detection of biallelic markers include LCR (ligase chain reaction), Gap LCR (GLCR) which are described above in III.B. As mentioned above LCR uses two pairs of probes to exponentially amplify a specific target. The sequences of each pair of oligonucleotides, is selected to permit the pair to hybridize to abutting sequences of the same strand of the target. Such hybridization forms a substrate for a template-dependant ligase. In accordance with the present invention, LCR can be performed with oligonucleotides having the proximal and distal sequences of the same strand of a biallelic marker site. In one embodiment, either oligonucleotide will be designed to include the biallelic marker site. In such an embodiment, the reaction conditions are selected such that the oligonucleotides can be ligated together only if the target molecule either contains or lacks the specific nucleotide(s) that is complementary to the biallelic marker on the oligonucleotide. In an alternative embodiment, the oligonucleotides will not include the biallelic marker, such that when they hybridize to the target molecule, a "gap" is

created as described in WO 90/01069. This gap is then "filled" with complementary dNTPs (as mediated by DNA polymerase), or by an additional pair of oligonucleotides. Thus at the end of each cycle, each single strand has a complement capable of serving as a target during the next cycle and exponential allele-specific amplification of the desired sequence is obtained.

Ligase/Polymerase-mediated Genetic Bit Analysis™ is another method for determining the identity of a nucleotide at a preselected site in a nucleic acid molecule (WO 95/21271). This method involves the incorporation of a nucleoside triphosphate that is complementary to the nucleotide present at the preselected site onto the terminus of a primer molecule, and their subsequent ligation to a second oligonucleotide. The reaction is monitored by detecting a specific label attached to the reaction's solid phase or by detection in solution.

4) Hybridization assay methods

A preferred method of determining the identity of the nucleotide present at a biallelic marker site involves nucleic acid hybridization. The hybridization probes, which can be conveniently used in such reactions, preferably include the probes defined herein. Any hybridization assay may be used including Southern hybridization, Northern hybridization, dot blot hybridization and solid-phase hybridization (see Sambrook et al., Molecular Cloning – A Laboratory Manual, Second Edition, Cold Spring Harbor Press, N.Y., 1989).

Hybridization refers to the formation of a duplex structure by two single stranded nucleic acids due to complementary base pairing. Hybridization can occur between exactly complementary nucleic acid strands or between nucleic acid strands that contain minor regions of mismatch. Specific probes can be designed that hybridize to one form of a biallelic marker and not to the other and therefore are able to discriminate between different allelic forms. Allele-specific probes are often used in pairs, one member of a pair showing perfect match to a target sequence containing the original allele and the other showing a perfect match to the target sequence containing the alternative allele. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe hybridizes to only one of the alleles. Stringent, sequence specific hybridization conditions, under which a probe will hybridize only to the exactly complementary target sequence are well known in the art (Sambrook et al., Molecular Cloning – A Laboratory Manual, Second Edition. Cold Spring Harbor Press, N.Y., 1989). Stringent conditions are sequence dependent and will be different in different

circumstances. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (Tm) for the specific sequence at a defined ionic strength and pH. By wy of example and not limitation, procedures using conditions of high stringency are as follows: Prehybridization of filters containing DNA is carried out for 8 h to overnight at 65°C in buffer composed of 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 μg/ml denatured salmon sperm DNA. Filters are hybridized for 48 h at 65°C, the preferred hybridization temperature, in prehybridization mixture containing 100 μg/ml denatured salmon sperm DNA and 5-20 X 10^6 cpm of ^{32}P-labeled probe. Alternatively, the hybridization step can be performed at 65°C in the presence of SSC buffer, 1 x SSC corresponding to 0.15M NaCl and 0.05 M Na citrate. Subsequently, filter washes can be done at 37°C for 1 h in a solution containing 2X SSC, 0.01% PVP, 0.01% Ficoll, and 0.01% BSA, followed by a wash in 0.1X SSC at 50°C for 45 min. Alternatively, filter washes can be performed in a solution containing 2 x SSC and 0.1% SDS, or 0.5 x SSC and 0.1% SDS, or 0.1 x SSC and 0.1% SDS at 68°C for 15 minute intervals. Following the wash steps, the hybridized probes are detectable by autoradiography. By way of example and not limitation, procedures using conditions of intermediate stringency are as follows: Filters containing DNA are prehybridized, and then hybridized at a temperature of 60°C in the presence of a 5 x SSC buffer and labeled probe. Subsequently, filters washes are performed in a solution containing 2x SSC at 50°C and the hybridized probes are detectable by autoradiography. Other conditions of high and intermediate stringency which may be used are well known in the art and as cited in Sambrook et al. (Molecular Cloning - A Laboratory Manual, Second Edition, Cold Spring Harbor Press, N.Y., 1989) and Ausubel et al. (Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y., 1989).

Although such hybridizations can be performed in solution, it is preferred to employ a solid-phase hybridization assay. The target DNA comprising a biallelic marker of the present invention may be amplified prior to the hybridization reaction. The presence of a specific allele in the sample is determined by detecting the presence or the absence of stable hybrid duplexes formed between the probe and the target DNA. The detection of hybrid duplexes can be carried out by a number of methods. Various detection assay formats are well known which utilize detectable labels bound to either the target or the probe to enable detection of the hybrid duplexes. Typically, hybridization duplexes are separated from unhybridized nucleic acids and the labels bound to the duplexes are then detected. Those skilled in the art will recognize that wash steps may be employed to wash away excess

target DNA or probe. Standard heterogeneous assay formats are suitable for detecting the hybrids using the labels present on the primers and probes.

Two recently developed assays allow hybridization-based allele discrimination with no need for separations or washes (see Landegren U. et al., *Genome Research*, 8:769-776,1998). The TaqMan assay takes advantage of the 5' nuclease activity of Taq DNA polymerase to digest a DNA probe annealed specifically to the accumulating amplification product. TaqMan probes are labeled with a donor-acceptor dye pair that interacts via fluorescence energy transfer. Cleavage of the TaqMan probe by the advancing polymerase during amplification dissociates the donor dye from the quenching acceptor dye, greatly increasing the donor fluorescence. All reagents necessary to detect two allelic variants can be assembled at the beginning of the reaction and the results are monitored in real time (see Livak et al., *Nature Genetics*, 9:341-342, 1995). In an alternative homogeneous hybridization-based procedure, molecular beacons are used for allele discriminations. Molecular beacons are hairpin-shaped oligonucleotide probes that report the presence of specific nucleic acids in homogeneous solutions. When they bind to their targets they undergo a conformational reorganization that restores the fluorescence of an internally quenched fluorophore (Tyagi et al., *Nature Biotechnology*, 16:49-53, 1998).

The polynucleotides provided herein can be used in hybridization assays for the detection of biallelic marker alleles in biological samples. These probes are characterized in that they preferably comprise between 8 and 50 nucleotides, and in that they are sufficiently complementary to a sequence comprising a biallelic marker of the present invention to hybridize thereto and preferably sufficiently specific to be able to discriminate the targeted sequence for only one nucleotide variation. The GC content in the probes of the invention usually ranges between 10 and 75 %, preferably between 35 and 60 %, and more preferably between 40 and 55 %. The length of these probes can range from 10, 15, 20, or 30 to at least 100 nucleotides, preferably from 10 to 50, more preferably from 18 to 35 nucleotides. A particularly preferred probe is 25 nucleotides in length. Preferably the biallelic marker is within 4 nucleotides of the center of the polynucleotide probe. In particularly preferred probes the biallelic marker is at the center of said polynucleotide. Shorter probes may lack specificity for a target nucleic acid sequence and generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. Longer probes are expensive to produce and can sometimes self-hybridize to form hairpin structures. Methods for the synthesis of oligonucleotide probes have been described above and can be applied to the probes of the present invention.

Preferably the probes of the present invention are labeled or immobilized on a solid support. Labels and solid supports are further described in I. Detection probes are generally nucleic acid sequences or uncharged nucleic acid analogs such as, for example peptide nucleic acids which are disclosed in International Patent Application WO 92/20702, d, morpholino analogs which are described in U.S. Patents Numbered 5,185,444; 5,034,506 and 5,142,047. The probe may have to be rendered "non-extendable" in that additional dNTPs cannot be added to the probe. In and of themselves analogs usually are non-extendable and nucleic acid probes can be rendered non-extendable by modifying the 3' end of the probe such that the hydroxyl group is no longer capable of participating in elongation. For example, the 3' end of the probe can be functionalized with the capture or detection label to thereby consume or otherwise block the hydroxyl group. Alternatively, the 3' hydroxyl group simply can be cleaved, replaced or modified, U.S. Patent Application Serial No. 07/049,061 filed April 19, 1993 describes modifications, which can be used to render a probe non-extendable.

The probes of the present invention are useful for a number of purposes. They can be used in Southern hybridization to genomic DNA or Northern hybridization to mRNA. The probes can also be used to detect PCR amplification products. By assaying the hybridization to an allele specific probe, one can detect the presence or absence of a biallelic marker allele in a given sample.

High-Throughput parallel hybridizations in array format are specifically encompassed within "hybridization assays" and are described below.

Hybridization to addressable arrays of oligonucleotides

Hybridization assays based on oligonucleotide arrays rely on the differences in hybridization stability of short oligonucleotides to perfectly matched and mismatched target sequence variants. Efficient access to polymorphism information is obtained through a basic structure comprising high-density arrays of oligonucleotide probes attached to a solid support (the chip) at selected positions. Each DNA chip can contain thousands to millions of individual synthetic DNA probes arranged in a grid-like pattern and miniaturized to the size of a dime.

The chip technology has already been applied with success in numerous cases. For example, the screening of mutations has been undertaken in the BRCA1 gene, in *S. cerevisiae* mutant strains, and in the protease gene of HIV-1 virus (Hacia et al., *Nature Genetics*, 14(4):441-447, 1996; Shoemaker et al., *Nature Genetics*, 14(4):450-456, 1996 ; Kozal et al., *Nature Medicine*, 2:753-759, 1996). Chips of various formats for use in

detecting biallelic polymorphisms can be produced on a customized basis by Affymetrix (GeneChip™), Hyseq (HyChip and HyGnostics), and Protogene Laboratories.

In general, these methods employ arrays of oligonucleotide probes that are complementary to target nucleic acid sequence segments from an individual which, target sequences include a polymorphic marker. EP785280, describes a tiling strategy for the detection of single nucleotide polymorphisms. Briefly, arrays may generally be "tiled" for a large number of specific polymorphisms. By "tiling" is generally meant the synthesis of a defined set of oligonucleotide probes which is made up of a sequence complementary to the target sequence of interest, as well as preselected variations of that sequence, e.g., substitution of one or more given positions with one or more members of the basis set of monomers, i.e. nucleotides. Tiling strategies are further described in PCT application No. WO 95/11995. In a particular aspect, arrays are tiled for a number of specific, identified biallelic marker sequences. In particular the array is tiled to include a number of detection blocks, each detection block being specific for a specific biallelic marker or a set of biallelic markers. For example, a detection block may be tiled to include a number of probes, which span the sequence segment that includes a specific polymorphism. To ensure probes that are complementary to each allele, the probes are synthesized in pairs differing at the biallelic marker. In addition to the probes differing at the polymorphic base, monosubstituted probes are also generally tiled within the detection block. These monosubstituted probes have bases at and up to a certain number of bases in either direction from the polymorphism, substituted with the remaining nucleotides (selected from A, T, G, C and U). Typically the probes in a tiled detection block will include substitutions of the sequence positions up to and including those that are 5 bases away from the biallelic marker. The monosubstituted probes provide internal controls for the tiled array, to distinguish actual hybridization from artefactual cross-hybridization. Upon completion of hybridization with the target sequence and washing of the array, the array is scanned to determine the position on the array to which the target sequence hybridizes. The hybridization data from the scanned array is then analyzed to identify which allele or alleles of the biallelic marker are present in the sample. Hybridization and scanning may be carried out as described in PCT application No. WO 92/10092 and WO 95/11995 and US patent No. 5,424,186, .

Thus, in some embodiments, the chips may comprise an array of nucleic acid sequences of fragments of about 15 nucleotides in length. In further embodiments, the chip may comprise an array including at least one of the sequences selected from the group

consisting of SEQ ID No. 1-38, 40-54, 56-463, 465-487, 490-493 and the sequences complementary thereto, or a fragment thereof at least about 8 consecutive nucleotides, preferably 10, 15, 20, more preferably 25, 30, 40, 47, or 50 consecutive nucleotides. In some embodiments, the chip may comprise an array of at least 2, 3, 4, 5, 6, 7, 8 or more of these polynucleotides of the invention. Solid supports and polynucleotides of the present invention attached to solid supports are further described in I. "Biallelic Markers and Polynucleotides Comprising Biallelic Markers."

5) Integrated Systems

Another technique, which may be used to analyze polymorphisms, includes multicomponent integrated systems, which miniaturize and compartmentalize processes such as PCR and capillary electrophoresis reactions in a single functional device. An example of such technique is disclosed in US patent 5,589,136, which describes the integration of PCR amplification and capillary electrophoresis in chips.

Integrated systems can be envisaged mainly when microfluidic systems are used. These systems comprise a pattern of microchannels designed onto a glass, silicon, quartz, or plastic wafer included on a microchip. The movements of the samples are controlled by electric, electroosmotic or hydrostatic forces applied across different areas of the microchip. For genotyping biallelic markers, the microfluidic system may integrate nucleic acid amplification, microsequencing, capillary electrophoresis and a detection method such as laser-induced fluorescence detection.

IV. Methods of Genetic Analysis Using the Biallelic Markers of the Present Invention

Different methods are available for the genetic analysis of complex traits (see Lander and Schork, *Science*, 265, 2037-2048, 1994). The search for disease-susceptibility genes is conducted using two main methods: the linkage approach in which evidence is sought for cosegregation between a locus and a putative trait locus using family studies, and the association approach in which evidence is sought for a statistically significant association between an allele and a trait or a trait causing allele (Khoury J. et al., *Fundamentals of Genetic Epidemiology, Oxford University Press, NY*, 1993). In general, the biallelic markers of the present invention find use in any method known in the art to demonstrate a statistically significant correlation between a genotype and a phenotype. The biallelic markers may be used in parametric and non-parametric linkage analysis methods. Preferably, the biallelic markers of the present invention are used to identify genes associated with detectable traits using association studies, an approach which does not

require the use of affected families and which permits the identification of genes associated with complex and sporadic traits.

The genetic analysis using the biallelic markers of the present invention may be conducted on any scale. The whole set of biallelic markers of the present invention or any subset of biallelic markers of the present invention may be used. In some embodiments a subset of biallelic markers corresponding to one or several candidate genes of the present invention may be used. In other embodiments a subset of biallelic markers corresponding to candidate genes from a given metabolic pathway may be used. Such pathways include glucoronidation and glutathione conjugation. Alternatively, a subset of biallelic markers of the present invention localised on a specific chromosome segment may be used. Further, any set of genetic markers including a biallelic marker of the present invention may be used. A set of biallelic polymorphisms that, could be used as genetic markers in combination with the biallelic markers of the present invention, has been described in WO 98/20165. As mentioned above, it should be noted that the biallelic markers of the present invention may be included in any complete or partial genetic map of the human genome. These different uses are specifically contemplated in the present invention and claims.

IV.A. Linkage Analysis

Linkage analysis is based upon establishing a correlation between the transmission of genetic markers and that of a specific trait throughout generations within a family. Thus, the aim of linkage analysis is to detect marker loci that show cosegregation with a trait of interest in pedigrees.

Parametric methods

When data are available from successive generations there is the opportunity to study the degree of linkage between pairs of loci. Estimates of the recombination fraction enable loci to be ordered and placed onto a genetic map. With loci that are genetic markers, a genetic map can be established, and then the strength of linkage between markers and traits can be calculated and used to indicate the relative positions of markers and genes affecting those traits (Weir, B.S., *Genetic data Analysis II: Methods for Discrete population genetic Data, Sinauer Assoc., Inc., Sunderland, MA, USA*, 1996). The classical method for linkage analysis is the logarithm of odds (lod) score method (see Morton N.E., *Am.J. Hum.Genet.*, 7:277-318, 1955; Ott J., *Analysis of Human Genetic Linkage, John Hopkins University Press, Baltimore*, 1991). Calculation of lod scores requires specification of the mode of inheritance for the disease (parametric method). Generally, the length of the candidate region identified using linkage analysis is between 2 and 20Mb. Once a candidate

region is identified as described above, analysis of recombinant individuals using additional markers allows further delineation of the candidate region. Linkage analysis studies have generally relied on the use of a maximum of 5,000 microsatellite markers, thus limiting the maximum theoretical attainable resolution of linkage analysis to about 600 kb on average.

Linkage analysis has been successfully applied to map simple genetic traits that show clear Mendelian inheritance patterns and have a high penetrance (i.e., the ratio between the number of trait positive carriers of allele *a* and the total number of *a* carriers in the population). However, parametric linkage analysis suffers from a variety of drawbacks. First, it is limited by its reliance on the choice of a genetic model suitable for each studied trait. Furthermore, as already mentioned, the resolution attainable using linkage analysis is limited, and complementary studies are required to refine the analysis of the typical 2Mb to 20Mb regions initially identified through linkage analysis. In addition, parametric linkage analysis approaches have proven difficult when applied to complex genetic traits, such as those due to the combined action of multiple genes and/or environmental factors. It is very difficult to model these factors adequately in a lod score analysis. In such cases, too large an effort and cost are needed to recruit the adequate number of affected families required for applying linkage analysis to these situations, as recently discussed by Risch, N. and Merikangas, K. (*Science*, 273:1516-1517, 1996).

Non-parametric methods

The advantage of the so-called non-parametric methods for linkage analysis is that they do not require specification of the mode of inheritance for the disease, they tend to be more useful for the analysis of complex traits. In non-parametric methods, one tries to prove that the inheritance pattern of a chromosomal region is not consistent with random Mendelian segregation by showing that affected relatives inherit identical copies of the region more often than expected by chance. Affected relatives should show excess "allele sharing" even in the presence of incomplete penetrance and polygenic inheritance. In non-parametric linkage analysis the degree of agreement at a marker locus in two individuals can be measured either by the number of alleles identical by state (IBS) or by the number of alleles identical by descent (IBD). Affected sib pair analysis is a well-known special case and is the simplest form of these methods.

The biallelic markers of the present invention may be used in both parametric and non-parametric linkage analysis. Preferably biallelic markers may be used in non-parametric methods which allow the mapping of genes involved in complex traits. The biallelic markers of the present invention may be used in both IBD- and IBS- methods to

map genes affecting a complex trait. In such studies, taking advantage of the high density of biallelic markers, several adjacent biallelic marker loci may be pooled to achieve the efficiency attained by multi-allelic markers (Zhao et al., *Am. J. Hum. Genet.*, 63:225-240, 1998).

However, both parametric and non-parametric linkage analysis methods analyse affected relatives, they tend to be of limited value in the genetic analysis of drug responses or in the analysis of side effects to treatments. This type of analysis is impractical in such cases due to the lack of availability of familial cases. In fact, the likelihood of having more than one individual in a family being exposed to the same drug at the same time is extremely low.

IV.B. Population Association Studies

The present invention comprises methods for identifying one or several genes among a set of candidate genes that are associated with a detectable trait using the biallelic markers of the present invention. In one embodiment the present invention comprises methods to detect an association between a biallelic marker allele or a biallelic marker haplotype and a trait. Further, the invention comprises methods to identify a trait causing allele in linkage disequilibrium with any biallelic marker allele of the present invention.

As described above, alternative approaches can be employed to perform association studies: genome-wide association studies, candidate region association studies and candidate gene association studies. In a preferred embodiment, the biallelic markers of the present invention are used to perform candidate gene association studies. The candidate gene analysis clearly provides a short-cut approach to the identification of genes and gene polymorphisms related to a particular trait when some information concerning the biology of the trait is available. Further, the biallelic markers of the present invention may be incorporated in any map of genetic markers of the human genome in order to perform genome-wide association studies. Methods to generate a high-density map of biallelic markers has been described in US Provisional Patent application serial number 60/082,614. The biallelic markers of the present invention may further be incorporated in any map of a specific candidate region of the genome (a specific chromosome or a specific chromosomal segment for example).

As mentioned above, association studies may be conducted within the general population and are not limited to studies performed on related individuals in affected families. Association studies are extremely valuable as they permit the analysis of sporadic or multifactor traits. Moreover, association studies represent a powerful method for fine-

scale mapping enabling much finer mapping of trait causing alleles than linkage studies. Studies based on pedigrees often only narrow the location of the trait causing allele. Association studies using the biallelic markers of the present invention can therefore be used to refine the location of a trait causing allele in a candidate region identified by Linkage Analysis methods. Moreover, once a chromosome segment of interest has been identified, the presence of a candidate gene such as a candidate gene of the present invention, in the region of interest can provide a shortcut to the identification of the trait causing allele. Biallelic markers of the present invention can be used to demonstrate that a candidate gene is associated with a trait. Such uses are specifically contemplated in the present invention and claims.

1) Determining the frequency of a biallelic marker allele or of a biallelic marker haplotype in a population

Association studies explore the relationships among frequencies for sets of alleles between loci.

Determining the frequency of an allele in a population

Allelic frequencies of the biallelic markers in a population can be determined using one of the methods described above under the heading "Methods for genotyping an individual for biallelic markers", or any genotyping procedure suitable for this intended purpose. Genotyping pooled samples or individual samples can determine the frequency of a biallelic marker allele in a population. One way to reduce the number of genotypings required is to use pooled samples. A major obstacle in using pooled samples is in terms of accuracy and reproducibility for determining accurate DNA concentrations in setting up the pools. Genotyping individual samples provides higher sensitivity, reproducibility and accuracy and; is the preferred method used in the present invention. Preferably, each individual is genotyped separately and simple gene counting is applied to determine the frequency of an allele of a biallelic marker or of a genotype in a given population.

Determining the frequency of a haplotype in a population

The gametic phase of haplotypes is unknown when diploid individuals are heterozygous at more than one locus. Using genealogical information in families gametic phase can sometimes be inferred (Perlin et al., *Am. J. Hum. Genet.*, 55:777-787, 1994). When no genealogical information is available different strategies may be used. One possibility is that the multiple-site heterozygous diploids can be eliminated from the analysis, keeping only the homozygotes and the single-site heterozygote individuals, but this approach might lead to a possible bias in the sample composition and the underestimation of

low-frequency haplotypes. Another possibility is that single chromosomes can be studied independently, for example, by asymmetric PCR amplification (see Newton et al., *Nucleic Acids Res.*, 17:2503-2516, 1989; Wu et al., *Proc. Natl. Acad. Sci. USA*, 86:2757, 1989), or by isolation of single chromosome by limit dilution followed by PCR amplification (see Ruano et al., *Proc. Natl. Acad. Sci. USA*, 87:6296-6300, 1990). Further, a sample may be haplotyped for sufficiently close biallelic markers by double PCR amplification of specific alleles (Sarkar, G. and Sommer S.S., *Biotechniques*, 1991). These approaches are not entirely satisfying either because of their technical complexity, the additional cost they entail, their lack of generalisation at a large scale, or the possible biases they introduce. To overcome these difficulties, an algorithm to infer the phase of PCR-amplified DNA genotypes introduced by Clark A.G. (*Mol. Biol. Evol.*, 7:111-122, 1990), may be used. Briefly, the principle is to start filling a preliminary list of haplotypes present in the sample by examining unambiguous individuals, that is, the complete homozygotes and the single-site heterozygotes. Then other individuals in the same sample are screened for the possible occurrence of previously recognised haplotypes. For each positive identification, the complementary haplotype is added to the list of recognised haplotypes, until the phase information for all individuals is either resolved or identified as unresolved. This method assigns a single haplotype to each multiheterozygous individual, whereas several haplotypes are possible when there are more than one heterozygous site. Alternatively, one can use methods estimating haplotype frequencies in a population without assigning haplotypes to each individual. Preferably, a method based on an expectation-maximization (EM) algorithm (Dempster et al., *J. R. Stat. Soc.*, 39B: 1-38, 1977), leading to maximum-likelihood estimates of haplotype frequencies under the assumption of Hardy-Weinberg proportions (random mating) is used (see Excoffier L. and Slatkin M., *Mol. Biol. Evol.*, 12(5): 921-927, 1995). The EM algorithm is a generalised iterative maximum-likelihood approach to estimation that is useful when data are ambiguous and/or incomplete. The EM algorithm is used to resolve heterozygotes into haplotypes. Haplotype estimations are further described below under the heading "Statistical methods." Any other method known in the art to determine or to estimate the frequency of a haplotype in a population may also be used.

2) Linkage Disequilibrium analysis

Linkage disequilibrium is the non-random association of alleles at two or more loci and represents a powerful tool for mapping genes involved in disease traits (see Ajioka R.S. et al., *Am. J. Hum. Genet.*, 60:1439-1447, 1997). Biallelic markers, because they are

densely spaced in the human genome and can be genotyped in more numerous numbers than other types of genetic markers (such as RFLP or VNTR markers), are particularly useful in genetic analysis based on linkage disequilibrium. The biallelic markers of the present invention may be used in any linkage disequilibrium analysis method known in the art.

Briefly, when a disease mutation is first introduced into a population (by a new mutation or the immigration of a mutation carrier), it necessarily resides on a single chromosome and thus on a single "background" or "ancestral" haplotype of linked markers. Consequently, there is complete disequilibrium between these markers and the disease mutation: one finds the disease mutation only in the presence of a specific set of marker alleles. Through subsequent generations recombinations occur between the disease mutation and these marker polymorphisms, and the disequilibrium gradually dissipates. The pace of this dissipation is a function of the recombination frequency, so the markers closest to the disease gene will manifest higher levels of disequilibrium than those that are further away. When not broken up by recombination, "ancestral" haplotypes and linkage disequilibrium between marker alleles at different loci can be tracked not only through pedigrees but also through populations. Linkage disequilibrium is usually seen as an association between one specific allele at one locus and another specific allele at a second locus.

The pattern or curve of disequilibrium between disease and marker loci is expected to exhibit a maximum that occurs at the disease locus. Consequently, the amount of linkage disequilibrium between a disease allele and closely linked genetic markers may yield valuable information regarding the location of the disease gene. For fine-scale mapping of a disease locus, it is useful to have some knowledge of the patterns of linkage disequilibrium that exist between markers in the studied region. As mentioned above the mapping resolution achieved through the analysis of linkage disequilibrium is much higher than that of linkage studies. The high density of biallelic markers combined with linkage disequilibrium analysis provides powerful tools for fine-scale mapping. Different methods to calculate linkage disequilibrium are described below under the heading "Statistical Methods."

3) Population-based case-control studies of trait-marker associations

As mentioned above, the occurrence of pairs of specific alleles at different loci on the same chromosome is not random and the deviation from random is called linkage disequilibrium. Association studies focus on population frequencies and rely on the phenomenon of linkage disequilibrium. If a specific allele in a given gene is directly

involved in causing a particular trait, its frequency will be statistically increased in an affected (trait positive) population, when compared to the frequency in a trait negative population or in a random control population. As a consequence of the existence of linkage disequilibrium, the frequency of all other alleles present in the haplotype carrying the trait-causing allele will also be increased in trait positive individuals compared to trait negative individuals or random controls. Therefore, association between the trait and any allele (specifically a biallelic marker allele) in linkage disequilibrium with the trait-causing allele will suffice to suggest the presence of a trait-related gene in that particular region. Case-control populations can be genotyped for biallelic markers to identify associations that narrowly locate a trait causing allele. As any marker in linkage disequilibrium with one given marker associated with a trait will be associated with the trait. Linkage disequilibrium allows the relative frequencies in case-control populations of a limited number of genetic polymorphisms (specifically biallelic markers) to be analysed as an alternative to screening all possible functional polymorphisms in order to find trait-causing alleles. Association studies compare the frequency of marker alleles in unrelated case-control populations, and represent powerful tools for the dissection of complex traits.

Case-control populations (inclusion criteria)

Population-based association studies do not concern familial inheritance but compare the prevalence of a particular genetic marker, or a set of markers, in case-control populations. They are case-control studies based on comparison of unrelated case (affected or trait positive) individuals and unrelated control (unaffected or trait negative or random) individuals. Preferably the control group is composed of unaffected or trait negative individuals. Further, the control group is ethnically matched to the case population. Moreover, the control group is preferably matched to the case-population for the main known confusion factor for the trait under study (for example age-matched for an age-dependent trait). Ideally, individuals in the two samples are paired in such a way that they are expected to differ only in their disease status. In the following "trait positive population", "case population" and "affected population" are used interchangeably.

An important step in the dissection of complex traits using association studies is the choice of case-control populations (see Lander and Schork, *Science*, 265, 2037-2048, 1994). A major step in the choice of case-control populations is the clinical definition of a given trait or phenotype. Any genetic trait may be analysed by the association method proposed here by carefully selecting the individuals to be included in the trait positive and trait negative phenotypic groups. Four criteria are often useful: clinical phenotype, age at onset,

family history and severity. The selection procedure for continuous or quantitative traits (such as blood pressure for example) involves selecting individuals at opposite ends of the phenotype distribution of the trait under study, so as to include in these trait positive and trait negative populations individuals with non-overlapping phenotypes. Preferably, case-control populations consist of phenotypically homogeneous populations. Trait positive and trait negative populations consist of phenotypically uniform populations of individuals representing each between 1 and 98%, preferably between 1 and 80%, more preferably between 1 and 50%, and more preferably between 1 and 30%, most preferably between 1 and 20% of the total population under study, and selected among individuals exhibiting non-overlapping phenotypes. The clearer the difference between the two trait phenotypes, the greater the probability of detecting an association with biallelic markers. The selection of those drastically different but relatively uniform phenotypes enables efficient comparisons in association studies and the possible detection of marked differences at the genetic level, provided that the sample sizes of the populations under study are significant enough.

In preferred embodiments, a first group of between 50 and 300 trait positive individuals, preferably about 100 individuals, are recruited according to their phenotypes. A similar number of trait negative individuals are included in such studies.

In the present invention, typical examples of inclusion criteria include a disease involving the metabolic conversion of xenobiotics or the evaluation of the response to a drug or side effects to treatment with drugs.

Suitable examples of association studies using biallelic markers including the biallelic markers of the present invention, are studies involving the following populations:

a case population suffering from a disease involving the metabolic conversion of xenobiotics and a healthy unaffected control population, or

a case population treated with therapeutic agents suffering from side-effects resulting from the treatment and a control population treated with the same agents showing no side-effects, or

a case population treated with therapeutic agents showing a beneficial response and a control population treated with same agents showing no beneficial response.

In a preferred embodiment, the trait considered was a side-effect upon drug treatment, the study involved two populations derived from a clinical study of the anti-asthmatic drug zileuton. The case population was composed of asthmatic individuals treated with zileuton showing zileuton-associated hepatotoxicity monitored by the serum level of alanine aminotransferase (ALT) and the control population was composed of

asthmatic individuals treated with zileuton and having no increased serum level of ALT. Inclusion criteria and association between the biallelic markers of the present invention and zileuton-associated hepatotoxicity are further described below and in Example 4.

Association analysis

The general strategy to perform association studies using biallelic markers derived from a region carrying a candidate gene is to scan two groups of individuals (case-control populations) in order to measure and statistically compare the allele frequencies of the biallelic markers of the present invention in both groups.

If a statistically significant association with a trait is identified for at least one or more of the analysed biallelic markers, one can assume that: either the associated allele is directly responsible for causing the trait (the associated allele is the trait causing allele), or more likely the associated allele is in linkage disequilibrium with the trait causing allele. The specific characteristics of the associated allele with respect to the candidate gene function usually gives further insight into the relationship between the associated allele and the trait (causal or in linkage disequilibrium). If the evidence indicates that the associated allele within the candidate gene is most probably not the trait causing allele but is in linkage disequilibrium with the real trait causing allele, then the trait causing allele can be found by sequencing the vicinity of the associated marker.

Association studies are usually run in two successive steps. In a first phase, the frequencies of a reduced number of biallelic markers from one or several candidate genes are determined in the trait positive and trait negative populations. In a second phase of the analysis, the identity of the candidate gene and the position of the genetic loci responsible for the given trait is further refined using a higher density of markers from the relevant region. However, if the candidate gene under study is relatively small in length, as it is the case for many of the candidate genes analysed included in the present invention, a single phase may be sufficient to establish significant associations.

Haplotype analysis

As described above, when a chromosome carrying a disease allele first appears in a population as a result of either mutation or migration, the mutant allele necessarily resides on a chromosome having a set of linked markers: the ancestral haplotype. This haplotype can be tracked through populations and its statistical association with a given trait can be analysed. Complementing single point (allelic) association studies with multi-point association studies also called haplotype studies increases the statistical power of association studies. Thus, a haplotype association study allows one to define the frequency

and the type of the ancestral carrier haplotype. A haplotype analysis is important in that it increases the statistical power of an analysis involving individual markers.

In a first stage of a haplotype frequency analysis, the frequency of the possible haplotypes based on various combinations of the identified biallelic markers of the invention is determined. The haplotype frequency is then compared for distinct populations of trait positive and control individuals. The number of trait positive individuals, which should be, subjected to this analysis to obtain statistically significant results usually ranges between 30 and 300, with a preferred number of individuals ranging between 50 and 150. The same considerations apply to the number of unaffected individuals (or random control) used in the study. The results of this first analysis provide haplotype frequencies in case-control populations, for each evaluated haplotype frequency a p-value and an odd ratio are calculated. If a statistically significant association is found, the relative risk for an individual carrying the given haplotype of being affected with the trait under study can be approximated.

The preferred 2, 3 and 4 marker haplotypes of the invention are listed in Table 3 below:

Table 3

GENE	MARKER 1	MARKER 2	MARKER 3	MARKER 4
MGST-II	12-455-326	12-453-429	12-424-198	
MGST-II	12-455-326	12-453-429	12-424-198	12-454-363
MGST-II	12-447-58	12-455-326	12-461-299	12-453-429
MGST-II	12-441-233	12-461-299	12-453-429	
MGST-II	12-441-233	12-461-299	12-453-429	12-426-154
MGST-II	12-426-154	12-424-198		
MGST-II	12-426-154	12-461-299	12-424-198	
ME1	10-428-219	12-724-225		
UGT1A7	12-128-225	12-156-91	12-139-380	12-140-134
UGT1A7	12-148-311	12-156-91	12-139-380	12-140-134
UGT2B4	10-470-25	12-652-203		
UGT2B4	10-470-25	12-637-219	12-652-203.	

The most preferred 2, 3 and 4 marker haplotypes of the invention are listed in Table 4 below:

Table 4

GENE	MARKER 1	MARKER 2	MARKER 3	MARKER 4
MGST-II	12-455-326	12-453-429	12-424-198	
MGST-II	12-455-326	12-453-429	12-424-198	12-454-363
MGST-II	12-447-58	12-455-326	12-461-299	12-453-429
MGST-II	12-426-154	12-424-198		
ME1	10-428-219	12-724-225		

UGT1A7	12-128-225	12-156-91	12-139-380	12-140-134
UGT2B4	10-470-25	12-652-203		

Interaction Analysis

The biallelic markers of the present invention may also be used to identify patterns of biallelic markers associated with detectable traits resulting from polygenic interactions. The analysis of genetic interaction between alleles at unlinked loci requires individual genotyping using the techniques described herein. The analysis of allelic interaction among a selected set of biallelic markers with appropriate level of statistical significance can be considered as a haplotype analysis. Interaction analysis consists in stratifying the case-control populations with respect to a given haplotype for the first loci and performing a haplotype analysis with the second loci with each subpopulation.

Statistical methods used in association studies are further described below in IV.C. "Statistical Methods."

4) Testing for linkage in the presence of association

The biallelic markers of the present invention may further be used in TDT (transmission/disequilibrium test). TDT tests for both linkage and association and is not affected by population stratification. TDT requires data for affected individuals and their parents or data from unaffected sibs instead of from parents (see Spielmann S. et al., *Am. J. Hum. Genet.*, 52:506-516, 1993; Schaid D.J. et al., *Genet. Epidemiol.*,13:423-450, 1996, Spielmann S. and Ewens W.J., *Am. J. Hum. Genet.*, 62:450-458, 1998). Such combined tests generally reduce the false–positive errors produced by separate analyses.

IV.C. Statistical Methods

In general, any method known in the art to test whether a trait and a genotype show a statistically significant correlation may be used.

1) Methods in linkage analysis

Statistical methods and computer programs useful for linkage analysis are well-known to those skilled in the art (see Terwilliger J.D. and Ott J., *Handbook of Human Genetic Linkage, John Hopkins University Press, London*, 1994; Ott J., *Analysis of Human Genetic Linkage, John Hopkins University Press, Baltimore,* 1991).

2) Methods to estimate haplotype frequencies in a population

As described above, when genotypes are scored, it is often not possible to distinguish heterozygotes so that haplotype frequencies cannot be easily inferred. When the gametic phase is not known, haplotype frequencies can be estimated from the multilocus genotypic data. Any method known to person skilled in the art can be used to estimate

haplotype frequencies (see Lange K., *Mathematical and Statistical Methods for Genetic Analysis, Springer, New York,* 1997; Weir, B.S., *Genetic data Analysis II: Methods for Discrete population genetic Data, Sinauer Assoc., Inc., Sunderland, MA, USA,* 1996). Preferably, maximum-likelihood haplotype frequencies are computed using an Expectation-Maximization (EM) algorithm (see Dempster et al., *J. R. Stat. Soc.*, 39B:1-38, 1977; Excoffier L. and Slatkin M., *Mol. Biol. Evol.*, 12(5): 921-927, 1995). This procedure is an iterative process aiming at obtaining maximum-likelihood estimates of haplotype frequencies from multi-locus genotype data when the gametic phase is unknown. Haplotype estimations are usually performed by applying the EM algorithm using for example the EM-HAPLO program (Hawley M.E. et al., *Am. J. Phys. Anthropol.*, 18:104, 1994) or the Arlequin program (Schneider et al., *Arlequin: a software for population genetics data analysis*, University of Geneva, 1997). The EM algorithm is a generalised iterative maximum likelihood approach to estimation and is briefly described below.

In the following part of this text, phenotypes will refer to multi-locus genotypes with unknown phase. Genotypes will refer to known-phase multi-locus genotypes.

Suppose a sample of N unrelated individuals typed for K markers. The data observed are the unknown-phase K-locus phenotypes that can categorised in F different phenotypes. Suppose that we have H underlying possible haplotypes (in case of K biallelic markers, $H=2^K$).

For phenotype j, suppose that c_j genotypes are possible. We thus have the following equation

$$P_j = \sum_{i=1}^{c_j} pr(genotype_i) = \sum_{i=1}^{c_j} pr(h_k, h_l) \qquad \underline{\text{Equation 1}}$$

where Pj is the probability of the phenotype j, h_k and h_l are the two haplotypes constituent the genotype i. Under the Hardy-Weinberg equilibrium, $pr(h_k, h_l)$ becomes :

$$pr(h_k, h_l) = pr(h_k)^2 \text{ if } h_k = h_l,\ pr(h_k, h_l) = 2pr(h_k).pr(h_l) \text{ if } h_k \neq h_l. \quad \underline{\text{Equation 2}}$$

The successive steps of the E-M algorithm can be described as follows:

Starting with initial values of the of haplotypes frequencies, noted $p_1^{(0)}, p_2^{(0)}, \ldots\ldots p_H^{(0)}$, these initial values serve to estimate the genotype frequencies (Expectation step) and then estimate another set of haplotype frequencies (Maximisation step), noted $p_1^{(1)}, p_2^{(1)}, \ldots\ldots p_H^{(1)}$, these two steps are iterated until changes in the sets of haplotypes frequency are very small.

A stop criterion can be that the maximum difference between haplotype frequencies between two iterations is less than 10^{-7}. These values can be adjusted according to the desired precision of estimations.

In details, at a given iteration s, the Expectation step consists in calculating the genotypes frequencies by the following equation:

$$pr(genotype_i)^{(s)} = pr(phenotype_j).pr(genotype_i|phenotype_j)^{(s)}$$

$$= \frac{n_j}{N}.\frac{pr(h_k,h_l)^{(s)}}{P_j^{(s)}} \qquad \underline{\text{Equation 3}}$$

where genotype i occurs in phenotype j, and where h_k and h_l constitute genotype i. Each probability is derived according to eq.1, and eq.2 described above.

Then the Maximisation step simply estimates another set of haplotype frequencies given the genotypes frequencies. This approach is also known as gene-counting method (Smith, *Ann. Hum. Genet.*, 21:254-276, 1957).

$$p_t^{(s+1)} = \frac{1}{2}\sum_{j=1}^{F}\sum_{i=1}^{c_j}\delta_{it}.pr(genotype_i)^{(s)} \qquad \underline{\text{Equation 4}}$$

Where δ_{it} is an indicator variable which count the number of time haplotype t in genotype i. It takes the values of 0, 1 or 2.

To ensure that the estimation finally obtained is the maximum-likelihood estimation several values of departures are required. The estimations obtained are compared and if they are different the estimations leading to the best likelihood are kept.

3) Methods to calculate linkage disequilibrium between markers

A number of methods can be used to calculate linkage disequilibrium between any two genetic positions, in practice linkage disequilibrium is measured by applying a statistical association test to haplotype data taken from a population.

Linkage disequilibrium between any pair of biallelic markers comprising at least one of the biallelic markers of the present invention (M_i, M_j) having alleles (a_i/b_i) at marker M_i and alleles (a_j/b_j) at marker M_j can be calculated for every allele combination (a_i,a_j ; a_i,b_j; b_i,a_j and b_i,b_j), according to the Piazza formula :

$\Delta_{aiaj} = \sqrt{\theta 4} - \sqrt{(\theta 4 + \theta 3)(\theta 4 + \theta 2)}$, where :

$\theta 4$= - - = frequency of genotypes not having allele a_i at M_i and not having allele a_j at M_j

$\theta 3$= - + = frequency of genotypes not having allele a_i at M_i and having allele a_j at M_j

$\theta 2$= + - = frequency of genotypes having allele a_i at M_i and not having allele a_j at M_j

Linkage disequilibrium (LD) between pairs of biallelic markers (M_i, M_j) can also be calculated for every allele combination (ai,aj; ai,bj ; b_i,a_j and b_i,b_j), according to the maximum-likelihood estimate (MLE) for delta (the composite genotypic disequilibrium coefficient), as described by Weir (Weir B.S., *Genetic Data Analysis, Sinauer Ass. Eds,* 1996). The MLE for the composite linkage disequilibrium is:

$$D_{aiaj}= (2n_1 + n_2 + n_3 + n_4/2)/N - 2(pr(a_i).pr(a_j))$$

Where $n_1 = \Sigma$ phenotype (a_i/a_i, a_j/a_j), $n_2 = \Sigma$ phenotype (a_i/a_i, a_j/b_j), $n_3 = \Sigma$ phenotype (a_i/b_i, a_j/a_j), n4= Σ phenotype (a_i/b_i, a_j/b_j) and N is the number of individuals in the sample.

This formula allows linkage disequilibrium between alleles to be estimated when only genotype, and not haplotype, data are available.

Another means of calculating the linkage disequilibrium between markers is as follows. For a couple of biallelic markers, M_i (a_i/b_i) and M_j (a_j/b_j), fitting the Hardy-Weinberg equilibrium, one can estimate the four possible haplotype frequencies in a given population according to the approach described above.

The estimation of gametic disequilibrium between *ai* and *aj* is simply:

$$D_{aiaj} = pr(haplotype(a_i, a_j)) - pr(a_i).pr(a_j).$$

Where $pr(a_i)$ is the probability of allele a_i and $pr(a_j)$ is the probability of allele a_j and where *pr(haplotype* (a_i, a_j)) is estimated as in Equation 3 above.

For a couple of biallelic marker only one measure of disequilibrium is necessary to describe the association between M_i and M_j.

Then a normalised value of the above is calculated as follows:

$$D'_{aiaj} = D_{aiaj} / \max(-pr(a_i).pr(a_j), -pr(b_i).pr(b_j)) \quad \text{with } D_{aiaj}<0$$

$$D'_{aiaj} = D_{aiaj} / \max(pr(b_i).pr(a_j), pr(a_i).pr(b_j)) \quad \text{with } D_{aiaj}>0$$

The skilled person will readily appreciate that other LD calculation methods can be used without undue experimentation.

Linkage disequilibrium among a set of biallelic markers having an adequate heterozygosity rate can be determined by genotyping between 50 and 1000 unrelated individuals, preferably between 75 and 200, more preferably around 100.

4) Testing for association

Methods for determining the statistical significance of a correlation between a phenotype and a genotype, in this case an allele at a biallelic marker or a haplotype made up of such alleles, may be determined by any statistical test known in the art and with any accepted threshold of statistical significance being required. The application of particular

methods and thresholds of significance are well with in the skill of the ordinary practitioner of the art.

Testing for association is performed by determining the frequency of a biallelic marker allele in case and control populations and comparing these frequencies with a statistical test to determine if their is a statistically significant difference in frequency which would indicate a correlation between the trait and the biallelic marker allele under study. Similarly, a haplotype analysis is performed by estimating the frequencies of all possible haplotypes for a given set of biallelic markers in case and control populations, and comparing these frequencies with a statistical test to determine if their is a statistically significant correlation between the haplotype and the phenotype (trait) under study. Any statistical tool useful to test for a statistically significant association between a genotype and a phenotype may be used. Preferably the statistical test employed is a chi-square test with one degree of freedom. A P-value is calculated (the P-value is the probability that a statistic as large or larger than the observed one would occur by chance).

Statistical significance

In preferred embodiments, significance for diagnosis purposes, either as a positive basis for further diagnostic tests or as a preliminary starting point for early preventive therapy, the p value related to a biallelic marker association is preferably about 1 x 10-2 or less, more preferably about 1 x 10-4 or less, for a single biallelic marker analysis and about 1 x 10-3 or less, still more preferably 1 x 10-6 or less and most preferably of about 1 x 10-8 or less, for a haplotype analysis involving several markers. These values are believed to be applicable to any association studies involving single or multiple marker combinations.

The skilled person can use the range of values set forth above as a starting point in order to carry out association studies with biallelic markers of the present invention. In doing so, significant associations between the biallelic markers of the present invention and responses to drugs or side effects upon treatment with drugs or diseases involving the metabolic conversion of xenobiotics can be revealed and used for diagnosis and drug screening purposes.

Phenotypic permutation

In order to confirm the statistical significance of the first stage haplotype analysis described above, it might be suitable to perform further analyses in which genotyping data from case-control individuals are pooled and randomised with respect to the trait phenotype. Each individual genotyping data is randomly allocated to two groups, which contain the same number of individuals as the case-control populations used to compile the data

obtained in the first stage. A second stage haplotype analysis is preferably run on these artificial groups, preferably for the markers included in the haplotype of the first stage analysis showing the highest relative risk coefficient. This experiment is reiterated preferably at least between 100 and 10000 times. The repeated iterations allow the determination of the percentage of obtained haplotypes with a significant p-value level.

Assessment of statistical association

To address the problem of false positives similar analysis may be performed with the same case-control populations in random genomic regions. Results in random regions and the candidate region are compared as described in US Provisional Patent Application entitled "Methods, software and apparati for identifying genomic regions harbouring a gene associated with a detectable trait".

5) Evaluation of risk factors

The association between a risk factor (in genetic epidemiology the risk factor is the presence or the absence of a certain allele or haplotype at marker loci) and a disease is measured by the odds ratio (OR) and by the relative risk (RR). If $P(R^+)$ is the probability of developing the disease for individuals with R and $P(R^-)$ is the probability for individuals without the risk factor, then the relative risk is simply the ratio of the two probabilities, that is:

$$RR = P(R^+)/P(R^-)$$

In case-control studies, direct measures of the relative risk cannot be obtained because of the sampling design. However, the odds ratio allows a good approximation of the relative risk for low-incidence diseases and can be calculated:

$$OR = \left[\frac{F^+}{1-F^+}\right] \Big/ \left[\frac{F^-}{(1-F^-)}\right]$$

F^+ is the frequency of the exposure to the risk factor in cases and F^- is the frequency of the exposure to the risk factor in controls. F^+ and F^- are calculated using the allelic or haplotype frequencies of the study and further depend on the underlying genetic model (dominant, recessive, additive...).

One can further estimate the attributable risk (AR) which describes the proportion of individuals in a population exhibiting a trait due to a given risk factor. This measure is important in quantitating the role of a specific factor in disease etiology and in terms of the public health impact of a risk factor. The public health relevance of this measure lies in

estimating the proportion of cases of disease in the population that could be prevented if the exposure of interest were absent. AR is determined as follows:

$$AR = P_E\,(RR\text{-}1) \,/\, (P_E\,(RR\text{-}1)+1)$$

AR is the risk attributable to a biallelic marker allele or a biallelic marker haplotype. P_E is the frequency of exposure to an allele or a haplotype within the population at large; and RR is the relative risk which, is approximated with the odds ratio when the trait under study has a relatively low incidence in the general population.

IV.D. Identification of Biallelic Markers in Linkage Disequilibrium with the Biallelic Markers of the Invention

Once a first biallelic marker has been identified in a genomic region of interest, the practitioner of ordinary skill in the art, using the teachings of the present invention, can easily identify additional biallelic markers in linkage disequilibrium with this first marker. As mentioned before any marker in linkage disequilibrium with a first marker associated with a trait will be associated with the trait. Therefore, once an association has been demonstrated between a given biallelic marker and a trait, the discovery of additional biallelic markers associated with this trait is of great interest in order to increase the density of biallelic markers in this particular region. The causal gene or mutation will be found in the vicinity of the marker or set of markers showing the highest correlation with the trait.

Identification of additional markers in linkage disequilibrium with a given marker involves: (a) amplifying a genomic fragment comprising a first biallelic marker from a plurality of individuals; (b) identifying of second biallelic markers in the genomic region harboring said first biallelic marker; (c) conducting a linkage disequilibrium analysis between said first biallelic marker and second biallelic markers; and (d) selecting said second biallelic markers as being in linkage disequilibrium with said first marker. Subcombinations comprising steps (b) and (c) are also contemplated.

Methods to identify biallelic markers and to conduct linkage disequilibrium analysis are described herein and can be carried out by the skilled person without undue experimentation. The present invention then also concerns biallelic markers which are in linkage disequilibrium with the specific biallelic markers shown in Figure 1 and which are expected to present similar characteristics in terms of their respective association with a given trait.

IV.E. Identification of Functional Mutations

Once a positive association is confirmed with a biallelic marker of the present invention, the associated candidate gene can be scanned for mutations by comparing the

sequences of a selected number of trait positive and trait negative or control individuals. In a preferred embodiment, functional regions such as exons and splice sites, promoters and other regulatory regions of the candidate gene are scanned for mutations. Preferably, trait positive individuals carry the haplotype shown to be associated with the trait and trait negative individuals do not carry the haplotype or allele associated with the trait. The mutation detection procedure is essentially similar to that used for biallelic site identification.

The method used to detect such mutations generally comprises the following steps: (a) amplification of a region of the candidate gene comprising a biallelic marker or a group of biallelic markers associated with the trait from DNA samples of trait positive patients and trait negative controls; (b) sequencing of the amplified region; (c) comparison of DNA sequences from trait-positive patients and trait-negative controls; and (d) determination of mutations specific to trait-positive patients. Subcombinations which comprise steps (b) and (c) are specifically contemplated.

It is preferred that candidate polymorphisms be then verified by screening a larger population of cases and controls by means of any genotyping procedure such as those described herein, preferably using a microsequencing technique in an individual test format. Polymorphisms are considered as candidate mutations when present in cases and controls at frequencies compatible with the expected association results.

Identification of mutations and low frequency polymorphisms in exons 3-5, in the 5'UTR region and in the 3' flanking region of the MGST-II gene is further described in Example 5. Eight polymorphisms were identified in the region of the MGST-II gene that was scanned. Three mutations were identified in the 3'UTR region. One mutation in exon 4 causes an amino acid substitution (Tyr→His) at the polypeptide level. A mutation in exon 5 introduces a stop codon into the ORF leading to the expression of a truncated MGST-II polypeptide. These mutations modify the specificity, activity and function of the MGST-II enzyme and therefore represent functional mutations of the MGST-II gene. Candidate polymorphisms and mutations suspected of being responsible for the detectable phenotype, such as hepatoxicity to zileuton or asthma, can be confirmed by screening a larger population of affected and unaffected individuals using any of the genotyping procedures described herein. Preferably the microsequencing technique is used. In a preferred embodiement trait positive and trait negative populations are genotyped for the candidate polymorphisms identified in Example 5 (10-286-289, 10-286-345, 10-286-375, 10-523-232, 10-289-201, 10-290-37, 10-290-326 and 10-290-328) most preferably for the

mutations in exons 4 and 5 (10-289-201 and 10-290-37). Polymorphisms are considered as candidate "trait-causing" mutations when they exhibit a statistically significant correlation with the detectable phenotype.

V. Biallelic Markers of the Invention in Methods of Genetic Diagnostics

The biallelic markers of the present invention can also be used to develop diagnostics tests capable of identifying individuals who express a detectable trait as the result of a specific genotype or individuals whose genotype places them at risk of developing a detectable trait at a subsequent time. The trait analyzed using the present diagnostics may be any detectable trait, including a response to a drug or side effects to a drug upon treatment or a disease involving the metabolic conversion of xenobiotics.

The diagnostic techniques of the present invention may employ a variety of methodologies to determine whether a test subject has a biallelic marker pattern associated with an increased risk of developing a detectable trait or whether the individual suffers from a detectable trait as a result of a particular mutation, including methods which enable the analysis of individual chromosomes for haplotyping, such as family studies, single sperm DNA analysis or somatic hybrids.

The present invention provides diagnostic methods to determine whether an individual is at risk of developing a disease or suffers from a disease resulting from a mutation or a polymorphism in a candidate gene of the present invention. The present invention also provides methods to determine whether an individual is likely to respond positively to a therapeutic agent or whether an individual is at risk of developing an adverse side effect to a therapeutic agent.

These methods involve obtaining a nucleic acid sample from the individual and, determining, whether the nucleic acid sample contains at least one allele or at least one biallelic marker haplotype, indicative of a risk of developing the trait or indicative that the individual expresses the trait as a result of possessing a particular candidate gene polymorphism or mutation (trait-causing allele).

Preferably, in such diagnostic methods, a nucleic acid sample is obtained from the individual and this sample is genotyped using methods described above in III. "Methods of Genotyping an Individual for Biallelic Markers." The diagnostics may be based on a single biallelic marker or a on group of biallelic markers.

In each of these methods, a nucleic acid sample is obtained from the test subject and the biallelic marker pattern of one or more of the biallelic markers listed in Figure 1 is determined.

In one embodiment, a PCR amplification is conducted on the nucleic acid sample to amplify regions in which polymorphisms associated with a detectable phenotype have been identified. The amplification products are sequenced to determine whether the individual possesses one or more polymorphisms associated with a detectable phenotype. The primers used to generate amplification products may comprise the primers listed in Figure 7. Alternatively, the nucleic acid sample is subjected to microsequencing reactions as described above to determine whether the individual possesses one or more polymorphisms associated with a detectable phenotype resulting from a mutation or a polymorphism in a candidate gene. The primers used in the microsequencing reactions may include the primers listed in Figure 6. In another embodiment, the nucleic acid sample is contacted with one or more allele specific oligonucleotide probes which, specifically hybridize to one or more candidate gene alleles associated with a detectable phenotype. The probes used in the hybridization assay may include the probes listed in Figure 8. Diagnostic kits comprising polynucleotides of the present invention are further described in section I.

These diagnostic methods are extremely valuable as they can, in certain circumstances, be used to initiate preventive treatments or to allow an individual carrying a significant haplotype to foresee warning signs such as minor symptoms. For diseases in which attacks may be extremely violent and sometimes fatal if not treated on time, the knowledge of a potential predisposition, even if this predisposition is not absolute, might contribute in a very significant manner to treatment efficacy. Similarly, a diagnosed predisposition to a potential side effect could immediately direct the physician toward a treatment for which such side effects have not been observed during clinical trials.

Diagnostics, which analyze and predict response to a drug or side effects to a drug, may be used to determine whether an individual should be treated with a particular drug. For example, if the diagnostic indicates a likelihood that an individual will respond positively to treatment with a particular drug, the drug may be administered to the individual. Conversely, if the diagnostic indicates that an individual is likely to respond negatively to treatment with a particular drug, an alternative course of treatment may be prescribed. A negative response may be defined as either the absence of an efficacious response or the presence of toxic side effects.

Clinical drug trials represent another application for the markers of the present invention. One or more markers indicative of response to a drug or to side effects to a drug may be identified using the methods described above. Thereafter, potential participants in clinical trials of such an agent may be screened to identify those individuals most likely to

respond favorably to the drug and exclude those likely to experience side effects. In that way, the effectiveness of drug treatment may be measured in individuals who respond positively to the drug, without lowering the measurement as a result of the inclusion of individuals who are unlikely to respond positively in the study and without risking undesirable safety problems.

In a preferred embodiment the identity of the nucleotide present at, at least one, biallelic marker selected from the group consisting of 12-455-326, 12-453-429, 12-454-363, 12-441-233, 12-461-299, 12-426-154, 12-424-198, 12-716-295, 10-428-219,12-720-80, 12-156-91, 12-140-134, 12-653-423, 10-471-84, 10-471-85, 10-470-25, 12-652-203, 12-637-219, 12-721-440 and 10-420-284 is determined, and optionally wherein the detectable trait is asthma, or optionally the detectable trait is hepatoxicity to the anti-asthmatic drug zileuton. In another preferred embodiment the identity of the nucleotide present at, at least one of the polymorphic sites selected from the group consisting of 12-447-58, 12-455-326, 12-461-299, 12-453-429, 12-424-198, 12-454-363, 12-716-295, 10-428-219, 12-720-80, 10-420-248, 12-721-440, 12-653-423, 10-470-25, 10-471-84, 10-471-85, 12-637-219 and 12-652-203 is determined, and optionally wherein the detectable trait is asthma. In another preferred embodiment the identity of the nucleotide present at, at least one of the polymorphic sites selected from the group consisting of 12-453-429, 12-455-326, 12-453-429, 12-454-363, 12-441-233, 12-461-299, 12-426-154, 12-424-198, 12-716-295, 10-428-219,12-720-80, 12-156-91, 12-140-134, 12-653-423, 10-471-84, 10-471-85, 10-470-25, 12-652-203, 12-637-219, 12-721-440, and 10-420-284 is determined, and optionally wherein the detectable trait is hepatoxicity to the anti-asthmatic drug zileuton. Diagnostic kits comprising polynucleotides of the present invention are further described in section I. "Biallelic Markers and Polynucleotides Comprising Biallelic Markers."

VI. Association of Biallelic Markers of the Invention With Asthma

In the context of the present invention, an association between the MGST-II, ME1, UGT1A7 and UGT2B4 genes and asthma was established.

Asthma affects over 5% of the population in industrialized countries. It is increasing in prevalence and severity and has a rising mortality (Rang H.P., Ritter J.M. and Dale M.M.; *Pharmacology*; Churchill Livingstone, NY, 1995). Bronchial asthma is a multifactorial syndrome rather than a single disease, defined as airway obstruction characterized by inflammatory changes in the airways and bronchial hyper-responsiveness. In addition to the evidenced impact of environmental factors on the development of asthma, patterns of clustering and segregation in asthmatic families have suggested a genetic

component to asthma. However the lack of a defined and specific asthma phenotype and of suitable markers for genetic analysis is proving to be a major hurdle for reliably identifying genes associated with asthma. The identification of genes implicated in asthma would represent a major step towards the identification of new molecular targets for the development of anti-asthma drugs. Moreover there is no straightforward physiological or biological blood test for the asthmatic state. As a result, adequate asthma treatment is often delayed, thereby allowing the inflammation process to better establish itself. Thus, there is a need for the identification of asthma susceptibility genes in order to develop an efficient and reliable asthma diagnostic test.

As mentioned above, products of arachidonic acid metabolism are important inflammatory mediators and have been involved in a number of inflammatory diseases, including asthma. More specifically, prostaglandins and leukotrienes are thought to play a major role in the inflammatory process observed in asthma patients.

In order to investigate and identify a genetic origin to asthma, a candidate gene scan was conducted. This approach comprised:

- selecting candidate genes potentially involved in the pathological pathway of interest, in this case arachidonic acid metabolism, and
- identifying biallelic markers in those genes, and finally
- conducting association studies to identify biallelic marker alleles or haplotypes associated with asthma.

Further details concerning this association study are provided in Example 3, results are briefly summarized below.

Two groups of independent individuals were used in this association study in accordance with the invention: the case-control populations. The two groups corresponded to 297 asthmatic individuals and 178 control individuals. The trait positive asthma population was mostly composed of individuals from Caucasian ethnic background (>90 %). The control population was composed of individuals from a random US Caucasian population.

In the association study described in Example 3, several biallelic marker haplotypes were shown to be significantly associated with asthma. A preferred haplotype consisting of three biallelic markers (12-455-326, 12-453-429 and 12-424-198) presented a p-value of $3.2\ 10^{-5}$. Another preferred haplotype consisting of four biallelic markers (12-455-326, 12-453-429, 12-424-198 and 12-454-363) had a p-value of $1.2\ 10^{-6}$. Phenotypic permutation

tests confirmed the statistical significance of these results. These haplotypes can therefore be considered to be significantly associated with asthma.

This information is extremely valuable. The knowledge of a potential genetic predisposition to asthma, even if this predisposition is not absolute, might contribute in a very significant manner to treatment efficacy of asthma patients and to the development of new therapeutic and diagnostic tools.

VII. Association of Biallelic Markers of the Invention with Hepatotoxicity to Anti-Asthma Drug Zileuton (Zyflo™)

In the context of the present invention, an association between the MGST-II gene and side effects related to treatment with the anti-asthmatic drug zileuton was discovered.

As mentioned above, bronchial asthma is a multifactorial syndrome rather than a single disease, defined as airway obstruction characterized by inflammatory changes in the airways and bronchial hyper-responsiveness. Although initially reversible with bronchiodilators, airway obstruction becomes increasingly irreversible if treated poorly. Asthma management therefore relies on early and regular use of drugs that control the disease. As a consequence, there is a strong need for efficient and safe therapeutic opportunities for patients with asthma. There are two main categories of anti-asthmatic drugs– bronchodilators and anti-inflammatory agents. There is now general agreement on the need to implement early anti-inflammatory treatment rather than relying on symptomatic treatment with bronchiodilators alone. The leukotrienes, a family of proinflammatory mediators arising via arachidonic acid metabolism, have been implicated in the inflammatory cascade that occurs in asthmatic airways. Of great relevance to the pathogenesis of asthma are the 5-lipoxygenase and the 5-lipoxygenase activating protein (FLAP), which catalyze the initial steps in the biosynthesis of leukotrienes from arachidonic acid. Given the significant role of the inflammatory process in asthma, pharmacological agents, such as leukotriene antagonists, FLAP inhibitors and 5-lipoxygenase inhibitors have been developed.

Zileuton (Zyflo™) is an active inhibitor of 5-lipoxygenase, the enzyme that catalyzes the formation of leukotrienes from arachidonic acid, indicated for prophylaxis and chronic treatment of asthma. A minority of zileuton-treated patients develop liver function abnormalities as close monitoring revealed that elevations of liver function tests may occur during treatment with zileuton. In the present invention the ALT test (serum level of alanine aminotransferase) was used, which is considered the most sensitive indicator of liver injury.

In order to investigate and identify a genetic origin to zileuton-associated hepatotoxicity, a candidate gene scan was conducted. This approach comprised:

- selecting candidate genes potentially involved in the pathological pathway of interest or in the metabolism of zileuton, and
- identifying biallelic markers in those genes, and finally
- conducting association studies to identify biallelic marker alleles or haplotypes associated with elevations of liver function tests upon treatment with zileuton.

Further details concerning this association study are provided in Example 4, results are briefly summarized below.

Two groups of unrelated individuals were used in this association study in accordance with the invention: the case-control populations. The case population was composed of 89 asthmatic individuals treated with zileuton showing zileuton-associated hepatotoxicity monitored by the serum level of alanine aminotransferase (ALT) and the control population was composed of 208 asthmatic individuals treated with zileuton and having no increased serum ALT level.

The association study conducted with the biallelic markers derived from the MGST-II locus showed that several haplotypes were significantly associated with zileuton-associated hepatotoxicity. A preferred haplotype consisting of three biallelic markers (12-441-233, 12-461-299 and 12-453-429) presented a p-value of 1.5 10^{-5} and an odd ratio of 3.63. A second preferred haplotype consisting of four biallelic markers (12-441-233, 12-461-299, 12-453-429 and 12-426-154) had a p-value of 5.2 10^{-7} and an odd ratio of 5.75.

This information is extremely valuable. The knowledge of a potential genetic predisposition to hepatoxicity upon treatment with zileuton, even if this predisposition is not absolute, might contribute in a very significant manner to the safety of asthma treatment and to the development of diagnostic tools.

Similar association studies, with different case-control populations, can be routinely carried out by the skilled technician using the biallelic markers of the present invention in order to identify other association between traits and MGST-II-related biallelic marker alleles or haplotypes.

VI. Computer-Related Embodiments

As used herein the term "nucleic acid codes of the invention" encompass the nucleotide sequences comprising, consisting essentially of, or consisting of any one of the following: a) a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500 or 1000 nucleotides, to the extent that a polynucleotide of these lengths

is consistent with the lengths of the particular Sequence ID, of a sequence selected from the group consisting of the sequences described in Figure 2, and the complements thereof; b) a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500 or 1000 nucleotides, to the extent that a polynucleotide of these lengths is consistent with the lengths of the particular Sequence ID, of a sequence selected from the group consisting of the sequences described in Figure 3, and the complements thereof; c) a contiguous span of at least 12, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, or 500 nucleotides, to the extent that a polynucleotide of these lengths is consistent with the lengths of the particular Sequence ID, of a sequence selected from the group consisting of the sequences described in Figure 6, more preferably a set of markers or sequences consisting of those markers or sequences found in SEQ ID Nos. 3, 5, 9, 13-15, 25, 31, 33, 37, 38, 41, 323, 345, 351-353, 357, 377, and 380, and the complements thereof, wherein said span includes an DME-related biallelic marker, preferably an DME-related biallelic marker described in Figure 1, preferably the biallelic markers found in Figures 9, 10, 11 and 12; or more preferably the biallelic markers found in SEQ ID Nos. 3, 5, 9, 13-15, 25, 31, 33, 37, 38, 41, 323, 345, 351-353, 357, 377, 380, in said sequence with the alternative allele present at said biallelic marker.

The "nucleic acid codes of the invention" further encompass nucleotide sequences homologous to a contiguous span of at least 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, 500 or 1000 nucleotides, to the extent that a contiguous span of these lengths is consistent with the lengths of the particular Sequence ID, of a sequence selected from the group consisting of the sequences described in Figure 2, Figure 3 and Figure 6 and the complements thereof. Homologous sequences refer to a sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, 80%, or 75% homology to these contiguous spans. Homology may be determined using any method described herein, including BLAST2N with the default parameters or with any modified parameters. Homologous sequences also may include RNA sequences in which uridines replace the thymines in the nucleic acid codes of the invention. It will be appreciated that the nucleic acid codes of the invention can be represented in the traditional single character format (See the inside back cover of Stryer, Lubert. *Biochemistry*, 3rd edition. W. H Freeman & Co., New York.) or in any other format or code which records the identity of the nucleotides in a sequence.

It will be appreciated by those skilled in the art that the nucleic acid codes of the invention, one or more of the polypeptide codes of SEQ ID Nos. 488 and 489 can be stored, recorded, and manipulated on any medium which can be read and accessed by a computer. As

used herein, the words "recorded" and "stored" refer to a process for storing information on a computer medium. A skilled artisan can readily adopt any of the presently known methods for recording information on a computer readable medium to generate manufactures comprising one or more of the nucleic acid codes of the invention and one or more of the polypeptide codes of SEQ ID Nos. 488 and 489. Another aspect of the present invention is a computer readable medium having recorded thereon at least 2, 5, 10, 15, 20, 25, 30, or 50 nucleic acid codes of the invention, and the complements thereof. Another aspect of the present invention is a computer readable medium having recorded thereon at least 2, 5, 10, 15, 20, 25, 30, or 50 polypeptide codes of SEQ ID Nos. 488 and 489.

Computer readable media include magnetically readable media, optically readable media, electronically readable media and magnetic/optical media. For example, the computer readable media may be a hard disk, a floppy disk, a magnetic tape, CD-ROM, Digital Versatile Disk (DVD), Random Access Memory (RAM), or Read Only Memory (ROM) as well as other types of other media known to those skilled in the art.

Embodiments of the present invention include systems, particularly computer systems which store and manipulate the sequence information described herein. One example of a computer system 100 is illustrated in block diagram form in Figure 17. As used herein, "a computer system" refers to the hardware components, software components, and data storage components used to analyze the nucleotide sequences of the nucleic acid codes of the invention , or the amino acid sequences of the polypeptide codes of SEQ ID Nos. 488 and 489. In one embodiment, the computer system 100 is a Sun Enterprise 1000 server (Sun Microsystems, Palo Alto, CA). The computer system 100 preferably includes a processor for processing, accessing and manipulating the sequence data. The processor 105 can be any well-known type of central processing unit, such as the Pentium III from Intel Corporation, or similar processor from Sun, Motorola, Compaq or International Business Machines. Preferably, the computer system 100 is a general purpose system that comprises the processor 105 and one or more internal data storage components 110 for storing data, and one or more data retrieving devices for retrieving the data stored on the data storage components. A skilled artisan can readily appreciate that any one of the currently available computer systems are suitable. In one particular embodiment, the computer system 100 includes a processor 105 connected to a bus which is connected to a main memory 115 (preferably implemented as RAM) and one or more internal data storage devices 110, such as a hard drive and/or other computer readable media having data recorded thereon. In some embodiments, the computer system 100 further includes one or more data retrieving device 118 for reading the data stored on the internal data

storage devices 110. The data retrieving device 118 may represent, for example, a floppy disk drive, a compact disk drive, a magnetic tape drive, etc. In some embodiments, the internal data storage device 110 is a removable computer readable medium such as a floppy disk, a compact disk, a magnetic tape, etc. containing control logic and/or data recorded thereon. The computer system 100 may advantageously include or be programmed by appropriate software for reading the control logic and/or the data from the data storage component once inserted in the data retrieving device. The computer system 100 includes a display 120 which is used to display output to a computer user. It should also be noted that the computer system 100 can be linked to other computer systems 125a-c in a network or wide area network to provide centralized access to the computer system 100. Software for accessing and processing the nucleotide sequences of the nucleic acid codes of the invention, or the amino acid sequences of the polypeptide codes of SEQ ID Nos. 488 and 489 (such as search tools, compare tools, and modeling tools etc.) may reside in main memory 115 during execution. In some embodiments, the computer system 100 may further comprise a sequence comparer for comparing the above-described nucleic acid codes of the invention or polypeptide codes of SEQ ID Nos. 488 and 489 stored on a computer readable medium to reference nucleotide or polypeptide sequences stored on a computer readable medium. A "sequence comparer" refers to one or more programs which are implemented on the computer system 100 to compare a nucleotide or polypeptide sequence with other nucleotide or polypeptide sequences and/or compounds including but not limited to peptides, peptidomimetics, and chemicals stored within the data storage means. For example, the sequence comparer may compare the nucleotide sequences of the nucleic acid codes of the invention, or the amino acid sequences of the polypeptide codes of SEQ ID Nos. 488 and 489 stored on a computer readable medium to reference sequences stored on a computer readable medium to identify homologies, motifs implicated in biological function, or structural motifs. The various sequence comparer programs identified elsewhere in this patent specification are particularly contemplated for use in this aspect of the invention.

Figure 18 is a flow diagram illustrating one embodiment of a process 200 for comparing a new nucleotide or protein sequence with a database of sequences in order to determine the homology levels between the new sequence and the sequences in the database. The database of sequences can be a private database stored within the computer system 100, or a public database such as GENBANK, PIR OR SWISSPROT that is available through the Internet.

The process 200 begins at a start state 201 and then moves to a state 202 wherein the new sequence to be compared is stored to a memory in a computer system 100. As discussed

above, the memory could be any type of memory, including RAM or an internal storage device. The process 200 then moves to a state 204 wherein a database of sequences is opened for analysis and comparison. The process 200 then moves to a state 206 wherein the first sequence stored in the database is read into a memory on the computer. A comparison is then performed at a state 210 to determine if the first sequence is the same as the second sequence. It is important to note that this step is not limited to performing an exact comparison between the new sequence and the first sequence in the database. Well-known methods are known to those of skill in the art for comparing two nucleotide or protein sequences, even if they are not identical. For example, gaps can be introduced into one sequence in order to raise the homology level between the two tested sequences. The parameters that control whether gaps or other features are introduced into a sequence during comparison are normally entered by the user of the computer system. Once a comparison of the two sequences has been performed at the state 210, a determination is made at a decision state 210 whether the two sequences are the same. Of course, the term "same" is not limited to sequences that are absolutely identical. Sequences that are within the homology parameters entered by the user will be marked as "same" in the process 200. If a determination is made that the two sequences are the same, the process 200 moves to a state 214 wherein the name of the sequence from the database is displayed to the user. This state notifies the user that the sequence with the displayed name fulfills the homology constraints that were entered. Once the name of the stored sequence is displayed to the user, the process 200 moves to a decision state 218 wherein a determination is made whether more sequences exist in the database. If no more sequences exist in the database, then the process 200 terminates at an end state 220. However, if more sequences do exist in the database, then the process 200 moves to a state 224 wherein a pointer is moved to the next sequence in the database so that it can be compared to the new sequence. In this manner, the new sequence is aligned and compared with every sequence in the database. It should be noted that if a determination had been made at the decision state 212 that the sequences were not homologous, then the process 200 would move immediately to the decision state 218 in order to determine if any other sequences were available in the database for comparison. Accordingly, one aspect of the present invention is a computer system comprising a processor, a data storage device having stored thereon a nucleic acid code of the invention or a polypeptide code of SEQ ID Nos. 488 and 489, a data storage device having retrievably stored thereon reference nucleotide sequences or polypeptide sequences to be compared to the nucleic acid code of the invention or polypeptide code of SEQ ID Nos. 488 and 489 and a sequence comparer for conducting the comparison. The sequence

comparer may indicate a homology level between the sequences compared or identify structural motifs in the above described nucleic acid code of the invention and polypeptide codes of SEQ ID Nos. 488 and 489 or it may identify structural motifs in sequences which are compared to these nucleic acid codes and polypeptide codes. In some embodiments, the data storage device may have stored thereon the sequences of at least 2, 5, 10, 15, 20, 25, 30, or 50 of the nucleic acid codes of the invention or polypeptide codes of SEQ ID Nos. 488 and 489.

Another aspect of the present invention is a method for determining the level of homology between a nucleic acid code of the invention and a reference nucleotide sequence, comprising the steps of reading the nucleic acid code and the reference nucleotide sequence through the use of a computer program which determines homology levels and determining homology between the nucleic acid code and the reference nucleotide sequence with the computer program. The computer program may be any of a number of computer programs for determining homology levels, including those specifically enumerated herein, including BLAST2N with the default parameters or with any modified parameters. The method may be implemented using the computer systems described above. The method may also be performed by reading 2, 5, 10, 15, 20, 25, 30, or 50 of the above described nucleic acid codes of the invention through use of the computer program and determining homology between the nucleic acid codes and reference nucleotide sequences .

Figure 19 is a flow diagram illustrating one embodiment of a process 250 in a computer for determining whether two sequences are homologous. The process 250 begins at a start state 252 and then moves to a state 254 wherein a first sequence to be compared is stored to a memory. The second sequence to be compared is then stored to a memory at a state 256. The process 250 then moves to a state 260 wherein the first character in the first sequence is read and then to a state 262 wherein the first character of the second sequence is read. It should be understood that if the sequence is a nucleotide sequence, then the character would normally be either A, T, C, G or U. If the sequence is a protein sequence, then it should be in the single letter amino acid code so that the first and sequence sequences can be easily compared.

A determination is then made at a decision state 264 whether the two characters are the same. If they are the same, then the process 250 moves to a state 268 wherein the next characters in the first and second sequences are read. A determination is then made whether the next characters are the same. If they are, then the process 250 continues this loop until two characters are not the same. If a determination is made that the next two

characters are not the same, the process 250 moves to a decision state 274 to determine whether there are any more characters either sequence to read. If there aren't any more characters to read, then the process 250 moves to a state 276 wherein the level of homology between the first and second sequences is displayed to the user. The level of homology is determined by calculating the proportion of characters between the sequences that were the same out of the total number of sequences in the first sequence. Thus, if every character in a first 100 nucleotide sequence aligned with a every character in a second sequence, the homology level would be 100%. Alternatively, the computer program may be a computer program which compares the nucleotide sequences of the nucleic acid codes of the present invention, to reference nucleotide sequences in order to determine whether the nucleic acid code of SEQ ID Nos. 1-652 differs from a reference nucleic acid sequence at one or more positions. Optionally such a program records the length and identity of inserted, deleted or substituted nucleotides with respect to the sequence of either the reference polynucleotide or the nucleic acid code of SEQ ID Nos. 1-652. In one embodiment, the computer program may be a program which determines whether the nucleotide sequences of the nucleic acid codes of the invention contain a biallelic marker or single nucleotide polymorphism (SNP) with respect to a reference nucleotide sequence. This single nucleotide polymorphism may comprise a single base substitution, insertion, or deletion, while this biallelic marker may comprise about one to ten consecutive bases substituted, inserted or deleted.

Another aspect of the present invention is a method for determining the level of homology between a polypeptide code of SEQ ID Nos. 488 and 489 and a reference polypeptide sequence, comprising the steps of reading the polypeptide code of SEQ ID Nos. 488 and 489 and the reference polypeptide sequence through use of a computer program which determines homology levels and determining homology between the polypeptide code and the reference polypeptide sequence using the computer program.

Accordingly, another aspect of the present invention is a method for determining whether a nucleic acid code of the invention differs at one or more nucleotides from a reference nucleotide sequence comprising the steps of reading the nucleic acid code and the reference nucleotide sequence through use of a computer program which identifies differences between nucleic acid sequences and identifying differences between the nucleic acid code and the reference nucleotide sequence with the computer program. In some embodiments, the computer program is a program which identifies single nucleotide polymorphisms. The method may be implemented by the computer systems described above and the method illustrated in Figure 19. The method may also be performed by

reading at least 2, 5, 10, 15, 20, 25, 30, or 50 of the nucleic acid codes of the invention and the reference nucleotide sequences through the use of the computer program and identifying differences between the nucleic acid codes and the reference nucleotide sequences with the computer program. In other embodiments the computer based system may further comprise an identifier for identifying features within the nucleotide sequences of the nucleic acid codes of the invention or the amino acid sequences of the polypeptide codes of SEQ ID Nos. 488 and 489. An "identifier" refers to one or more programs which identifies certain features within the above-described nucleotide sequences of the nucleic acid codes of the invention or the amino acid sequences of the polypeptide codes of SEQ ID Nos. 488 and 489. In one embodiment, the identifier may comprise a program which identifies an open reading frame in the cDNAs codes of SEQ ID Nos. 486 and 487.

Figure 20 is a flow diagram illustrating one embodiment of an identifier process 300 for detecting the presence of a feature in a sequence. The process 300 begins at a start state 302 and then moves to a state 304 wherein a first sequence that is to be checked for features is stored to a memory 115 in the computer system 100. The process 300 then moves to a state 306 wherein a database of sequence features is opened. Such a database would include a list of each feature's attributes along with the name of the feature. For example, a feature name could be "Initiation Codon" and the attribute would be "ATG." Another example would be the feature name "TAATAA Box" and the feature attribute would be "TAATAA". An example of such a database is produced by the University of Wisconsin Genetics Computer Group (www.gcg.com). Once the database of features is opened at the state 306, the process 300 moves to a state 308 wherein the first feature is read from the database. A comparison of the attribute of the first feature with the first sequence is then made at a state 310. A determination is then made at a decision state 316 whether the attribute of the feature was found in the first sequence. If the attribute was found, then the process 300 moves to a state 318 wherein the name of the found feature is displayed to the user. The process 300 then moves to a decision state 320 wherein a determination is made whether move features exist in the database. If no more features do exist, then the process 300 terminates at an end state 324. However, if more features do exist in the database, then the process 300 reads the next sequence feature at a state 326 and loops back to the state 310 wherein the attribute of the next feature is compared against the first sequence. It should be noted, that if the feature attribute is not found in the first sequence at the decision state 316, the process 300 moves directly to the decision state 320 in order to determine if any more features exist in the database. In another embodiment, the identifier may comprise a

molecular modeling program which determines the 3-dimensional structure of the polypeptides codes of SEQ ID Nos. 488 and 489. In some embodiments, the molecular modeling program identifies target sequences that are most compatible with profiles representing the structural environments of the residues in known three-dimensional protein structures. (See, e.g., Eisenberg et al., U.S. Patent No. 5,436,850 issued July 25, 1995). In another technique, the known three-dimensional structures of proteins in a given family are superimposed to define the structurally conserved regions in that family. This protein modeling technique also uses the known three-dimensional structure of a homologous protein to approximate the structure of the polypeptide codes of SEQ ID Nos. 488 and 489. (See e.g., Srinivasan, et al., U.S. Patent No. 5,557,535 issued September 17, 1996). Conventional homology modeling techniques have been used routinely to build models of proteases and antibodies. (Sowdhamini et al., Protein Engineering 10:207, 215 (1997)). Comparative approaches can also be used to develop three-dimensional protein models when the protein of interest has poor sequence identity to template proteins. In some cases, proteins fold into similar three-dimensional structures despite having very weak sequence identities. For example, the three-dimensional structures of a number of helical cytokines fold in similar three-dimensional topology in spite of weak sequence homology. The recent development of threading methods now enables the identification of likely folding patterns in a number of situations where the structural relatedness between target and template(s) is not detectable at the sequence level. Hybrid methods, in which fold recognition is performed using Multiple Sequence Threading (MST), structural equivalencies are deduced from the threading output using a distance geometry program DRAGON to construct a low resolution model, and a full-atom representation is constructed using a molecular modeling package such as QUANTA.

According to this 3-step approach, candidate templates are first identified by using the novel fold recognition algorithm MST, which is capable of performing simultaneous threading of multiple aligned sequences onto one or more 3-D structures. In a second step, the structural equivalencies obtained from the MST output are converted into interresidue distance restraints and fed into the distance geometry program DRAGON, together with auxiliary information obtained from secondary structure predictions. The program combines the restraints in an unbiased manner and rapidly generates a large number of low resolution model confirmations. In a third step, these low resolution model confirmations are converted into full-atom models and subjected to energy minimization using the

molecular modeling package QUANTA. (See e.g., Aszódi et al., Proteins: Structure, Function, and Genetics, Supplement 1:38-42 (1997)).

The results of the molecular modeling analysis may then be used in rational drug design techniques to identify agents which modulate the activity of the polypeptide codes of SEQ ID Nos. 488 and 489. Accordingly, another aspect of the present invention is a method of identifying a feature within the nucleic acid codes of the invention or the polypeptide codes of SEQ ID Nos. 488 and 489 comprising reading the nucleic acid code(s) or the polypeptide code(s) through the use of a computer program which identifies features therein and identifying features within the nucleic acid code(s) or polypeptide code(s) with the computer program. In one embodiment, computer program comprises a computer program which identifies open reading frames. In a further embodiment, the computer program identifies structural motifs in a polypeptide sequence. In another embodiment, the computer program comprises a molecular modeling program. The method may be performed by reading a single sequence or at least 2, 5, 10, 15, 20, 25, 30, or 50 of the nucleic acid codes of the invention or the polypeptide codes of SEQ ID Nos. 488 and 489 through the use of the computer program and identifying features within the nucleic acid codes or polypeptide codes with the computer program. The nucleic acid codes of the invention or the polypeptide codes of SEQ ID Nos. 488 and 489 may be stored and manipulated in a variety of data processor programs in a variety of formats. For example, the nucleic acid codes of the invention or the polypeptide codes of SEQ ID Nos. 488 and 489 may be stored as text in a word processing file, such as MicrosoftWORD or WORDPERFECT or as an ASCII file in a variety of database programs familiar to those of skill in the art, such as DB2, SYBASE, or ORACLE. In addition, many computer programs and databases may be used as sequence comparers, identifiers, or sources of reference nucleotide or polypeptide sequences to be compared to the nucleic acid codes of the invention or the polypeptide codes of SEQ ID Nos. 488 and 489. The following list is intended not to limit the invention but to provide guidance to programs and databases which are useful with the nucleic acid codes of the invention or the polypeptide codes of SEQ ID No. 488 and 489. The programs and databases which may be used include, but are not limited to: MacPattern (EMBL), DiscoveryBase (Molecular Applications Group), GeneMine (Molecular Applications Group), Look (Molecular Applications Group), MacLook (Molecular Applications Group), BLAST and BLAST2 (NCBI), BLASTN and BLASTX (Altschul et al, *J. Mol. Biol.* 215: 403 (1990)), FASTA (Pearson and Lipman, *Proc. Natl. Acad. Sci. USA*, 85: 2444 (1988)), FASTDB (Brutlag et al. Comp. App. Biosci. 6:237-245. 1990), Catalyst (Molecular Simulations Inc.), Catalyst/SHAPE

(Molecular Simulations Inc.), Cerius^2.DBAccess (Molecular Simulations Inc.), HypoGen (Molecular Simulations Inc.), Insight II, (Molecular Simulations Inc.), Discover (Molecular Simulations Inc.), CHARMm (Molecular Simulations Inc.), Felix (Molecular Simulations Inc.), DelPhi, (Molecular Simulations Inc.), QuanteMM, (Molecular Simulations Inc.), Homology (Molecular Simulations Inc.), Modeler (Molecular Simulations Inc.), ISIS (Molecular Simulations Inc.), Quanta/Protein Design (Molecular Simulations Inc.), WebLab (Molecular Simulations Inc.), WebLab Diversity Explorer (Molecular Simulations Inc.), Gene Explorer (Molecular Simulations Inc.), SeqFold (Molecular Simulations Inc.), the EMBL/Swissprotein database, the MDL Available Chemicals Directory database, the MDL Drug Data Report data base, the Comprehensive Medicinal Chemistry database, Derwents's World Drug Index database, the BioByteMasterFile database, the Genbank database, and the Genseqn database. Many other programs and data bases would be apparent to one of skill in the art given the present disclosure. Motifs which may be detected using the above programs include sequences encoding leucine zippers, helix-turn-helix motifs, glycosylation sites, ubiquitination sites, alpha helices, and beta sheets, signal sequences encoding signal peptides which direct the secretion of the encoded proteins, sequences implicated in transcription regulation such as homeoboxes, acidic stretches, enzymatic active sites, substrate binding sites, and enzymatic cleavage sites.

It should be noted that the nucleic acid codes of the invention further encompass all of the polynucleotides disclosed, described or claimed in the present invention. Also, it should be noted that the polypeptide codes of SEQ ID Nos. 488 and 489 further encompass all of the polypeptides disclosed, described or claimed in the present invention. Moreover, the present invention specifically contemplates the storage of such codes on computer readable media and computer systems individually or in combination, as well as the use of such codes and combinations in the methods of section "VI. Computer-Related Embodiments."

EXAMPLES

Several of the methods of the present invention are described in the following examples, which are offered by way of illustration and not by way of limitation. Many other modifications and variations of the invention as herein set forth can be made without departing from the spirit and scope thereof and therefore only such limitations should be imposed as are indicated by the appended claims.

Example 1

De Novo Identification Of Biallelic Markers

The biallelic markers set forth in this application were isolated from human genomic sequences. To identify biallelic markers, genomic fragments were amplified, sequenced and compared in a plurality of individuals.

DNA samples

Donors were unrelated and healthy. They represented a sufficient diversity for being representative of a French heterogeneous population. The DNA from 100 individuals was extracted and tested for the *de novo* identification of biallelic markers.

DNA samples were prepared from peripheral venous blood as follows. Thirty ml of peripheral venous blood were taken from each donor in the presence of EDTA. Cells (pellet) were collected after centrifugation for 10 minutes at 2000 rpm. Red cells were lysed in a lysis solution (50 ml final volume: 10 mM Tris pH7.6; 5 mM $MgCl_2$; 10 mM NaCl). The solution was centrifuged (10 minutes, 2000 rpm) as many times as necessary to eliminate the residual red cells present in the supernatant, after resuspension of the pellet in the lysis solution. The pellet of white cells was lysed overnight at 42°C with 3.7 ml of lysis solution composed of: (a) 3 ml TE 10-2 (Tris-HCl 10 mM, EDTA 2 mM) / NaCl 0.4 M; (b) 200 µl SDS 10%; and (c) 500 µl proteinase K (2 mg proteinase K in TE 10-2 / NaCl 0.4 M).

For the extraction of proteins, 1 ml saturated NaCl (6M) (1/3.5 v/v) was added. After vigorous agitation, the solution was centrifuged for 20 minutes at 10000 rpm. For the precipitation of DNA, 2 to 3 volumes of 100% ethanol were added to the previous supernatant, and the solution was centrifuged for 30 minutes at 2000 rpm. The DNA solution was rinsed three times with 70% ethanol to eliminate salts, and centrifuged for 20 minutes at 2000 rpm. The pellet was dried at 37°C, and resuspended in 1 ml TE 10-1 or 1 ml water. The DNA concentration was evaluated by measuring the OD at 260 nm (1 unit OD = 50 µg/ml DNA). To determine the presence of proteins in the DNA solution, the OD 260 / OD 280 ratio was determined. Only DNA preparations having a OD 260 / OD 280 ratio between 1.8 and 2 were used in the subsequent examples described below. DNA pools were constituted by mixing equivalent quantities of DNA from each individual.

Amplification of genomic DNA by PCR

Amplification of specific genomic sequences was carried out on pooled DNA samples obtained as described above.

Amplification primers

The primers used for the amplification of human genomic DNA fragments were defined with the OSP software (Hillier & Green, 1991). Preferably, primers included, upstream of the specific bases targeted for amplification, a common oligonucleotide tail useful for sequencing. Primers PU contain the following additional PU 5' sequence : TGTAAAACGACGGCCAGT; primers RP contain the following RP 5' sequence : CAGGAAACAGCTATGACC. Primers are listed in Figure 7.

Amplification

PCR assays were performed using the following protocol:

Final volume	25 µl
DNA	2 ng/µl
$MgCl_2$	2 mM
dNTP (each)	200 µM
primer (each)	2.9 ng/µl
Ampli Taq Gold DNA polymerase	0.05 unit/µl
PCR buffer (10x = 0.1 M TrisHCl pH8.3 0.5M KCl)	1x

DNA amplification was performed on a Genius II thermocycler. After heating at 94°C for 10 min, 40 cycles were performed. Cycling times and temperatures were: 30 sec at 94°C, 55°C for 1 min and 30 sec at 72°C. Holding for 7 min at 72°C allowed final elongation. The quantities of the amplification products obtained were determined on 96-well microtiter plates, using a fluorometer and Picogreen as intercalant agent (Molecular Probes).

Sequencing of amplified genomic DNA and identification of biallelic polymorphisms

Sequencing of the amplified DNA was carried out on ABI 377 sequencers. The sequences of the amplification products were determined using automated dideoxy terminator sequencing reactions with a dye terminator cycle sequencing protocol. The products of the sequencing reactions were run on sequencing gels and the sequences were determined using gel image analysis (ABI Prism DNA Sequencing Analysis software 2.1.2 version).

The sequence data were further evaluated to detect the presence of biallelic markers within the amplified fragments. The polymorphism search was based on the presence of superimposed peaks in the electrophoresis pattern resulting from different bases occurring at the same position. However, the presence of two peaks can be an artifact due to background noise. To exclude such an artifact, the two DNA strands were sequenced and a comparison between the two strands was carried out. In order to be registered as a polymorphic

sequence, the polymorphism had to be detected on both strands. Further, some biallelic single nucleotide polymorphisms were confirmed by microsequencing as described below.

Biallelic markers were identified in the analyzed fragments and are shown in Figure 1 and Table 2.

Example 2

Genotyping Of Biallelic Markers

The biallelic markers identified as described above were further confirmed and their respective frequencies were determined through microsequencing. Microsequencing was carried out on individual DNA samples obtained as described herein.

Microsequencing primers

Amplification of genomic DNA fragments from individual DNA samples was performed as described in Example 1 using the same set of PCR primers (Figure 7). Microsequencing was carried out on the amplified fragments using specific primers. See Figure 6. The preferred primers used in microsequencing had about 19 nucleotides in length and hybridized just upstream of the considered polymorphic base.

The microsequencing reactions were performed as follows: 5 µl of PCR products were added to 5 µl purification mix (2U SAP (Shrimp alkaline phosphate) (Amersham E70092X)); 2U Exonuclease I (Amersham E70073Z); and 1 µl SAP buffer (200 mM Tris-HCl pH8, 100 mM $MgCl_2$) in a microtiter plate. The reaction mixture was incubated 30 minutes at 37°C, and denatured 10 minutes at 94°C afterwards. To each well was then added 20 µl of microsequencing reaction mixture containing: 10 pmol microsequencing oligonucleotide (19mers, GENSET, crude synthesis, 5 OD), 1 U Thermosequenase (Amersham E79000G), 1.25 µl Thermosequenase buffer (260 mM Tris HCl pH 9.5, 65 mM $MgCl_2$), and the two appropriate fluorescent ddNTPs complementary to the nucleotides at the polymorphic site corresponding to both polymorphic bases (11.25 nM TAMRA-ddTTP ; 16.25 nM ROX-ddCTP ; 1.675 nM REG-ddATP ; 1.25 nM RHO-ddGTP ; Perkin Elmer, Dye Terminator Set 401095). After 4 minutes at 94°C, 20 PCR cycles of 15 sec at 55°C, 5 sec at 72°C, and 10 sec at 94°C were carried out in a Tetrad PTC-225 thermocycler (MJ Research). The microtiter plate was centrifuged 10 sec at 1500 rpm. The unincorporated dye terminators were removed by precipitation with 19 µl $MgCl_2$ 2mM and 55 µl 100 % ethanol. After 15 minute incubation at room temperature, the microtiter plate was centrifuged at 3300 rpm 15 minutes at 4°C. After discarding the supernatants, the microplate was evaporated to dryness under reduced pressure (Speed Vac). Samples were resuspended in 2.5 µl formamide EDTA loading buffer and heated for 2 min at 95°C. 0.8 µl

microsequencing reaction were loaded on a 10 % (19:1) polyacrylamide sequencing gel. The data were collected by an ABI PRISM 377 DNA sequencer and processed using the GENESCAN software (Perkin Elmer).

Frequency of biallelic markers

Frequencies are reported for the less common allele only and are shown in Figure 1. The frequencies for both alleles are shown for the MGST-II, ME1, UGT1A7 and UGT2B4 genes in Figures 9, 10, 11, and 12, respectively.

Example 3

Association Between Asthma and the Biallelic Markers of the MGST-II Gene

Collection of DNA samples from trait positive and control individuals

The disease trait followed in this association study was asthma, a disease involving the leukotriene pathway. The asthmatic population corresponded to 298 individuals that took part in a clinical study for the evaluation of the anti-asthmatic drug zileuton. More than 90 % of these 297 asthmatic individuals had a Caucasian ethnic background. The control population corresponded to 178 individuals from a random US Caucasian population.

Genotyping of affected and control individuals

The general strategy to perform the association studies was to individually scan the DNA samples from all individuals in each of the populations described above in order to establish the allele frequencies of the above described biallelic markers in each of these populations.

Allelic frequencies of the above-described biallelic marker alleles in each population were determined by performing microsequencing reactions on amplified fragments obtained by genomic PCR performed on the DNA samples from each individual. Genomic PCR and microsequencing were performed as detailed above in Examples 1 and 2 using the described PCR and microsequencing primers.

Haplotype frequency analysis

None of the single marker alleles showed a significant association with asthma however, significant results were obtained in haplotype studies. Allelic frequencies were useful to check that the markers used in the haplotype studies meet the Hardy-Weinberg proportions (random mating).

The results of the haplotype analysis using 13 biallelic markers (12-421-135, 12-421-140, 12-430-80, 12-441-233, 12-442-133, 12-447-58, 12-455-326, 12-461-299, 12-453-429, 12-424-198, 12-454-363, 12-458-196 and 12-426-154) are shown in Figure 13.

Haplotype analysis for association of MGST-II biallelic markers and asthma was performed by estimating the frequencies of all possible 2, 3 and 4 marker haplotypes in the asthmatic and control populations described above. Haplotype estimations were performed by applying the Expectation-Maximization (EM) algorithm (Excoffier and Slatkin, *Mol. Biol. Evol.*, 12:921-927, 1995), using the EM-HAPLO program (Hawley et al., *Am. J. Phys. Anthropol.*,18:104, 1994) as described above. Estimated haplotype frequencies in the asthmatic and control population were compared by means of a chi-square statistical test (one degree of freedom).

Figure 13 shows the most significant haplotypes obtained. Haplotype No. 6 consisting of three biallelic markers (12-455-326, 12-453-429 and 12-424-198) had a p-value of $3.2e10^{-5}$ and an odds ratio of 12.22. Estimated haplotype frequencies were 11.8 % in the cases and 1.1 % in the controls. Haplotype No. 18 consisting of four biallelic markers (12-455-326, 12-453-429,12-424-198 and 12-454-363) had a p-value of $1.2e10^{-6}$ and an odds ratio of 100.00. Both haplotypes are related as three out of four biallelic marker alleles (G at 12-455-326, C at 12-453-429 and T and 12-454-363) are common to both haplotypes. Haplotype No. 19 consisting of four biallelic markers (12-447-58, 12-455-326, 12-461-299 and 12-453-429) had a p-value of $8.2e10^{-6}$ and an odds ratio of 100.00. Markers 12-455-326 and 12-453-429 are common in all three significant haplotypes; therefore, they represent preferred markers for the diagnosis of asthma. Haplotypes Nos. 6, 18 and 19 are strongly associated with asthma. Haplotypes Nos. 7-17 and 20-30 also showed very significant association (see Figure 13).

The statistical significance of the results obtained for the haplotype analysis was evaluated by a phenotypic permutation test reiterated 1000 or 10,000. For this computer simulation, data from the asthmatic and control individuals were pooled and randomly allocated to two groups which contained the same number of individuals as the case-control populations used to produce the data summarized in Figure 13. A haplotype analysis was then run on these artificial groups for the 3 markers included in haplotype No. 6 (haplotype GCT), the 4 markers included in haplotype No. 18 (haplotype GCTG) and the 4 markers included in haplotype No. 19 (haplotype CATT), all of which showed a strong association with asthma. This experiment was reiterated 1000 and 10,000 times and the results are shown in Figure 14. These results demonstrate that among 1000 iterations only 3 and among 10,000 iterations only 31 of the obtained haplotypes had a p-value comparable to the one obtained for haplotype No. 6 (haplotype GCT). These results demonstrate that among 1000 iterations 0 and among 10,000 iterations only 5 of the obtained haplotypes had a p-

value comparable to the one obtained for haplotype No. 18 (haplotype GCTG). These results further demonstrate that among 1000 iterations only 12 and among 10,000 iterations only 76 of the obtained haplotypes had a p-value comparable to the one obtained for haplotype No. 19 (haplotype CATT). These results clearly validate the statistical significance of the association between the haplotypes shown in Figure 13 and asthma.

Example 4

Association Between Side Effects Upon Treatment With the Anti-Asthmatic Drug Zileuton (Zyflo™) and the Biallelic Markers of the MGST-II Gene

Collection of DNA samples from trait positive and control individuals

The side effect examined in this study was the hepatotoxicity experienced by asthmatic individuals as a result of their treatment with Zileuton as part of a clinical study. Asthmatic individuals were unrelated and more than 90% of the individuals had a Caucasian ethnic background. Hepatotoxicity was monitored by measuring the serum levels of alanine aminotransferase (ALT), which is a sensitive indicator of liver cell damage.

More than 90% of the asthmatic individuals participating in this study did not experience Zileuton-associated ALT increase compared to their ALT levels prior to zileuton intake. As mentioned above, an association study is more informative if the populations considered present extreme phenotypes. Therefore, the asthmatic individuals, which were selected for the side effect positive trait (ALT+), corresponded to 89 individuals that presented at least 3 times the upper limit of normal (ULN) level of ALT. On the other side, the asthmatic individuals that were selected for the side effect negative trait (ALT-) corresponded to 208 individuals that presented less than 1xULN of ALT. ALT+ and ALT- populations corresponded to 4% and 35% respectively of the total asthmatic individuals that participated in this study.

Genotyping of affected and control individuals

The general strategy to perform the Association studies was to individually scan the DNA samples from all individuals in each of the populations described above in order to establish the allele frequencies of the above described biallelic markers in each of these populations.

Allelic frequencies of the above-described biallelic marker alleles in each population were determined by performing microsequencing reactions on amplified fragments obtained by genomic PCR performed on the DNA samples from each individual. Genomic PCR and microsequencing were performed as detailed above in Examples 1 and 2 using the described PCR and microsequencing primers.

Haplotype frequency analysis

None of the single marker alleles showed a significant association with hepatoxicity to zileuton however, significant results were obtained in haplotype studies.

The results of the haplotype analysis using 13 biallelic markers (12-421-135, 12-421-140, 12-430-80, 12-441-233, 12-442-133, 12-447-58, 12-455-326, 12-461-299, 12-453-429, 12-424-198, 12-454-363, 12-458-196 and 12-426-154) are shown in Figure 15. Haplotype analysis for association of MGST-II biallelic markers and asthma was performed by estimating the frequencies of all possible 2, 3 and 4 marker haplotypes in the ALT+ and ALT- populations described above. Haplotype estimations were performed by applying the Expectation-Maximization (EM) algorithm (Excoffier and Slatkin, *Mol. Biol. Evol.*, 12:921-927, 1995), using the EM-HAPLO program (Hawley et al., *Am. J. Phys. Anthropol.*,18:104, 1994) as described above. Estimated haplotype frequencies in the ALT+ and ALT- populations were compared by means of a chi-square statistical test (one degree of freedom).

Figure 15 shows the most significant haplotypes obtained. Haplotype No. 6 consisting of three biallelic markers (12-441-233, 12-461-299 and 12-453-429) presented a p-value of $1.5\ 10^{-5}$ and an odd-ratio of 3.63. Estimated haplotype frequencies were 15.7 % in the cases and 4.9 % in the controls. Haplotype No. 19 consisting of four biallelic markers (12-441-233, 12-461-299, 12-453-429 and 12-426-154) had a p-value of $5.2\ 10^{-7}$ and an odd ratio of 5.75. Estimated haplotype frequencies were 14.1 % in the cases and 2.8 % in the controls. Both haplotypes showed strong association with elevated serum ALT level upon treatment with zileuton. Both haplotypes are related as three out of four biallelic marker alleles (C at 12-441-233, T at 12-461-299 and T at 12-453-429) are common to both haplotypes. Haplotypes Nos. 7-18 and 20-31 of Figure 15 also showed very significant association.

The statistical significance of the results obtained for the haplotype analysis was evaluated by a phenotypic permutation test reiterated 1000 or 10,000 times on a computer. For this computer simulation, data from the ALT+ and ALT- populations were pooled and randomly allocated to two groups which contained the same number of individuals as the ALT+ and ALT- populations used to produce the data summarized in Figure 15. A haplotype analysis was then run on these artificial groups for the 3 markers included in haplotype No. 6 (haplotype CTT) and for the 4 markers included in haplotype No. 19 (haplotype CTTA) which. showed the strongest association with secondary effects to zileuton. This experiment was reiterated 1000 and 10,000 times and the results are shown in

Figure 16. These results demonstrate that among 1000 iterations only 1 and among 10,000 iterations only 12 of the obtained haplotypes had a p-value comparable to the one obtained for haplotype No. 6 (haplotype CTT). These results further demonstrate that among 1000 iterations only 1 and among 10,000 iterations only 7 of the obtained haplotypes had a p-value comparable to the one obtained for haplotype No. 19 (haplotype CTTA). These results clearly validate the statistical significance of the association between hepatotoxicity to Zyflo™ and the haplotypes shown in Figure 15.

Example 5

Identification of Mutations and of Low Frequency Alleles of the MGST-II Gene

Exons 3-5, the 5'UTR region and the 3'region of the MGST-II gene were screened for mutations by comparing their sequence in individuals exhibiting elevated ALT levels upon treatment with zileuton (ALT+) and in individuals showing normal ALT levels upon treatment with zileuton (ALT-). ALT + and ALT- individuals are further described in Example 4. Intron sequences immediately flanking the exons were also screened.

To identify mutations, fragments of the MGST-II gene were amplified, sequenced and compared in ALT+ and ALT- individuals. DNA samples from each individual were processed separately.

DNA samples

Individual DNA samples were obtained as described in Example 1.

Amplification of the MGST-II gene

Amplification primers are described in Table 5 and PCR assays were performed as described in Example 1.

Sequencing of amplified genomic DNA: identification of mutations and of low frequency polymorphisms

Sequencing of the amplified DNA was carried out on ABI 377 sequencers. The sequences of the amplification products were determined using automated dideoxy terminator sequencing reactions with a dye terminator cycle sequencing protocol. The products of the sequencing reactions were run on sequencing gels and the sequences were determined using gel image analysis (ABI Prism DNA Sequencing Analysis software 2.1.2 version).

The sequence data was further analyzed to detect the presence of mutations and of low frequency alleles. The sequences obtained with 79 ALT+ individuals and 105 ALT- individuals were compared. New polymorphisms/mutations were detected and the genotype of each individual for these markers was determined. Results are shown below:

Marker ID	Position in MGST-II gene	Least common allele/ mutation	Original allele	Genotype of ALT+ and ALT- individuals
10-286-289	5'UTR	G	C	79 ALT+ C/C 104 ALT- C/C 1 ALT- GC
10-286-345	5'UTR	T	A	65 ALT + A/A 12 ALT + A/T 2 ALT + T/T 82 ALT- A/A 19 ALT- A/T 3 ALT- T/T
10-286-375	5'UTR	G	A	78 ALT + A/A 1 ALT+ A/G 104 ALT- A/A
10-523-232	Exon 3	T	C	75 ALT+ C/C 100 ALT- C/C 1 ALT- C/T
10-289-201	Exon 4	C	T	76 ALT+ T/T 2 ALT+ C/T 100 ALT- T/T 1 ALT- C/T
10-290-37	Exon 5	T	C	78 ALT+ C/C 1 ALT+ C/T 104 ALT- C/C
10-290-326	3' region	A	G	79 ALT+ G/G 103 ALT- G/G 1 ALT- A/G
10-290-328	3'region	deletion	-	1 ALT+ deletion 78 ALT+ - 104 ALT- -

Eight polymorphisms were identified in the region of the MGST-II gene that was scanned. Three mutations were identified in the 3'UTR region. One mutation in exon 4 causes an amino acid substitution (Tyr→His) at the polypeptide level. A mutation in exon 5 introduces a stop codon into the ORF leading to the expression of a truncated MGST-II polypeptide. These mutations modify the specificity, activity and function of the MGST-II enzyme and therefore represent functional mutations of the MGST-II gene.

Example 6

Preparation of Antibody Compositions to MGST-II Variants

Preferably antibody compositions, specifically binding the 93-His variant or the SEQ ID No. 489 variant of MGST-II, are prepared.

Substantially pure protein or polypeptide is isolated from transfected or transformed cells containing an expression vector encoding the MGST-II protein or a portion thereof. The concentration of protein in the final preparation is adjusted, for example, by concentration on

an Amicon filter device, to the level of a few micrograms per ml. Monoclonal or polyclonal antibodies to the protein can then be prepared as follows:

Monoclonal Antibody Production by Hybridoma Fusion

Monoclonal antibody to epitopes in the MGST-II protein or a portion thereof can be prepared from murine hybridomas according to the classical method of Kohler and Milstein (*Nature*, 256:495. 1975) or derivative methods thereof (see Harlow and Lane, *Antibodies A Laboratory Manual*, Cold Spring Harbor Laboratory, pp. 53-242, 1988).

Briefly, a mouse is repetitively inoculated with a few micrograms of the MGST-II protein or a portion thereof over a period of a few weeks. The mouse is then sacrificed, and the antibody producing cells of the spleen isolated. The spleen cells are fused by means of polyethylene glycol with mouse myeloma cells, and the excess unfused cells destroyed by growth of the system on selective media comprising aminopterin (HAT media). The successfully fused cells are diluted and aliquots of the dilution placed in wells of a microtiter plate where growth of the culture is continued. Antibody-producing clones are identified by detection of antibody in the supernatant fluid of the wells by immunoassay procedures, such as ELISA, as originally described by Engvall, E., Meth. Enzymol. 70:419 (1980), and derivative methods thereof. Selected positive clones can be expanded and their monoclonal antibody product harvested for use. Detailed procedures for monoclonal antibody production are described in Davis, L. et al. Basic Methods in Molecular Biology Elsevier, New York. Section 21-2.

Polyclonal Antibody Production by Immunization

Polyclonal antiserum containing antibodies to heterogeneous epitopes in the MGST-II protein or a portion thereof can be prepared by immunizing suitable non-human animal with the MGST-II protein or a portion thereof, which can be unmodified or modified to enhance immunogenicity. A suitable non-human animal is preferably a non-human mammal is selected, usually a mouse, rat, rabbit, goat, or horse. Alternatively, a crude preparation which, has been enriched for MGST-II concentration can be used to generate antibodies. Such proteins, fragments or preparations are introduced into the non-human mammal in the presence of an appropriate adjuvant (e.g. aluminum hydroxide, RIBI, etc.) which is known in the art. In addition the protein, fragment or preparation can be pretreated with an agent which will increase antigenicity, such agents are known in the art and include, for example, methylated bovine serum albumin (mBSA), bovine serum albumin (BSA), Hepatitis B surface antigen, and keyhole limpet hemocyanin (KLH). Serum from the immunized animal is collected, treated and tested according to known procedures. If the serum contains

polyclonal antibodies to undesired epitopes, the polyclonal antibodies can be purified by immunoaffinity chromatography.

Effective polyclonal antibody production is affected by many factors related both to the antigen and the host species. Also, host animals vary in response to site of inoculations and dose, with both inadequate or excessive doses of antigen resulting in low titer antisera. Small doses (ng level) of antigen administered at multiple intradermal sites appears to be most reliable. Techniques for producing and processing polyclonal antisera are known in the art, see for example, Mayer and Walker (1987). An effective immunization protocol for rabbits can be found in Vaitukaitis, J. et al. J. *Clin. Endocrinol. Metab.* 33:988-991 (1971).

Booster injections can be given at regular intervals, and antiserum harvested when antibody titer thereof, as determined semi-quantitatively, for example, by double immunodiffusion in agar against known concentrations of the antigen, begins to fall. (See, for example, Ouchterlony, O. et al., Chap. 19 in: Handbook of Experimental Immunology D. Wier (ed) Blackwell,1973). Plateau concentration of antibody is usually in the range of 0.1 to 0.2 mg/ml of serum. Affinity of the antisera for the antigen is determined by preparing competitive binding curves, as described, for example, by Fisher, D., (Chap. 42: *Manual of Clinical Immunology*, 2d Ed. Rose and Friedman, Eds., *Amer. Soc. For Microbiol.*, Washington, D.C., 1980).

Antibody preparations prepared according to either the monoclonal or the polyclonal protocol are useful in quantitative immunoassays which determine concentrations of antigen-bearing substances in biological samples; they are also used semi-quantitatively or qualitatively to identify the presence of antigen in a biological sample. The antibodies may also be used in therapeutic compositions for killing cells expressing the protein or reducing the levels of the protein in the body.

It should be noted that in the accompanying Sequence Listing, all instances of the symbol "n" in the nucleic acid sequences mean that the nucleotide can be adenine, guanine, cytosine or thymine.

In some instances, the polymorphic bases of the biallelic markers alter the identity of amino acids in the encoded polypeptide. This is indicated in the accompanying Sequence Listing by use of the feature VARIANT, placement of a Xaa at the position of the polymorphic amino acid, and definition of Xaa as the two alternative amino acids. For example, if one allele of a biallelic marker is the codon CAC, which encodes histidine, while the other allele of the biallelic marker is CAA, which encodes glutamine, the

Sequence Listing for the encoded polypeptide will contain an Xaa at the location of the polymorphic amino acid. In this instance, Xaa would be defined as being histidine or glutamine.

In other instances, Xaa may indicate an amino acid whose identity is unknown because of nucleotide sequence ambiguity. In this instance, the feature UNSURE is used, Xaa is placed at the position of the unknown amino acid, and Xaa is defined as being any of the 20 amino acids or a limited number of amino acids suggested by the genetic code.

SEQUENCE LISTING FREE TEXT

The following free text appears in the accompanying sequence listing:

biallelic

marker

drug metabolism

Homo Sapiens

allele

polymorphic base

misc_binding

potential

complement

potential complement

primer_bind

upstream amplification primer

upstream amplification primer, complement

downstream amplification primer

potential probe

misc_feature

5' regulatory region

exon

5'UTR

CDS

3'UTR

polyA_signal

PRT

VARIANT

Stop

Artificial Sequence

sequencing oligonucleotide PrimerPU

sequencing oligonucleotide PrimerRP

WHAT IS CLAIMED IS:

1. An isolated, purified or recombinant polynucleotide comprising a contiguous span of at least 12 nucleotides of a sequence selected from the group consisting of the sequences described in Figure 2 and the complements thereof.

2. A polynucleotide according to claim 1, wherein said span includes a DME-related biallelic marker in said sequence.

3. An isolated, purified or recombinant polynucleotide comprising a contiguous span of at least 12 nucleotides of a sequence selected from the group consisting of the sequences described in Figure 3 and the complements thereof, wherein said span includes a DME-related biallelic marker in said sequence with the alternative allele present at said biallelic marker.

4. An isolated, purified or recombinant polynucleotide consisting essentially of a contiguous span of 8 to 50 nucleotides of a sequence selected from the group consisting of the sequences described in Figure 3 and the complements thereof, wherein said span includes a DME-related biallelic marker in said sequence with the original allele present at said biallelic marker.

5. An isolated, purified or recombinant polynucleotide consisting essentially of a contiguous span of 8 to 50 nucleotides of a sequence selected from the group consisting of the sequences described in Figure 4 and the complements thereof, wherein said span includes a DME-related biallelic marker in said sequence.

6. A polynucleotide according to any one of claims 2 to 5, wherein said contiguous span is 18 to 35 nucleotides in length and said biallelic marker is within 4 nucleotides of the center of said polynucleotide.

7. A polynucleotide according to claim 6. wherein said polynucleotide consists of said contiguous span and said contiguous span is 25 nucleotides in length and said biallelic marker is at the center of said polynucleotide.

8. A polynucleotide according to claim 1, wherein the 3' end of said contiguous span is present at the 3' end of said polynucleotide.

9. A polynucleotide according to any one of claims 2 to 5, wherein the 3' end of said contiguous span is located at the 3' end of said polynucleotide and said biallelic marker is present at the 3' end of said polynucleotide.

10. A polynucleotide according to claim 8, wherein the 3' end of said polynucleotide is located within 20 nucleotides upstream of a DME-related biallelic marker in said sequence.

11. An isolated, purified or recombinant polynucleotide consisting essentially of a contiguous span of 8 to 50 nucleotides in a sequence selected from the group consisting of the sequences described in Figure 3, the sequences described in Figure 4, and the complements thereof, wherein the 3' end of said contiguous span is located at the 3' end of said polynucleotide, and wherein the 3' end of said polynucleotide is located within 20 nucleotides upstream of a DME-related biallelic marker in said sequence.

12. A polynucleotide according to either claim 10 or 11, wherein the 3' end of said polynucleotide is located 1 nucleotide upstream of a DME-related biallelic marker in said sequence.

13. A polynucleotide according to claim 1, wherein said polynucleotide consists essentially of a sequence selected from the sequences described in Figure 6.

14. An isolated, purified or recombinant polynucleotide comprising a contiguous span of at least 12 nucleotides of a sequence selected from the sequences described in Figure 5.

15. A polynucleotide consisting essentially of a sequence selected from the sequences described in Figure 7.

16. A polynucleotide consisting essentially of a sequence selected from the sequences described in Figure 8.

17. A polynucleotide according to any one of claims 1, 3, 4, 5, 11, 14, 15 and 16 wherein said contiguous span comprises at least 15 contiguous nucleotides in said sequence.

18. A polynucleotide according to any one of claims 1, 3, 4, 5, 11, 14, 15 and 16 wherein said contiguous span comprises at least 20 contiguous nucleotides in said sequence.

19. A polynucleotide according to any one of claims 1, 3, 4, 5, 11, 14, 15 and 16 wherein said contiguous span comprises at least 25 contiguous nucleotides in said sequence.

20. A polynucleotide according to any one of claims 1, 3, 4, 5, 11, 14, 15 and 16 attached to a solid support.

21. An array of polynucleotides comprising at least one polynucleotide according to claim 20.

22. An array according to claim 21, wherein said array is addressable.

23. A polynucleotide according to any one of claims 1, 3, 4, 5, 11, 14, 15 and 16, further comprising a label.

24. A method of genotyping comprising determining the identity of a nucleotide at a DME-related biallelic marker or MGST-II-related biallelic marker in a biological sample.

25. A method according to claim 24, wherein said DME-related biallelic marker is selected from the biallelic markers described in Figure 1.

26. A method according to claim 25, wherein said DME-related biallelic marker is selected from the group consisting of the biallelic markers found in Figures 9, 10, 11 and 12.

27. A method according to claim 25, wherein said DME-related biallelic marker is selected from the group consisting of 12-455-326, 12-453-429, 12-454-363, 12-441-233, 12-461-299, 12-426-154, 12-424-198, 12-716-295, 10-428-219,12-720-80, 12-156-91, 12-140-134, 12-653-423, 10-471-84, 10-471-85, 10-470-25, 12-652-203, 12-637-219, 12-721-440, and 10-420-284.

28. A method according to claim 24, wherein said biological sample is derived from a single subject.

29. A method according to claim 28, wherein the identity of the nucleotides at said biallelic marker is determined for both copies of said biallelic marker present in said subject's genome.

30. A method according claim 24, wherein said biological sample is derived from multiple subjects.

31. A method according to claim 24, further comprising amplifying a portion of said sequence comprising the biallelic marker prior to said determining step.

32. A method according to claim 31, wherein said amplifying is performed by PCR.

33. A method according to claim 24, wherein said determining is performed by a hybridization assay.

34. A method according to claim 24, wherein said determining is performed by a sequencing assay.

35. A method according to claim 24, wherein said determining is performed by a microsequencing assay.

36. A method according to claim 24, wherein said determining is performed by an enzyme-based mismatch detection assay.

37. A method of determining the frequency in a population of an allele of a DME-related biallelic marker or MGST-II-related biallelic marker, comprising:

a) genotyping individuals from said population for said biallelic marker according to the method of claim 24; and

b) determining the proportional representation of said biallelic marker in said population.

38. A method according to claim 37, wherein said DME-related biallelic marker is selected from the biallelic markers described in Figure 1.

39. A method according to claim 38, wherein said DME-related biallelic marker is selected from the group consisting of the biallelic markers found in Figures 9, 10, 11 and 12.

40. A method according to claim 38, wherein said DME-related biallelic marker is selected from the group consisting of 12-455-326, 12-453-429, 12-454-363, 12-441-233, 12-461-299, 12-426-154, 12-424-198, 12-716-295, 10-428-219,12-720-80, 12-156-91, 12-140-134, 12-653-423, 10-471-84, 10-471-85, 10-470-25, 12-652-203, 12-637-219, 12-721-440, and 10-420-284.

41. A method according to claim 37, wherein said genotyping of step a) is performed on each individual of said population.

42. A method according to claim 37, wherein said genotyping is performed on a single biological sample derived from said population.

43. A method of detecting an association between an allele and a phenotype, comprising the steps of:

a) determining the frequency of at least one DME-related biallelic marker or MGST-II-related biallelic marker allele in a trait positive population according to the method of claim 37;

b) determining the frequency of said DME-related biallelic marker or MGST-II-related biallelic marker allele in a control population according to the method of claim 37; and

c) determining whether a statistically significant association exists between said allele and said phenotype.

44. A method of estimating the frequency of a haplotype for a set of biallelic markers in a population, comprising:

a) genotyping each individual in said population for at least one DME-related biallelic marker or MGST-II-related biallelic marker according to claim 24;

b) genotyping each individual in said population for a second biallelic marker by determining the identity of the nucleotides at said second biallelic marker for both copies of said second biallelic marker present in the genome; and

c) applying a haplotype determination method to the identities of the nucleotides determined in steps a) and b) to obtain an estimate of said frequency.

45. A method according to claim 44, wherein said haplotype determination method is selected from the group consisting of asymmetric PCR amplification, double PCR amplification of specific alleles, the Clark method, and an expectation maximization algorithm.

46. A method according to claim 44, wherein said DME-related biallelic marker is selected from the biallelic markers described in Figure 1.

47. A method according to claim 46, wherein said DME-related biallelic marker is selected from the group consisting of the biallelic markers found in Figures 9, 10, 11 and 12.

48. A method according to claim 46, wherein said DME-related biallelic marker is selected from the group consisting of 12-455-326, 12-453-429, 12-454-363, 12-441-233, 12-461-299, 12-426-154, 12-424-198, 12-716-295, 10-428-219,12-720-80, 12-156-91, 12-140-134, 12-653-423, 10-471-84, 10-471-85, 10-470-25, 12-652-203, 12-637-219, 12-721-440, and 10-420-284.

49. A method according to claim 46, wherein said haplotype comprises one of the following sets of biallelic markers:

12-455-326, 12-453-429 and 12-424-198;

12-455-326, 12-453-429,12-424-198 and 12-454-363;

12-447-58, 12-455-326, 12-461-299 and 12-453-429;

12-441-233, 12-461-299 and 12-453-429;

12-441-233, 12-461-299, 12-453-429 and 12-426-154;

12-426-154, and 12-424-198;

12-426-154, 12-461-299, and 12-424-198;

10-428-219, and 12-724-225;

12-128-225, 12-156-91, 12-139-380, and 12-140-134;

12-148-311, 12-156-91, 12-139-380, 12-140-134;
10-470-25, and 12-652-203; and
10-470-25, 12-637-219, and 12-652-203.

50. A method according to claim 46, wherein said haplotype comprises one of the following sets of biallelic markers:

12-455-326, 12-453-429 and 12-424-198;
12-455-326, 12-453-429,12-424-198 and 12-454-363;
12-447-58, 12-455-326, 12-461-299 and 12-453-429;
12-426-154, and 12-424-198;
10-428-219, and 12-724-225;
12-128-225, 12-156-91, 12-139-380, and 12-140-134; and
10-470-25, and 12-652-203.

51. A method of detecting an association between a haplotype and a phenotype, comprising the steps of:

a) estimating the frequency of at least one haplotype in a trait positive population according to the method of claim 44;

b) estimating the frequency of said haplotype in a control population according to the method of claim 44; and

c) determining whether a statistically significant association exists between said haplotype and said phenotype.

52. A method according to either claim 43 or 51, wherein said control population is a trait negative population.

53. A method according to either claim 43 or 51, wherein said case control population is a random population.

54. A method according to claim 51, wherein said haplotype is selected from the group of DME-related biallelic marker consisting of the biallelic markers found in Figures 9, 10, 11 and 12.

55. A method according to claim 51, wherein said haplotype is selected from the group of DME-related biallelic marker consisting of 12-455-326, 12-453-429, 12-454-363, 12-441-233, 12-461-299, 12-426-154, 12-424-198, 12-716-295, 10-428-219,12-720-80, 12-156-91, 12-140-134, 12-653-423, 10-471-84, 10-471-85, 10-470-25, 12-652-203, 12-637-219, 12-721-440, and 10-420-284.

56. A method according to claim 51, wherein said haplotype comprises one of the following sets of DME-related biallelic preferred markers:

12-455-326, 12-453-429 and 12-424-198;
12-455-326, 12-453-429,12-424-198 and 12-454-363;
12-447-58, 12-455-326, 12-461-299 and 12-453-429;
12-441-233, 12-461-299 and 12-453-429;
12-441-233, 12-461-299, 12-453-429 and 12-426-154;
12-426-154, and 12-424-198;
12-426-154, 12-461-299, and 12-424-198;
10-428-219, and 12-724-225;
12-128-225, 12-156-91, 12-139-380, and 12-140-134;
12-148-311, 12-156-91, 12-139-380, 12-140-134;
10-470-25, and 12-652-203; and
10-470-25, 12-637-219, and 12-652-203.

57. A method according to claim 51, wherein said haplotype comprises one of the following sets of DME-related biallelic markers:

12-455-326, 12-453-429 and 12-424-198;
12-455-326, 12-453-429,12-424-198 and 12-454-363;
12-447-58, 12-455-326, 12-461-299 and 12-453-429;
12-426-154, and 12-424-198;
10-428-219, and 12-724-225;
12-128-225, 12-156-91, 12-139-380, and 12-140-134; and
10-470-25, and 12-652-203.

58. A method according to claim 43, wherein each of said determining of steps a) and b) is performed on a single pooled biological sample derived from each of said populations.

59. A method according to claim 43, wherein said genotyping of steps a) and b) is performed separately on biological samples derived from each individual in said populations.

60. A method according to either claim 43 or 51, wherein said phenotype is a response to a drug.

61. A method according to either claim 43 or 51, wherein said phenotype is a side effect to a drug.

62. A method according to either claim 43 or 51, wherein said phenotype is a disease involving the metabolic conversion of xenobiotics.

63. A method according to claim 43, wherein the identity of the nucleotides at all of the biallelic markers described in Figure 1 is determined in steps a) and b).

64. A computer readable medium having stored thereon a sequence selected from the group consisting of a nucleic acid code comprising a contiguous span of at least 12 nucleotides of a sequence described in Figure 2, Figure 3, Figure 5 and the complements thereof; wherein said contiguous span of a sequence described in Figure 3 comprises a DME-related biallelic marker with the alternative allele present at said biallelic marker.

65. A computer system comprising a processor and a data storage device wherein said data storage device has stored thereon a sequence selected from the group consisting of a nucleic acid code comprising a contiguous span of at least 12 nucleotides of a sequence described in Figure 2, Figure 3, Figure 5 and the complements thereof; wherein said contiguous span of a sequence described in Figure 3 comprises a DME-related biallelic marker with the alternative allele present at said biallelic marker.

66. The computer system of Claim 53 further comprising a sequence comparer and a data storage device having reference sequences stored thereon.

67. The computer system of Claim 54 wherein said sequence comparer comprises a computer program which indicates polymorphisms.

68. A method for comparing a first sequence to a reference sequence, comprising the steps of:

a) reading said first sequence and said reference sequence through use of a computer program which compares sequences; and

b) determining differences between said first sequence and said reference sequence with said computer program;

wherein said first sequence is selected from the group consisting of a nucleic acid comprising a contiguous span of at least 12 nucleotides of a sequence described in Figure 2, Figure 3, Figure 5 and the complements thereof; wherein said contiguous span of a sequence described in Figure 3 comprises a DME-related biallelic marker with the alternative allele present at said biallelic marker.

69. The method of Claim 68, wherein said step b) comprises identifying polymorphisms.

70. A method of administering a drug or treatment comprising:

a) obtaining a nucleic acid sample from an individual;

b) determining the identity of the polymorphic base of at least one DME-related biallelic marker or MGST-II-related biallelic marker according to the method of claim 24 which is associated with a positive response to said drug or treatment, or at least one DME-related biallelic marker or MGST-II-related biallelic marker or which is associated with a negative response to said drug or treatment; and

c) administering said drug or treatment to said individual if said nucleic acid sample contains at least one biallelic marker associated with a positive response to said drug or treatment, or if said nucleic acid sample lacks at least one biallelic marker associated with a negative response to said drug or treatment.

71. A method of selecting an individual for inclusion in a clinical trial of a drug or treatment comprising:

a) obtaining a nucleic acid sample from an individual;

b) determining the identity of the polymorphic base of at least one DME-related biallelic marker or MGST-II-related biallelic marker according to the method of claim 24 which is associated with a positive response to said drug or treatment, or

at least one biallelic marker associated with a negative response to said drug or treatment in said nucleic acid sample; and

c) including said individual in said clinical trial if said nucleic acid sample contains at least one biallelic marker which is associated with a positive response to said drug or treatment, or if said nucleic acid sample lacks at least one biallelic marker associated with a negative response to said drug or treatment.

72. A method according to claim 70, wherein said administering step comprises administering said drug or treatment to said individual if said nucleic acid sample contains at least one biallelic marker associated with a positive response to said drug treatment, and said nucleic acid sample lacks at least one biallelic marker associated with a negative response to said drug or treatment.

73. The method according to either claim 70 or 71, wherein said DME-related biallelic marker is selected from the group consisting of the biallelic markers found in Figure 1.

74. A method according to claim 73, wherein said DME-related biallelic marker is selected from the group consisting of the biallelic markers found in Figures 9, 10, 11 and 12.

75. A method according to claim 73, wherein said DME-related biallelic marker is selected from the group consisting of 12-455-326, 12-453-429, 12-454-363, 12-441-233, 12-461-299, 12-426-154, 12-424-198, 12-716-295, 10-428-219,12-720-80, 12-156-91, 12-140-134, 12-653-423, 10-471-84, 10-471-85, 10-470-25, 12-652-203, 12-637-219, 12-721-440, and 10-420-284.

76. A method according to claim 73, wherein said haplotype comprises one of the following sets of biallelic markers:

12-455-326, 12-453-429 and 12-424-198;

12-455-326, 12-453-429,12-424-198 and 12-454-363;

12-447-58, 12-455-326, 12-461-299 and 12-453-429;

12-441-233, 12-461-299 and 12-453-429;

12-441-233, 12-461-299, 12-453-429 and 12-426-154;

12-426-154, and 12-424-198;

12-426-154, 12-461-299, and 12-424-198;

10-428-219, and 12-724-225;

12-128-225, 12-156-91, 12-139-380, and 12-140-134;

12-148-311, 12-156-91, 12-139-380, 12-140-134;

10-470-25, and 12-652-203; and

10-470-25, 12-637-219, and 12-652-203.

77. A method according to claim 73, wherein said haplotype comprises one of the following sets of biallelic markers:

12-455-326, 12-453-429 and 12-424-198;

12-455-326, 12-453-429,12-424-198 and 12-454-363;

12-447-58, 12-455-326, 12-461-299 and 12-453-429;

12-426-154, and 12-424-198;

10-428-219, and 12-724-225;

12-128-225, 12-156-91, 12-139-380, and 12-140-134; and

10-470-25, and 12-652-203.

78. A diagnostic kit comprising a polynucleotide according to any one of claims 2, 3, 4, 5, 10, 11, 13, 14, 15, and 16.

79. A polynucleotide for use in a hybridization assay for determining the identity of a nucleotide at a DME-related biallelic marker or MGST-II-related biallelic marker.

80. A polynucleotide for use in a sequencing assay for determining the identity of a nucleotide at a DME-related biallelic marker or MGST-II-related biallelic marker.

81. A polynucleotide for use in an allele specific amplification assay for determining the identity of a DME-related biallelic marker or MGST-II-related biallelic marker.

82. A polynucleotide for use in amplifying a segment of nucleotides comprising a DME-related biallelic marker or MGST-II-related biallelic marker.

83. A use according to any one of claims 79 to 82. wherein said polynucleotide is selected from the sequences described in Figure 1.

84. A method according to claim 83, wherein said DME-related biallelic marker is selected from the group consisting of the biallelic markers found in Figures 9, 10, 11 and 12.

85. A method according to claim 83, wherein said DME-related biallelic marker is selected from the group consisting of 12-455-326, 12-453-429, 12-454-363, 12-441-233, 12-461-299, 12-426-154, 12-424-198, 12-716-295, 10-428-219,12-720-80, 12-156-91, 12-140-134, 12-653-423, 10-471-84, 10-471-85, 10-470-25, 12-652-203, 12-637-219, 12-721-440, and 10-420-284.

86. A method according to claim 83, wherein said haplotype comprises one of the following sets of biallelic markers:

12-455-326, 12-453-429 and 12-424-198;
12-455-326, 12-453-429,12-424-198 and 12-454-363;
12-447-58, 12-455-326, 12-461-299 and 12-453-429;
12-441-233, 12-461-299 and 12-453-429;
12-441-233, 12-461-299, 12-453-429 and 12-426-154;
12-426-154, and 12-424-198;
12-426-154, 12-461-299, and 12-424-198;
10-428-219, and 12-724-225;
12-128-225, 12-156-91, 12-139-380, and 12-140-134;
12-148-311, 12-156-91, 12-139-380, 12-140-134;
10-470-25, and 12-652-203; and
10-470-25, 12-637-219, and 12-652-203.

87. A method according to claim 83, wherein said haplotype comprises one of the following sets of biallelic markers:

12-455-326, 12-453-429 and 12-424-198;
12-455-326, 12-453-429,12-424-198 and 12-454-363;
12-447-58, 12-455-326, 12-461-299 and 12-453-429;
12-426-154, and 12-424-198;
10-428-219, and 12-724-225;
12-128-225, 12-156-91, 12-139-380, and 12-140-134; and
10-470-25, and 12-652-203.

88. An isolated, purified or recombinant, purified or recombinant polynucleotide comprising a contiguous span of at least 12 nucleotides of SEQ ID No. 485 or the complementary sequence thereof, wherein said contiguous span comprises at least 1 of the following nucleotide positions of SEQ ID No. 485: 1-7466, 7726-20255, 20356-36904, 36976-45166, 45249-45727 and 45966-49312.

89. An isolated, purified or recombinant polynucleotide comprising a contiguous span of at least 12 nucleotides of SEQ ID No. 485 or the complementary sequence thereof, wherein said contiguous span comprises a nucleotide selected from the group consisting of a T at position 36985, a C at position 45228 or a T at position 45755 of SEQ ID No. 485.

90. An isolated, purified, or recombinant polynucleotides comprising a contiguous span of at least 12 nucleotides of SEQ ID No. 486 or the complementary sequence thereof, wherein said contiguous span comprises at least 1 of nucleotide positions 1-198 of SEQ ID No. 486.

91. An isolated, purified or recombinant polynucleotide comprising a contiguous span of at least 12 nucleotides of SEQ ID No. 486 or the complementary sequence thereof, wherein said contiguous span comprises a nucleotide selected from the group consisting of a T at position 426, a C at position 478 or a T at position 526 of SEQ ID No. 486.

92. An isolated, purified, or recombinant polynucleotides comprising a contiguous span of at least 12 nucleotides of SEQ ID No. 487 or the complementary sequence thereof, wherein said contiguous span comprises at least 1 of nucleotide positions 1-198 of SEQ ID No. 487.

93. An isolated, purified or recombinant polynucleotide comprising a contiguous span of at least 12 nucleotides of SEQ ID No. 487 or the complementary sequence thereof, wherein said contiguous span comprises a nucleotide selected from the group consisting of a T at position 326, a C at position 378 or a T at position 426 of SEQ ID No. 487.

94. An isolated, purified, or recombinant polynucleotides comprising a contiguous span of at least 12 nucleotides of a sequence selected from the group consisting of SEQ ID Nos. 1-30, 436-441, 469-472, 474-477 and 484.

95. An isolated, purified, or recombinant polynucleotide comprising a contiguous span of 8 to 50 nucleotides of any one of SEQ ID Nos. 1-30, 436-441, 469-472, 474-477 and 484-487, or the complements thereof, wherein said contiguous span comprises a MGST-II-related biallelic marker.

96. A polynucleotide according to claim 95, wherein said MGST-II-related biallelic marker is selected from the group consisting of the biallelic markers described in Table 1; and the complements thereof.

97. A polynucleotide according to claim 95, wherein said MGST-II-related biallelic marker is selected from the group consisting of biallelic markers: 12-421-135, 12-421-140, 12-430-80, 12-441-233, 12-442-133, 12-447-58, 12-455-326, 12-461-299, 12-453-429, 12-424-198, 12-454-363, 12-458-196 and 12-426-154; and the complements thereof.

98. An isolated, purified, or recombinant polynucleotide which encodes a polypeptide comprising a contiguous span of at least 6 amino acids of SEQ ID No. 488, wherein said contiguous span includes a histidine residue at amino acid position 93 in SEQ ID No. 488.

99. An isolated, purified, or recombinant polynucleotide which encodes a polypeptide consisting essentially of amino acid residues 1-108 of SEQ ID No. 488.

100. An isolated, purified, or recombinant polynucleotide which encodes a polypeptide comprising a contiguous span of at least 6 amino acids of SEQ ID No. 489, wherein said contiguous span includes at least one of amino acid positions 20-30 of SEQ ID No. 489.

101. A recombinant vector comprising a polynucleotide according to any one of claims 88-95 and 98-100.

102. A host cell comprising a recombinant vector according to claim 101.

103. A non-human host animal or mammal comprising a recombinant vector according to claim 101.

104. A mammalian host cell comprising an MGST-II gene disrupted by homologous recombination with a knock out vector, comprising a polynucleotide according to any one of claims 88-95 and 98-100.

105. A non-human host mammal comprising a MGST-II gene disrupted by homologous recombination with a knock out vector, comprising a polynucleotide according to any one of claims 88-95 and 98-100.

106. An isolated, purified, or recombinant polypeptide comprising a contiguous span of at least 6 amino acids of SEQ ID No. 488, wherein said contiguous span includes a histidine residue at amino acid position 93 of SEQ ID No. 488.

107. An isolated or purified antibody composition capable of selectively binding to an epitope-containing fragment of a polypeptide according to claim 106, wherein said epitope comprises a histidine residue at amino acid position 93 in SEQ ID No. 488.

108. An isolated, purified, or recombinant polypeptide consisting essentially of amino acid residues 1-108 of SEQ ID No. 488.

109. An isolated, purified, or recombinant polypeptide comprising a contiguous span of at least 6 amino acids of SEQ ID No. 489, wherein said contiguous span includes at least one of amino acid positions 20-30 of SEQ ID No. 489.

110. An isolated or purified antibody composition capable of selectively binding to an epitope-containing fragment of a polypeptide according to claim 109, wherein said epitope comprises at least one of amino acid positions 20-30 of SEQ ID No. 489.

111. A method of determining whether an individual is at risk of developing asthma, or whether said individual suffers from asthma. comprising:

a) genotyping said individual for at least one MGST-II-related biallelic marker according to the method of claim 24; and

b) correlating the result of step a) with a risk of developing asthma.

112. A method of determining whether an individual is at risk of developing hepatoxicity upon treatment with zileuton, comprising:

a) genotyping said individual for at least one MGST-II-related biallelic marker according to the method of claim 24; and

b) correlating the result of step a) with a risk of developing asthma.

113. A method according to any one of claims 111 and 112, wherein said MGST-II-related biallelic marker is selected from the group consisting of biallelic markers: 12-455-326, 12-453-429, 12-424-198, 12-454-363, 12-447-58, 12-461-299, 12-441-233, and 12-426-154.

114. A diagnostic kit comprising a polynucleotide according to any one of claims 20, 23 and 88-97.

115. A computer readable medium having stored thereon a sequence selected from the group consisting of a nucleic acid code comprising one of the following:

a) a contiguous span of at least 12 nucleotides of SEQ ID No. 485 or the complementary sequence thereof, wherein said contiguous span comprises at least 1 of the following nucleotide positions of SEQ ID No. 485: 1-7667, 7726-20264, 20365-36918, 36991-45180, 45263-45741 and 45980-49327;

b) a contiguous span of at least 12 nucleotides of SEQ ID No. 485 or the complementary sequence thereof, wherein said contiguous span comprises a nucleotide selected from the group consisting of a T at position 36985, a C at position 45228 or a T at position 45755 of SEQ ID No. 485;

c) a contiguous span of at least 12 nucleotides of SEQ ID No. 486 or the complementary sequence thereof, wherein said contiguous span comprises at least 1 of nucleotide positions 1-198 of SEQ ID No. 486;

d) a contiguous span of at least 12 nucleotides of SEQ ID No. 486 or the complementary sequence thereof, wherein said contiguous span comprises a nucleotide selected from the group consisting of a T at position 426, a C at position 478 or a T at position 526 of SEQ ID No. 486;

e) a contiguous span of at least 12 nucleotides of SEQ ID No. 487 or the complementary sequence thereof. wherein said contiguous span comprises at least 1 of nucleotide positions 1-198 of SEQ ID No. 487:

f) a contiguous span of at least 12 nucleotides of SEQ ID No. 487 or the complementary sequence thereof, wherein said contiguous span comprises a nucleotide selected from the group consisting of a T at position 325, a C at position 378 or a T at position 426 of SEQ ID No. 487;

g) contiguous span of at least 12 nucleotides of a sequence selected from the group consisting of SEQ ID Nos. 2, 3, 5-30, 437-441, 472;

h) a contiguous span of 8 to 50 nucleotides of any one of SEQ ID Nos 1 to 3 and 8 to 44, or the complements thereof, wherein said contiguous span comprises a MGST-II-related biallelic marker.

i) a nucleotide sequence complementary to any one of the contiguous spans of a), b), c), d), e), f), g) and h).

116. A computer readable medium having stored thereon a sequence consisting of a polypeptide code comprising one of the following:

a) a contiguous span of at least 6 amino acids of SEQ ID No. 488, wherein said contiguous span includes a histidine residue at amino acid position 93 of SEQ ID No. 488;

b) a polypeptide consisting essentially of amino acid residues 1-108 of SEQ ID No. 488;

c) a contiguous span of at least 6 amino acids of SEQ ID No. 489, wherein said contiguous span includes at least one of amino acid positions 20-30 of SEQ ID No. 489.

117. A computer system comprising a processor and a data storage device wherein said data storage device a computer readable medium according to with claim 115 or 116.

118. A computer system according to claim 117, further comprising a sequence comparer and a data storage device having reference sequences stored thereon.

119. A computer system of claim 118 wherein said sequence comparer comprises a computer program which indicates polymorphisms.

120. A computer system of claim 118 further comprising an identifier which identifies features in said sequence.

121. A method for comparing a first sequence to a reference sequence, comprising the steps of:

a) reading said first sequence and said reference sequence through use of a computer program which compares sequences; and

b) determining differences between said first sequence and said reference sequence with said computer program,

wherein said first sequence is selected from the group consisting of a nucleic acid code comprising one of the following:

1) a contiguous span of at least 12 nucleotides of SEQ ID No. 485 or the complementary sequence thereof, wherein said contiguous span comprises at least 1 of the following nucleotide positions of SEQ ID No. 485: 1-7667, 7726-20264, 20365-36918, 36991-45180, 45263-45741 and 45980-49327;

2) a contiguous span of at least 12 nucleotides of SEQ ID No. 485 or the complementary sequence thereof, wherein said contiguous span comprises a nucleotide selected from the group consisting of a T at position 36985, a C at position 45228 or a T at position 45755 of SEQ ID No. 485;

3) a contiguous span of at least 12 nucleotides of SEQ ID No. 486 or the complementary sequence thereof, wherein said contiguous span comprises at least 1 of nucleotide positions 1-198 of SEQ ID No. 486;

4) a contiguous span of at least 12 nucleotides of SEQ ID No. 486 or the complementary sequence thereof, wherein said contiguous span comprises a nucleotide selected from the group consisting of a T at position 426, a C at position 478 or a T at position 526 of SEQ ID No. 486;

5) a contiguous span of at least 12 nucleotides of SEQ ID No. 487 or the complementary sequence thereof, wherein said contiguous span comprises at least 1 of nucleotide positions 1-198 of SEQ ID No. 487;

6) a contiguous span of at least 12 nucleotides of SEQ ID No. 487 or the complementary sequence thereof, wherein said contiguous span comprises a nucleotide selected from the group consisting of a T at position 325, a C at position 378 or a T at position 426 of SEQ ID No. 487;

7) contiguous span of at least 12 nucleotides of a sequence selected from the group consisting of SEQ ID Nos. 2, 3, 5-30, 437-441, 472;

8) a contiguous span of 8 to 50 nucleotides of any one of SEQ ID Nos. 1 to 3 and 8 to 44, or the complements thereof, wherein said contiguous span comprises a MGST-II-related biallelic marker.

9) a nucleotide sequence complementary to any one of the contiguous spans of 1-8.

and a polypeptide code comprising one of the following:

10) a contiguous span of at least 6 amino acids of SEQ ID No. 488, wherein said contiguous span includes a histidine residue at amino acid position 93 of SEQ ID No. 488;

11) a polypeptide consisting essentially of amino acid residues 1-108 of SEQ ID No. 488;

12) a contiguous span of at least 6 amino acids of SEQ ID No. 489, wherein said contiguous span includes at least one of amino acid positions 20-30 of SEQ ID No. 489.

122. A method according to Claim 121, wherein said step of determining differences between the first sequence and the reference sequence comprises identifying at least one polymorphism.

123. A method for identifying a feature in a sequence, comprising the steps of:

a) reading said sequence through the use of a computer program which identifies features in sequences; and

b) identifying features in said sequence with said computer program;

wherein said sequence is selected from the group consisting of a nucleic acid code comprising one of the following:

1) a contiguous span of at least 12 nucleotides of SEQ ID No. 485 or the complementary sequence thereof, wherein said contiguous span comprises at least 1 of the following nucleotide positions of SEQ ID No. 485: 1-7667, 7726-20264, 20365-36918, 36991-45180, 45263-45741 and 45980-49327;

2) a contiguous span of at least 12 nucleotides of SEQ ID No. 485 or the complementary sequence thereof, wherein said contiguous span comprises a nucleotide selected from the group consisting of a T at position 36985, a C at position 45228 or a T at position 45755 of SEQ ID No. 485;

3) a contiguous span of at least 12 nucleotides of SEQ ID No. 486 or the complementary sequence thereof, wherein said contiguous span comprises at least 1 of nucleotide positions 1-198 of SEQ ID No. 486;

4) a contiguous span of at least 12 nucleotides of SEQ ID No. 486 or the complementary sequence thereof, wherein said contiguous span comprises a nucleotide selected from the group consisting of a T at position 426, a C at position 478 or a T at position 526 of SEQ ID No. 486;

5) a contiguous span of at least 12 nucleotides of SEQ ID No. 487 or the complementary sequence thereof, wherein said contiguous span comprises at least 1 of nucleotide positions 1-198 of SEQ ID No. 487;

6) a contiguous span of at least 12 nucleotides of SEQ ID No. 487 or the complementary sequence thereof, wherein said contiguous span comprises a nucleotide selected from the group consisting of a T at position 325, a C at position 378 or a T at position 426 of SEQ ID No. 487;

7) contiguous span of at least 12 nucleotides of a sequence selected from the group consisting of SEQ ID Nos 2, 3, 5-30, 437-441, 472;

8) a contiguous span of 8 to 50 nucleotides of any one of SEQ ID Nos. 1 to 3 and 8 to 44, or the complements thereof, wherein said contiguous span comprises a MGST-II-related biallelic marker.

9) a nucleotide sequence complementary to any one of the contiguous spans of 1-8.

and a polypeptide code comprising one of the following:

10) a contiguous span of at least 6 amino acids of SEQ ID No. 488, wherein said contiguous span includes a histidine residue at amino acid position 93 of SEQ ID No. 488;

11) a polypeptide consisting essentially of amino acid residues 1-108 of SEQ ID No. 488;

12) a contiguous span of at least 6 amino acids of SEQ ID No. 489, wherein said contiguous span includes at least one of amino acid positions 20-30 of SEQ ID No. 489.

Fig. 1

GENE	BIALLELIC MARKER ID	SEQ ID NO.	BIALLELIC MARKER POSITION IN SEQ ID NO.	VALIDATION MICRO-SEQUENCING	GENOTYPING LEAST COMMON ALLELE FREQUENCY %	
MGST2	12-421-140	1	501	N		
MGST2	12-424-192	2	501	N		
MGST2	12-424-198	3	501	N		
MGST2	12-425-57	4	501	N		
MGST2	12-426-154	5	461	N		
MGST2	12-429-198	6	501	N		
MGST2	12-430-80	7	501	Y	T	5.38
MGST2	12-433-215	8	501	N		
MGST2	12-441-233	9	501	Y	G	34.48
MGST2	12-441-343	10	501	N		
MGST2	12-442-221	11	501	N		
MGST2	12-447-58	12	501	Y	G	34.27
MGST2	12-453-429	13	501	Y	T	42.55
MGST2	12-454-363	14	501	N		
MGST2	12-455-326	15	501	Y	C	41.94
MGST2	12-455-383	16	501	N		
MGST2	12-456-269	17	501	N		
MGST2	12-456-380	18	501	N		
MGST2	12-457-204	19	501	N		
MGST2	12-457-206	20	501	N		
MGST2	12-458-196	21	501	N		
MGST2	12-458-438	22	501	N		
MGST2	12-460-274	23	501	N		
MGST2	12-461-124	24	501	N		
MGST2	12-461-299	25	501	Y	C	42.39
MGST2	12-461-465	26	501	N		
MGST2	12-462-280	27	501	N		
MGST2	12-464-66	28	501	N		
MGST2	12-465-26	29	501	N		
MGST2	12-465-234	30	501	N		
ME1	10-428-219	31	501	N		
ME1	10-429-84	32	501	N		
ME1	10-420-284	33	501	N		
ME1	10-423-411	34	501	N		
ME1	12-713-95	35	232	Y	C	31.18
ME1	12-713-149	36	286	N		
ME1	12-716-295	37	500	Y	T	32.8
ME1	12-720-80	38	480	Y	C	33.69
ME1	12-721-281	40	426	N		
ME1	12-721-440	41	501	Y	A	1.6
ME1	12-723-293	42	503	Y	T	0.54
ME1	12-724-195	43	501	N		
ME1	12-724-225	44	501	Y	T	25.86
CYP1A2	10-153-329	45	330	Y	G	2.69

Fig. 1 (following)

CYP1A2	10-95-342	46	342	Y	A	0.54
CYP1A2	10-100-277	47	277	Y	C	2.33
CYP1A2	10-102-294	48	297	Y	C	30.85
CYP2C8	10-413-394	49	501	Y	A	38.07
CYP2C8	10-414-243	50	501	N		
CYP2C8	10-416-273	51	501	Y	T	39.25
CYP2C8	10-418-177	52	501	Y	G	11.41
CYP2C8	12-665-315	53	501	Y	T	22.58
CYP2C8	12-666-324	54	501	Y	C	10.87
CYP2C9	10-76-177	56	178	N		
CYP2C9	10-76-217	57	218	N		
CYP2C9	10-76-333	58	334	Y	G	13.04
CYP2C9	10-77-316	59	501	N		
CYP2C9	10-155-78	60	78	N		
CYP2C9	10-155-104	61	104	N		
CYP2C9	10-156-52	62	52	Y	A	4.79
CYP2C9	10-157-39	63	39	Y	C	30.65
CYP2C9	10-157-131	64	131	Y		
CYP2C9	10-157-166	65	166	N		
CYP2C9	10-157-246	66	246	N		
CYP2C9	10-159-161	67	161	Y	A	11.29
CYP2C9	10-159-162	68	162	N		
CYP2C18	10-83-169	69	169	Y	T	12.9
CYP2C18	10-84-152	70	152	N		
CYP2C18	10-84-243	71	243	Y	T	32.56
CYP2C18	10-84-277	72	277	N		
CYP2C18	10-84-295	73	295	Y		
CYP2C18	10-85-43	74	43	Y		
CYP2C18	10-85-117	75	117	Y	T	12.35
CYP2C18	10-85-320	76	320	N		
CYP2C18	10-86-121	77	121	Y		
CYP3A4-CYP3A7	12-244-275	78	501	N		
CYP3A4-CYP3A7	12-251-153	79	450	Y		
CYP3A4-CYP3A7	12-254-115	80	246	N		
CYP3A4-CYP3A7	12-254-180	81	311	Y		
CYP3A4-CYP3A7	12-265-300	82	499	N		
CYP3A4-CYP3A7	12-271-118	83	501	N		
CYP3A4-CYP3A7	12-272-112	84	501	Y		
CYP3A7	10-216-182	85	503	Y	A	6.59
CYP3A7	10-217-91	86	501	Y	T	12.64
CYP3A7	10-213-292	87	503	Y	G	12.9
CYP3A7	10-214-279	88	501	Y	C	13.3
CYP3A7	10-214-380	89	501	Y	G	13.44
FMO	2-1-216	90	216	N		

Fig. 1 (following)

FMO	2-1-397	91	397	N		
FMO	2-3-232	92	232	N		
FMO	2-4-51	93	51	N		
FMO	2-4-126	94	126	N		
FMO	2-5-202	95	202	N		
FMO	2-5-275	96	275	N		
FMO	2-5-346	97	346	N		
FMO	2-8-171	98	171	N		
FMO	2-9-188	99	188	N		
FMO	2-9-223	100	223	N		
FMO	2-10-107	101	107	N		
FMO	2-10-378	102	377	N		
FMO	2-11-284	103	284	N		
FMO	2-11-156	104	156	N		
FMO	2-11-379	105	379	N		
FMO	2-12-223	106	223	N		
FMO	2-14-239	107	239	N		
FMO	2-14-370	108	370	N		
FMO	2-17-104	109	104	N		
FMO	2-17-396	110	395	N		
FMO	2-22-43	111	43	N		
FMO	2-22-138	112	138	N		
FMO	2-23-82	113	82	N		
FMO	2-23-166	114	166	N		
FMO	2-23-244	115	244	N		
FMO	2-24-115	116	115	N		
FMO	2-25-36	117	36	N		
FMO	2-27-185	118	185	N		
FMO	2-27-378	119	378	N		
FMO	2-29-142	120	142	N		
FMO	2-29-166	121	166	N		
FMO	2-29-205	122	204	N		
FMO	2-29-206	123	205	N		
FMO	2-29-314	124	313	N		
FMO	2-32-68	125	68	N		
FMO	2-35-357	126	357	N		
FMO	2-36-256	127	256	N		
FMO	2-36-354	128	353	N		
FMO	2-42-236	129	236	N		
FMO	2-43-139	130	139	N		
FMO	2-44-215	131	213	N		
FMO	2-45-38	132	38	N		
FMO	2-45-183	133	183	N		
FMO	2-45-335	134	335	N		
FMO	2-45-394	135	394	N		
FMO	2-48-39	136	39	N		
FMO	2-48-72	137	72	N		
FMO	2-48-156	138	156	N		
FMO	2-48-285	139	285	N		
FMO	2-49-167	140	167	N		
GSHR	10-436-43	141	501	Y	C	19.44

Fig. 1 (following)

GSHR	10-436-376	142	501	Y	A	32.76
GSHR	10-431-51	143	501	Y	A	20.21
GSHR	10-432-93	144	477	Y		
GSHR	12-631-208	145	433	Y	G	17.39
GSHS	10-260-282	146	501	N		
GSHS	10-263-26	147	503	N		
GSHS	10-258-408	148	501	N		
GSHS	12-317-259	149	501	N		
GSHS	12-323-385	150	501	Y	T	47.85
GSHS	12-324-219	151	357	N		
GSHS	12-324-335	152	473	Y	C	35.16
GSHS	12-324-380	153	501	N		
GSHS	12-325-30	154	501	N		
GSHS	12-327-31	155	479	Y	G	47.87
GSHS	12-327-415	156	500	N		
GSHS	12-331-270	157	501	N		
GSHS	12-331-275	158	501	N		
GSHS	12-334-320	159	503	N		
GSHS	12-334-391	160	503	N		
GSHS	12-335-417	161	501	N		
GSHS	12-337-189	162	501	N		
GSHS	12-340-130	163	381	N		
GSHS	12-340-210	164	461	Y	T	46.81
GSHS	12-340-222	165	473	N		
GSHS	12-340-240	166	491	N		
GSHS	12-341-99	167	501	Y	A	17.2
GSHS	12-342-32	168	501	N		
GSHS	12-344-349	169	501	Y	G	43.75
GSHS	12-345-453	170	501	N		
GSHS	12-346-204	171	501	N		
GLCL	10-364-55	172	501	N		
GLCL	10-364-108	173	501	N		
GLCL	10-364-267	174	501	N		
GLCL	10-367-20	175	497	N		
GLCL	10-351-389	176	501	N		
GLCL	10-353-102	177	501	N		
GLCL	12-474-346	178	501	Y	A	25.28
GLCL	10-354-320	179	501	N		
GLCL	10-354-360	180	501	N		
GLCL	10-355-87	181	501	N		
GLCL	10-358-60	182	501	N		
GLCL	12-468-63	183	501	Y	C	46.24
GLCL	12-468-388	184	501	N		
GLCL	12-468-491	185	501	N		
GLCL	12-469-132	186	501	N		
GLCL	12-469-245	187	501	N		
GLCL	12-472-435	188	501	N		
GLCL	12-473-311	189	501	N		
GLCL	12-473-483	190	501	N		
GLCL	12-475-85	191	501	N		
GLCL	12-475-446	192	485	N		

Fig. 1 (following)

GLCL	12-477-100	193	501	N		
GLCL	12-477-331	194	501	N		
GLCL	12-477-332	195	501	N		
GLCL	12-477-44	196	501	N		
GLCL	12-478-223	197	501	N		
GLCL	12-478-320	198	501	N		
GLCL	12-479-289	199	501	N		
GLCL	12-482-237	200	501	N		
GLCL	12-482-285	201	501	N		
GLCL	12-482-482	202	501	N		
GLCL	12-483-322	203	499	N		
GLCL	12-484-46	204	501	N		
GLCL	12-490-312	205	501	N		
GLCL	12-491-295	206	501	N		
GLCL	12-493-417	207	501	N		
GLCL	12-494-373	208	501	N		
GLCL	12-495-166	209	501	N		
GLCL	12-495-272	210	501	N		
GLCL	12-495-424	211	501	N		
GLCL	12-500-220	212	501	N		
GLCL	12-501-155	213	501	N		
GLCL	12-503-52	214	501	N		
GLCL	12-503-62	215	501	N		
GLCL	12-504-54	216	499	N		
GLCL	12-504-96	217	501	N		
GLCL	12-504-428	218	501	Y	C	47.22
GLCL	12-507-53	219	474	Y	C	47.78
GLCL	12-507-92	220	501	N		
GLCL	12-507-159	221	500	N		
GLCL	12-507-177	222	501	N		
GLCL	12-508-29	223	501	N		
GLCL	12-509-42	224	501	N		
GLCL	12-509-126	225	501	N		
GLCL	12-510-59	226	501	N		
GLCL	12-511-74	227	501	Y	C	11.45
GGT5	10-325-311	228	501	N		
GGT5	10-327-120	229	501	N		
GGT5	10-331-179	230	501	N		
GGT5	10-331-357	231	501	N		
GGT5	10-334-263	232	501	N		
GGT5	10-321-226	233	501	N		
GGT5	12-183-98	234	501	N		
GGT5	12-185-78	235	501	N		
GGT5	12-186-154	236	501	Y	A	6.99
GGT5	12-186-397	237	501	Y	C	28.08
GGT5	12-187-65	238	501	Y	C	23.37
GGT5	12-187-66	239	501	N		
GGT5	12-189-348	240	501	Y	A	26.09
GGT5	12-192-63	241	501	N		
GGT5	12-192-64	242	502	N		
GGT5	12-192-268	243	501	N		

Fig. 1 (following)

GGT5	12-192-334	244	501	N		
GGT5	12-192-352	245	501	N		
GGT5	12-194-135	246	501	N		
GGT5	12-194-325	247	501	N		
GGT5	12-194-337	248	501	N		
GGT5	12-194-479	249	501	N		
DP	10-442-133	250	501	Y	C	7.06
DP	10-444-248	251	484	Y	G	42.78
DP	10-445-281	252	501	Y	T	13.3
DP	12-668-362	253	501	N		
DP	12-670-48	254	501	N		
DP	12-670-91	255	501	N		
DP	12-670-157	256	501	Y	T	47.83
DP	12-671-148	257	501	Y	C	41.49
DP	12-679-245	258	253	N		
DP	12-679-371	259	379	N		
DP	12-679-426	260	434	N		
DP	12-680-331	261	503	N		
G6PDH	10-151-154	262	154	Y	A	0.54
G6PDH	10-138-206	263	205	Y	T	8.51
G6PDH	10-138-352	264	351	Y	C	14.04
PGDH	12-586-414	265	501	Y	A	28.33
PGDH	12-587-379	266	499	N		
PGDH	12-588-103	267	501	Y	A	48.88
PGDH	12-589-152	268	501	N		
PGDH	12-592-118	269	501	Y	A	49.46
PGDH	12-593-174	270	501	Y	C	34.71
PGDH	12-596-124	271	501	Y	A	26.7
PGDH	12-602-196	272	501	Y	C	31.72
PGDH	12-602-350	273	501	N		
PGDH	12-603-191	274	501	Y	C	27.42
PGDH	12-783-73	275	501	N		
PGDH	12-783-421	276	501	N		
PGDH	12-785-200	277	501	N		
PGDH	12-785-393	278	501	N		
PGDH	12-787-103	279	501	N		
PGDH	12-790-396	280	501	N		
PGDH	12-791-211	281	501	N		
PGDH	12-792-233	282	501	N		
PGDH	12-793-383	283	505	N		
PGDH	12-803-125	284	501	N		
PGDH	12-805-115	285	501	N		
PGDH	12-808-52	286	501	N		
PGDH	12-808-75	287	501	N		
PGDH	12-809-119	288	501	N		
PGDH	12-810-77	289	501	N		
PGDH	10-265-178	290	501	N		
PGDH	10-266-203	291	503	N		
UGT1A7	10-403-312	292	501	N		
UGT1A7	10-405-54	293	501	N		
UGT1A7	10-408-356	294	501	N		

Fig. 1 (following)

UGT1A7	10-409-148	295	501	N		
UGT1A7	10-409-249	296	501	N		
UGT1A7	10-410-274	297	501	N		
UGT1A7	10-410-280	298	501	N		
UGT1A7	10-410-337	299	501	N		
UGT1A7	12-121-326	300	501	Y	A	26.88
UGT1A7	12-122-341	301	501	N		
UGT1A7	12-122-381	302	501	N		
UGT1A7	12-124-169	303	501	N		
UGT1A7	12-124-194	304	501	Y	C	19.41
UGT1A7	12-124-300	305	501	N		
UGT1A7	12-124-58	306	501	N		
UGT1A7	12-126-222	307	501	N		
UGT1A7	12-126-297	308	501	N		
UGT1A7	12-128-225	309	501	Y	G	47.44
UGT1A7	12-129-176	310	501	N		
UGT1A7	12-130-203	311	501	N		
UGT1A7	12-130-260	312	501	N		
UGT1A7	12-131-112	313	501	N		
UGT1A7	12-132-157	314	255	N		
UGT1A7	12-132-437	315	501	N		
UGT1A7	12-133-153	316	666	N		
UGT1A7	12-133-318	317	501	N		
UGT1A7	12-136-238	318	249	N		
UGT1A7	12-138-141	319	501	N		
UGT1A7	12-138-42	320	501	N		
UGT1A7	12-138-67	321	501	N		
UGT1A7	12-139-380	322	501	Y	A	21.24
UGT1A7	12-140-134	323	501	Y	T	41.01
UGT1A7	12-140-329	324	501	N		
UGT1A7	12-140-385	325	501	N		
UGT1A7	12-141-159	326	501	Y	T	37.5
UGT1A7	12-141-392	327	501	N		
UGT1A7	12-142-315	328	501	N		
UGT1A7	12-142-321	329	501	Y	G	45.56
UGT1A7	12-143-453	330	501	Y	G	49.39
UGT1A7	12-144-169	331	501	N		
UGT1A7	12-144-33	332	501	N		
UGT1A7	12-146-174	333	501	N		
UGT1A7	12-146-47	334	501	N		
UGT1A7	12-148-283	335	501	N		
UGT1A7	12-148-311	336	501	Y	T	43.17
UGT1A7	12-149-320	337	501	N		
UGT1A7	12-151-174	338	501	N		
UGT1A7	12-151-196	339	501	N		
UGT1A7	12-151-270	340	501	N		
UGT1A7	12-152-453	341	501	N		
UGT1A7	12-153-116	342	501	Y	T	37.78
UGT1A7	12-154-480	343	501	N		
UGT1A7	12-155-403	344	501	N		
UGT1A7	12-156-91	345	501	Y	A	50

Fig. 1 (following)

UGT1A7	12-157-437	346	501	N		
UGT1A7	12-158-213	347	501	N		
UGT1A7	12-158-450	348	480	N		
UGT1A7	12-161-157	349	501	N		
UGT1A7	12-162-21	350	498	N		
UGT2B4	10-470-25	351	503	Y	T	44.44
UGT2B4	10-471-84	352	503	Y	A	27.17
UGT2B4	10-471-85	353	503	Y		
UGT2B4	10-472-202	354	503	Y	C	9.68
UGT2B4	10-473-333	355	503	N		
UGT2B4	10-494-284	356	503	N		
UGT2B4	12-637-219	357	499	Y	G	36.17
UGT2B4	12-639-95	358	499	Y	G	34.95
UGT2B4	12-639-241	359	499	N		
UGT2B4	12-640-151	360	499	N		
UGT2B4	12-640-296	361	499	N		
UGT2B4	12-640-325	362	499	Y		
UGT2B4	12-640-413	363	499	N		
UGT2B4	12-641-120	364	499	N		
UGT2B4	12-641-122	365	499	N		
UGT2B4	12-641-223	366	432	N		
UGT2B4	12-641-267	367	388	N		
UGT2B4	12-642-387	368	503	N		
UGT2B4	12-642-417	369	503	Y	G	26.51
UGT2B4	12-646-429	370	434	N		
UGT2B4	12-646-433	371	438	N		
UGT2B4	12-647-145	372	503	N		
UGT2B4	12-648-123	373	251	N		
UGT2B4	12-648-300	374	428	Y	T	37.91
UGT2B4	12-648-402	375	501	N		
UGT2B4	12-652-115	376	298	N		
UGT2B4	12-652-203	377	386	Y	C	42.47
UGT2B4	12-652-274	378	457	N		
UGT2B4	12-652-371	379	501	N		
UGT2B4	12-653-423	380	499	N		
UGT2B4	12-654-115	381	499	N		
UGT2B4	12-654-207	382	499	N		
UGT2B4	12-657-396	383	503	N		
UGT2B4	12-658-120	384	503	N		
UGT2B4	12-659-382	385	501	N		
UGT2B4	12-660-134	386	306	N		
UGT2B4	12-662-80	387	497	N		
UGT2B7	12-906-149	388	501	Y		
UGT2B7	12-906-154	389	501	N		
UGT2B7	12-906-251	390	501	N		
UGT2B7	12-906-451	391	501	N		
UGT2B7	12-907-199	392	244	Y	G	3.23
UGT2B7	12-907-482	393	501	N		
UGT2B7	12-909-36	394	53	N		
UGT2B7	12-909-176	395	193	N		
UGT2B7	12-909-484	396	501	N		

Fig. 1 (following)

UGT2B7	12-910-76	397	347	Y	A	23.91
UGT2B7	12-910-295	398	503	N		
UGT2B7	12-911-22	399	240	Y	C	43.96
UGT2B7	12-912-65	400	501	N		
UGT2B7	12-914-106	401	384	Y	C	44.62
UGT2B7	12-914-252	402	503	N		
UGT2B10	10-448-266	403	503	N		
UGT2B10	10-453-330	404	503	N		
UGT2B10	10-455-367	405	503	N		
UGT2B10	12-5-158	406	503	Y	T	11.8
UGT2B10	12-9-367	407	499	Y	A	14.67
UGT2B10	12-10-303	408	501	Y	T	14.67
UGT2B10	12-14-264	409	501	Y	T	14.29
UGT2B10	12-17-86	410	499	Y	A	44.02
UGT2B10	12-19-163	411	501	Y	G	29.89
UGT2B15	10-457-284	412	503	N		
UGT2B15	10-460-221	413	503	N		
UGT2B15	10-460-232	414	503	N		
UGT2B15	10-460-235	415	503	N		
UGT2B15	10-460-236	416	503	N		
UGT2B15	10-460-285	417	503	N		
UGT2B15	12-605-58	418	501	Y	T	47.67
UGT2B15	12-607-207	419	501	N		
UGT2B15	12-609-119	420	499	Y	T	45.11
UGT2B15	12-609-180	421	499	N		
UGT2B15	12-609-233	422	499	N		
UGT2B15	12-611-294	423	501	Y	A	43.26
UGT2B15	12-612-41	424	501	Y	C	28.65
UGT2B15	12-613-302	425	499	N		
UGT2B15	12-614-471	426	501	Y	T	39.44
UGT2B15	12-620-192	427	503	Y	T	30.36
UGT2B15	12-621-49	428	503	N		
UGT2B15	12-622-325	429	364	N		
UGT2B15	12-624-82	430	501	N		
UGT2B15	12-624-83	431	501	N		
UGT2B15	12-624-107	432	489	N		
UGT2B15	12-624-146	433	501	N		
UGT2B15	12-624-288	434	501	N		
UGT2B15	12-624-293	435	501	N		
MGST2	12-421-135	436	501	N		
MGST2	12-442-133	437	501	Y	C	5.85
MGST2	12-449-63	438	501	N		
MGST2	12-454-242	439	501	N		
MGST2	12-463-250	440	501	N		
MGST2	12-462-199	441	501	N		
DME	10-430-287	442	501	N		
DME	12-718-432	443	501	N		
CYP3A4-CYP3A7	12-269-301	444	501	Y		
FMO	2-13-398	445	501	N		
FMO	2-28-132	446	501	N		

Fig. 1 (following)

FMO	2-39-27	447	501	N		
FMO	2-45-155	448	501	N		
FMO	2-4-391	14	501	N		
GSHS	12-345-410	450	501	N		
GLCL	10-358-353	451	501	N		
GLCL	10-360-190	452	501	N		
GLCL	10-365-374	453	501	N		
GLCL	10-367-58	454	501	N		
GLCL	12-468-424	455	501	N		
GLCL	12-481-293	456	501	N		
GLCL	12-499-86	457	501	N		
GLCL	12-500-217	458	501	N		
GLCL	12-511-101	459	501	N		
6PGD	12-586-443	460	501	N		
6PGD	12-593-287	461	501	N		
6PGD	12-795-383	462	501	N		
UGT2B4	10-494-332	463	501	N		
UGT2B4	12-659-251	465	429	N		
UGT2B7	12-912-419	466	501	N		
UGT2B7	12-914-28	467	306	N		
UGT2B15	12-624-307	468	501	N		
MGST2	10-290-326	469	501	N		
MGST2	10-290-37	470	501	N		
MGST2	10-523-232	471	501	N		
MGST2	12-449-300	472	501	N		
G6PDH	10-186-212	473	212	N		
MGST2	10-286-289	474	501	N		
MGST2	10-286-345	475	501	N		
MGST2	10-286-375	476	501	N		
MGST2	10-289-201	477	501	N		
GGT5	10-321-28	478	501	N		
CYP1A2	10-98-265	479	265	N		
UGT1A7	12-157-115	480	501	N		
GLCL	12-472-48	481	501	N		
GLCL	12-477-151	482	501	N		
GLCL	12-479-214	483	501	N		
MGST2	10-290-328	484	501	N		

FIG. 2

SEQ ID NO.	BIALLELIC MARKER ID	1ST ALLELE	2ND ALLELE	POSITION RANGE OF PREFERRED SEQUENCES
1	12-421-140	A	G	1-1001
2	12-424-192	A	G	190-801; 865-999
3	12-424-198	G	T	184-795; 859-993
4	12-425-57	G	A	208-225; 266-478
5	12-426-154	A	G	152-961
6	12-429-198	C	T	260-784; 822-1001
7	12-430-80	T	C	1-996
8	12-433-215	A	G	1-1001
12	12-447-58	G	C	1-36; 390-914
13	12-453-429	C	T	1-1001
14	12-454-363	A	G	1-315; 377-466; 598-619
15	12-455-326	T	C	1-357; 391-594; 760-827
16	12-455-383	G	A	1-414; 448-651; 817-884
17	12-456-269	A	G	1-536
19	12-457-204	A	G	437-527; 761-1001
20	12-457-206	C	T	435-525; 759-1001
21	12-458-196	T	A	1-727
22	12-458-438	T	C	1-21; 298-1001
23	12-460-274	A	G	1-499; 563-1001
24	12-461-124	A	C	1-203; 259-644; 687-773; 807-833
25	12-461-299	C	T	1-28; 84-469; 512-591
26	12-461-465	C	T	1-303; 346-432
27	12-462-280	C	T	1-1001
28	12-464-66	G	T	1-215; 261-1001
29	12-465-26	C	T	1-61; 99-1001
30	12-465-234	G	T	1-1001
31	10-428-219	A	G	1-398; 506-1000
33	10-420-284	C	T	1-302; 472-772
34	10-423-411	C	T	1-227; 333-821
35	12-713-95	C	T	1-668
36	12-713-149	G	C	1-668
37	12-716-295	C	T	1-902
38	12-720-80	G	C	1-982
40	12-721-281	A	C	1-926
41	12-721-440	A	G	1-1000
42	12-723-293	C	T	1-1001
43	12-724-195	C	T	277-1001
44	12-724-225	C	T	245-1001
49	10-413-394	A	G	1-139; 831-1001
51	10-416-273	A	T	1-258; 855-1001
53	12-665-315	T	C	180-1001
54	12-666-324	A	C	338-375; 414-501; 581-611

FIG. 2 (following)

78	12-244-275	A	G	
79	12-251-153	A	C	1-111; 158-950
82	12-265-300	T	C	1-999
84	12-272-112	A	C	396-416
85	10-216-182	A	G	77-151; 186-235; 320-488; 733-761
86	10-217-91	C	T	1-189; 434-462; 810-871; 925-1001
101	2-10-107	C	T	260-450
102	2-10-378	A	G	260-450
104	2-11-156	A	C	369-387
105	2-11-379	A	G	369-387
121	2-29-166	C	T	
141	10-436-43	G	C	1-630; 794-1001
142	10-436-376	A	G	1-297; 461-642; 977-1001
143	10-431-51	A	C	329-534; 682-860
144	10-432-93	A	G	1-40; 374-559; 705-885
146	10-260-282	G	T	1-24; 95-324; 482-1001
147	10-263-26	A	C	1-632; 754-1001
148	10-258-408	A	G	337-668
149	12-317-259	G	A	1-44; 116-150; 181-241; 281-673; 968-1001
150	12-323-385	T	C	340-1001
152	12-324-335	G	C	1-176; 395-906
153	12-324-380	A	G	1-159; 378-889
154	12-325-30	C	T	272-837; 977-1001
155	12-327-31	G	T	1-570; 655-821; 875-922; 973-999
156	12-327-415	A	G	1-208; 293-459; 513-1001
157	12-331-270	G	A	1-531; 834-1001
158	12-331-275	T	G	125-536; 839-1001
159	12-334-320	A	G	68-705
160	12-334-391	A	G	1-634; 982-1001
161	12-335-417	G	C	239-1001
162	12-337-189	A	G	1-1001
163	12-340-130	A	G	196-881
164	12-340-210	C	T	196-961
165	12-340-222	G	T	196-973
166	12-340-240	C	T	196-975
167	12-341-99	A	G	1-1001
168	12-342-32	T	C	238-397; 859-960
169	12-344-349	G	T	365-1001
170	12-345-453	G	C	1-606
192	12-475-446	G	A	
228	10-325-311	A	G	41-312; 421-891
231	10-331-357	G	T	76-218; 373-730; 938-1001
232	10-334-263	A	G	1-359; 481-604; 781-893
235	12-185-78	C	T	1-1001
236	12-186-154	A	G	335-876
237	12-186-397	C	T	92-633; 967-1001

FIG. 2 (following)

238	12-187-65	C	T	345-846
239	12-187-66	A	G	344-845
240	12-189-348	G	A	281-358; 407-1001
246	12-194-135	G	T	543-1001
247	12-194-325	A	G	351-1001
248	12-194-337	A	G	339-1001
249	12-194-479	C	T	197-1001
251	10-444-248	A	G	
254	12-670-48	G	C	1-961
255	12-670-91	C	T	1-918
256	12-670-157	C	T	1-852
257	12-671-148	C	T	1-908
258	12-679-245	A	G	96-465
259	12-679-371	A	G	96-465
260	12-679-426	C	T	96-465
265	12-586-414	A	G	1-71; 149-929
268	12-589-152	T	G	164-1001
269	12-592-118	A	T	353-1001
270	12-593-174	T	C	342-815
271	12-596-124	A	G	1-742
272	12-602-196	C	T	1-240; 436-641
274	12-603-191	T	C	1-709
275	12-783-73	G	C	1-769; 981-1001
277	12-785-200	C	T	351-510
279	12-787-103	G	A	1-47; 232-324; 401-1001
280	12-790-396	G	A	47-64; 393-1001
281	12-791-211	A	G	1-379; 467-818
284	12-803-125	T	A	125-1001
285	12-805-115	G	A	1-66; 278-838; 959-1001
286	12-808-52	A	G	400-1001
287	12-808-75	G	C	377-1001
289	12-810-77	G	A	99-1001
293	10-405-54	C	T	1-492
297	10-410-274	A	C	643-805
301	12-122-341	C	T	1-23; 150-282; 324-435; 593-620
302	12-122-381	A	C	110-242; 284-395; 553-580
303	12-124-169	G	T	1-727; 788-1001
304	12-124-194	C	T	1-702; 763-1001
305	12-124-300	G	T	1-596; 657-1001
306	12-124-58	A	C	1-837; 898-1001
308	12-126-297	T	C	1-508; 944-1001
310	12-129-176	G	T	163-1001
313	12-131-112	T	C	254-422
315	12-132-437	A	C	258-991
316	12-133-153	T	C	1-515; 607-666; 775-918; 976-1001
317	12-133-318	T	A	1-515; 607-666; 775-918; 976-1001

FIG. 2 (following)

318	12-136-238	A	G	1-643
319	12-138-141	G	A	1-393; 521-651
320	12-138-42	T	G	1-294; 422-552
321	12-138-67	G	A	1-319; 447-577
322	12-139-380	A	G	94-157; 276-663
323	12-140-134	G	T	1-142; 212-951
324	12-140-329	C	T	1-756
325	12-140-385	G	C	1-700
326	12-141-159	T	C	1-1001
327	12-141-392	C	A	1-1001
328	12-142-315	A	G	1-1001
329	12-142-321	A	G	1-1001
330	12-143-453	A	G	1-1001
331	12-144-169	G	A	97-1001
332	12-144-33	G	A	1-1001
333	12-146-174	T	C	1-529; 765-805
336	12-148-311	T	C	1-251; 684-1001
337	12-149-320	T	C	202-1001
338	12-151-174	G	T	313-1001
339	12-151-196	C	T	291-1001
340	12-151-270	A	G	217-1001
341	12-152-453	C	T	1-239; 526-576; 623-1001
342	12-153-116	C	T	1-819; 866-1001
346	12-157-437	A	C	1-865
347	12-158-213	T	C	1-1001
348	12-158-450	T	G	206-980
350	12-162-21	A	G	1-998
351	10-470-25	A	T	1-339; 413-539; 730-1001
355	10-473-333	C	T	461-744
356	10-494-284	C	T	89-349; 450-513
359	12-639-241	T	G	1-199; 652-667; 742-763
360	12-640-151	G	A	1-806; 943-1001
361	12-640-296	T	G	1-862
362	12-640-325	T	C	1-1001
363	12-640-413	C	G	1-1001
364	12-641-120	G	A	98-1001
365	12-641-122	T	G	100-1001
366	12-641-223	G	A	1-15; 134-1001
367	12-641-267	T	C	1-15; 134-1001
368	12-642-387	A	G	1-224; 292-1001
369	12-642-417	A	G	1-194; 262-1001
372	12-647-145	A	G	1-898
373	12-648-123	A	G	1-751
374	12-648-300	C	T	1-839
375	12-648-402	G	C	1-810; 909-1001
376	12-652-115	C	T	1-30; 191-798

FIG. 2 (following)

377	12-652-203	A	C	1-30; 191-886
378	12-652-274	G	T	1-30; 191-957
379	12-652-371	C	T	138-1001
380	12-653-423	T	A	1-603
381	12-654-115	T	C	161-1001
382	12-654-207	G	A	1-95; 253-1001
383	12-657-396	A	G	329-1001
384	12-658-120	A	T	1-1001
385	12-659-382	A	G	1-1001
386	12-660-134	A	G	291-608; 886-983
387	12-662-80	G	C	480-1001
391	12-906-451	A	C	447-532; 865-1001
392	12-907-199	G	T	
394	12-909-36	A	G	
397	12-910-76	A	G	1-785; 854-870
398	12-910-295	C	T	1-1001
399	12-911-22	G	C	1-740
400	12-912-65	C	T	1-183; 290-1001
401	12-914-106	C	T	1-1001
402	12-914-252	A	T	1-1001
404	10-453-330	C	T	1-207; 761-1001
406	12-5-158	C	T	672-1001
407	12-9-367	G	A	1-15; 249-283; 400-425; 493-666; 722-1001
409	12-14-264	C	T	1-1001
410	12-17-86	T	A	1-1001
411	12-19-163	A	G	230-388; 525-709; 824-866
414	10-460-232	A	G	1-349; 521-1001
415	10-460-235	C	T	1-346; 518-1001
416	10-460-236	A	G	1-345; 517-1001
417	10-460-285	A	T	1-296; 468-1001
418	12-605-58	G	T	1-1001
419	12-607-207	G	A	1-746; 885-902
420	12-609-119	T	G	1-234; 294-1001
421	12-609-180	T	G	40-295; 355-1001
422	12-609-233	G	A	138-348; 404-1001
423	12-611-294	G	A	1-617; 895-967
424	12-612-41	C	T	1-56; 398-708
425	12-613-302	C	G	1-86; 336-1001
426	12-614-471	T	A	1-1001
427	12-620-192	G	T	318-1001
428	12-621-49	A	G	1-242; 451-815
429	12-622-325	C	T	
430	12-624-82	T	C	1-1001
431	12-624-83	G	A	1-1001
432	12-624-107	T	C	1-989
433	12-624-146	T	C	1-1001

FIG. 2 (following)

434	12-624-288	T	G	1-1001
435	12-624-293	T	C	1-1001
436	12-421-135	T	-	1-1001
438	12-449-63	AT	-	1-107; 314-656
439	12-454-242	AT	-	1-436; 498-587; 719-740
440	12-463-250	CAT	-	1-30; 102-601; 752-1001
441	12-462-199		deletion	1-1001
442	10-430-287	T	-	1-330; 442-740; 782-1001
443	12-718-432	T	-	1-1001
444	12-269-301	T	-	774-820
450	12-345-410		deletion	1-649
460	12-586-443	C	-	1-42; 120-911
461	12-593-287		deletion	1-17; 455-942
462	12-795-383		insertion	166-500; 540-1001
465	12-659-251	deletion	-	1-929
466	12-912-419	A	-	1-686
467	12-914-28	T	-	1-806
468	12-624-307	T	-	1-1001
469	10-290-326	A	G	1-197; 437-1000
472	12-449-300	T	C	1-542; 908-1000
484	10-290-328	deletion		1-194; 434-1000

Fig. 3

SEQ ID NO.	BIALLELIC MARKER ID	ORIGINAL ALLELE	ALTERNATIVE ALLELE
10	12-441-343	G	A
18	12-456-380	G	T
32	10-429-84	T	C
45	10-153-329	T	G
46	10-95-342	G	A
47	10-100-277	T	C
57	10-76-217	C	T
59	10-77-316	A	T
60	10-155-78	T	C
61	10-155-104	C	G
62	10-156-52	G	A
63	10-157-39	C	T
64	10-157-131	A	G
65	10-157-166	G	A
66	10-157-246	G	A
67	10-159-161	T	A
68	10-159-162	C	A
69	10-83-169	T	C
70	10-84-152	C	T
71	10-84-243	C	T
74	10-85-43	C	T
76	10-85-320	A	T
81	12-254-180	G	A
83	12-271-118	T	C
87	10-213-292	C	G
90	2-1-216	G	A
91	2-1-397	T	C
92	2-3-232	C	T
93	2-4-51	A	C
94	2-4-126	A	G
95	2-5-202	A	G
96	2-5-275	G	A
97	2-5-346	C	T
98	2-8-171	A	G
99	2-9-188	G	A
100	2-9-223	T	G
103	2-11-284	A	G
106	2-12-223	A	T
107	2-14-239	C	T
108	2-14-370	C	G
109	2-17-104	A	G
110	2-17-396	A	C
111	2-22-43	A	G
112	2-22-138	G	A
113	2-23-82	A	G
114	2-23-166	G	A
115	2-23-244	G	T

FIG. 3 (following)

116	2-24-115	C	T
117	2-25-36	G	C
118	2-27-185	G	A
119	2-27-378	G	C
120	2-29-142	G	A
124	2-29-314	C	T
125	2-32-68	A	G
126	2-35-357	T	C
127	2-36-256	G	C
128	2-36-354	A	C
129	2-42-236	C	T
130	2-43-139	G	A
131	2-44-215	C	T
132	2-45-38	C	T
133	2-45-183	T	C
134	2-45-335	T	A
135	2-45-394	C	T
136	2-48-39	A	G
137	2-48-72	C	T
138	2-48-156	T	G
139	2-48-285	A	G
140	2-49-167	A	G
151	12-324-219	C	T
171	12-346-204	G	A
172	10-364-55	T	G
173	10-364-108	T	C
174	10-364-267	T	A
175	10-367-20	T	G
176	10-351-389	A	G
177	10-353-102	T	A
178	12-474-346	G	A
179	10-354-320	G	A
180	10-354-360	A	G
181	10-355-87	G	A
182	10-358-60	G	A
183	12-468-63	T	C
184	12-468-388	T	C
185	12-468-491	G	A
186	12-469-132	T	C
187	12-469-245	G	A
188	12-472-435	G	A
189	12-473-311	A	C
190	12-473-483	T	C
191	12-475-85	G	T
193	12-477-100	A	G
194	12-477-331	G	A
195	12-477-332	T	C
196	12-477-44	C	G
197	12-478-223	G	A
198	12-478-320	G	A
199	12-479-289	G	T

FIG. 3 (following)

200	12-482-237	A	G
201	12-482-285	T	A
202	12-482-482	A	T
203	12-483-322	A	T
204	12-484-46	G	A
205	12-490-312	A	T
206	12-491-295	A	G
207	12-493-417	G	C
208	12-494-373	C	T
209	12-495-166	C	T
210	12-495-272	A	T
211	12-495-424	T	C
212	12-500-220	A	G
213	12-501-155	G	T
214	12-503-52	T	G
215	12-503-62	T	A
216	12-504-54	G	A
217	12-504-96	C	T
218	12-504-428	G	C
219	12-507-53	T	C
220	12-507-92	A	G
221	12-507-159	T	G
222	12-507-177	C	G
223	12-508-29	G	A
224	12-509-42	G	A
225	12-509-126	G	A
226	12-510-59	G	A
227	12-511-74	T	C
229	10-327-120	C	T
230	10-331-179	G	A
233	10-321-226	A	G
234	12-183-98	G	A/T
241	12-192-63	C	G/T
243	12-192-268	G	C
245	12-192-352	G	A
250	10-442-133	G	C
252	10-445-281	C	T
253	12-668-362	T	A
261	12-680-331	C	T
262	10-151-154	G	A
264	10-138-352	T	C
266	12-587-379	A	C
267	12-588-103	G	A
273	12-602-350	C	A
278	12-785-393	G	A
283	12-793-383	T	G
288	12-809-119	C	G
290	10-265-178	G	A
292	10-403-312	C	T
298	10-410-280	C	T
299	10-410-337	A	G

FIG. 3 (following)

300	12-121-326	G	A
307	12-126-222	C	T
309	12-128-225	G	T
312	12-130-260	C	T
314	12-132-157	T	C
334	12-146-47	A	G
335	12-148-283	G	A
343	12-154-480	C	T
344	12-155-403	C	A
349	12-161-157	G	A
354	10-472-202	T	C
358	12-639-95	G	A
370	12-646-429	T	C
371	12-646-433	T	G
388	12-906-149	G	A
389	12-906-154	A	C
390	12-906-251	A	T
395	12-909-176	C	T
396	12-909-484	G	T
403	10-448-266	A	C
405	10-455-367	T	C
408	12-10-303	C	T
413	10-460-221	C	T
437	12-442-133	C	-
445	2-13-398	G	-
446	2-28-132	-	T
447	2-39-27		deletion
448	2-45-155		deletion
449	2-4-391	G	-
452	10-360-190	-	T
453	10-365-374	-	A
454	10-367-58	-	insertion
455	12-468-424	-	T
457	12-499-86		deletion
458	12-500-217		insertion
459	12-511-101	A	-
463	10-494-332	insertion	
470	10-290-37	C	T
471	10-523-232	C	T
473	10-186-212	G	C
474	10-286-289	C	G
475	10-286-345	A	T
476	10-286-375	A	G
477	10-289-201	T	C
478	10-321-28	G	A
479	10-98-265	A	G
480	12-157-115	T	C
481	12-472-48	T	G
482	12-477-151	A	G
483	12-479-214	G	T

Fig. 4

SEQ ID NO.	BIALLELIC MARKER ID	1ST ALLELE	2ND ALLELE
9	12-441-233	G	A
11	12-442-221	T	C
48	10-102-294	C	T
50	10-414-243	A	G
52	10-418-177	A	G
56	10-76-177	A	T
58	10-76-333	G	C
72	10-84-277	A	G
73	10-84-295	A	G
75	10-85-117	G	T
77	10-86-121	A	C
80	12-254-115	A	T
88	10-214-279	C	T
89	10-214-380	A	G
122	2-29-205	C	T
123	2-29-206	A	G
145	12-631-208	A	G
242	12-192-64	T	C
244	12-192-334	G	A
263	10-138-206	C	T
276	12-783-421	C	T
282	12-792-233	G	A
291	10-266-203	C	T
294	10-408-356	C	T
295	10-409-148	G	C
296	10-409-249	G	C
311	12-130-203	C	T
345	12-156-91	A	G
352	10-471-84	A	T
353	10-471-85	A	C
357	12-637-219	G	A
393	12-907-482	A	T
412	10-457-284	G	T
451	10-358-353		deletion
456	12-481-293	T	-

Fig. 5

SEQ ID NO.	POSITION RANGE OF PREFERRED SEQUENCES
9	940-1001
18	1-425; 920-1001
32	1-175; 713-787
50	683-1001
52	1-450; 606-1001
58	732-832
59	612-725
87	717-742; 881-899; 951-1001
88	1-24; 276-305
103	369-387
129	433-449
145	152-241; 540-933
151	1-176; 395-857
171	1-98; 753-798
212	986-1001
229	1-439; 639-1001
230	254-396; 551-908
233	1-161; 283-406; 583-695; 843-1001
261	1-452
267	552-1001
273	1-86; 282-487; 963-1001
276	1-421; 633-1001
278	158-317; 834-1001
283	1-112
288	1-174; 252-399; 583-987
290	1-342; 790-1001
291	86-460
292	654-1001
298	637-799
299	580-742
300	1-297; 727-803
307	1-433; 869-1001
309	1-17
311	928-953
312	871-896; 972-1001
314	289-755
334	1-402; 638-678; 969-1001
335	1-223; 656-923
343	629-1000
349	98-251; 960-1001
352	1-52; 399-436
353	1-52; 399-436
354	754-1001
357	527-810
358	1-53; 506-521; 596-617
370	1-80; 675-1001
371	1-80; 675-1001

FIG. 5 (following)

388	1-293; 748-833
389	1-288; 743-828
390	1-191; 646-731
403	745-1001
405	984-1001
408	797-897; 931-1001
412	1-207; 979-1001
455	1-22
463	1-299; 400-463
470	1-485; 725-1000
471	1-432; 514-1000
474	1-353; 656-1000
475	1-298; 601-1000
476	1-268; 571-1000
477	1-452; 538-1000
479	385-391
480	910-954
482	443-531; 730-854
483	347-392

Fig. 6

SEQ ID NO.	POSITION RANGE OF MICROSEQUENCING PRIMERS	COMPLEMENTARY POSITION RANGE OF MICROSEQUENCING PRIMERS
1	481-500	502-521
2	481-500	502-521
3	481-500	502-521
4	481-500	502-521
5	441-460	462-481
6	481-500	502-521
7	482-500*	502-521
8	481-500	502-521
9	482-500*	502-521
10	481-500	502-521
11	481-500	502-521
12	482-500*	502-521
13	481-500	502-520*
14	481-500	502-521
15	481-500	502-520*
16	481-500	502-521
17	481-500	502-521
18	481-500	502-521
19	481-500	502-521
20	481-500	502-521
21	481-500	502-521
22	481-500	502-521
23	481-500	502-521
24	481-500	502-521
25	481-500	502-520*
26	481-500	502-521
27	481-500	502-521
28	481-500	502-521
29	481-500	502-521
30	481-500	502-521
31	481-500	502-521
32	481-500	502-521
33	481-500	502-521
34	481-500	502-521
35	213-231*	233-252
36	266-285	287-306
37	477-499*	501-520
38	461-479*	481-500
40	406-425	427-446
41	481-500	502-520*
42	484-502*	504-523
43	481-500	502-521
44	482-500*	502-521
45	310-329	331-349*
46	322-341	343-361*
47	258-276*	278-297
48	278-296*	298-317

FIG. 6 (following)

49	482-500*	502-520*
50	481-500	502-521
51	482-500*	502-520*
52	481-500	502-520*
53	482-500*	502-521
54	482-500*	502-521
56	158-177	179-198
57	198-217	219-238
58	315-333*	335-354
59	481-500	502-521
60	58-77	79-98
61	84-103	105-124
62	32-51	53-71*
63	20-38*	40-59
64	111-130	132-150*
65	146-165	167-186
66	226-245	247-266
67	142-160*	162-181
68	142-161	163-182
69	150-168*	170-189
70	132-151	153-172
71	224-242*	244-263
72	257-276	278-297
73	275-294	296-314*
74	24-42*	44-63
75	97-116	118-136*
76	300-319	321-340
77	102-120*	122-141
78	481-500	502-521
79	431-449*	451-470
80	226-245	247-266
81	292-310*	312-331
82	479-498	500-519
83	481-500	502-521
84	482-500*	502-521
85	483-502	504-522*
86	482-500*	502-521
87	484-502*	504-523
88	481-500	502-521
89	481-500	502-520*
90	196-215	217-236
91	377-396	398-417
92	212-231	233-252
93	31-50	52-71
94	106-125	127-146
95	182-201	203-222
96	255-274	276-295
97	326-345	347-366
98	151-170	172-191
99	168-187	189-208
100	203-222	224-243

FIG. 6 (following)

101	87-106	108-127
102	357-376	378-397
103	264-283	285-304
104	136-155	157-176
105	359-378	380-399
106	203-222	224-243
107	219-238	240-259
108	350-369	371-390
109	84-103	105-124
110	375-394	396-415
111	23-42	44-63
112	118-137	139-158
113	62-81	83-102
114	146-165	167-186
115	224-243	245-264
116	95-114	116-135
117	16-35	37-56
118	165-184	186-205
119	358-377	379-398
120	122-141	143-162
121	146-165	167-186
122	184-203	205-224
123	185-204	206-225
124	293-312	314-333
125	48-67	69-88
126	337-356	358-377
127	236-255	257-276
128	333-352	354-373
129	216-235	237-256
130	119-138	140-159
131	193-212	214-233
132	18-37	39-58
133	163-182	184-203
134	315-334	336-355
135	374-393	395-414
136	19-38	40-59
137	52-71	73-92
138	136-155	157-176
139	265-284	286-305
140	147-166	168-187
141	482-500*	502-521
142	481-500	502-520*
143	482-500*	502-521
144	457-476	481-499*
145	414-432*	434-453
146	481-500	502-521
147	483-502	504-523
148	481-500	502-521
149	481-500	502-521
150	481-500	502-520*
151	337-356	358-377

FIG. 6 (following)

152	454-472*	474-493
153	481-500	502-521
154	481-500	502-521
155	459-478	480-498*
156	480-499	501-520
157	481-500	502-521
158	481-500	502-521
159	483-502	504-523
160	483-502	504-523
161	481-500	502-521
162	481-500	502-521
163	361-380	382-401
164	442-460*	462-481
165	453-472	474-493
166	471-490	492-511
167	481-500	502-520*
168	481-500	502-521
169	481-500	502-520*
170	481-500	502-521
171	481-500	502-521
172	481-500	502-521
173	481-500	502-521
174	481-500	502-521
175	477-496	498-517
176	481-500	502-521
177	481-500	502-521
178	482-500*	502-521
179	481-500	502-521
180	481-500	502-521
181	481-500	502-521
182	481-500	502-521
183	481-500	502-520*
184	481-500	502-521
185	481-500	502-521
186	481-500	502-521
187	481-500	502-521
188	481-500	502-521
189	481-500	502-521
190	481-500	502-521
191	481-500	502-521
192	465-484	486-505
193	481-500	502-521
194	481-500	502-521
195	481-500	502-521
196	481-500	502-521
197	481-500	502-521
198	481-500	502-521
199	481-500	502-521
200	481-500	502-521
201	481-500	502-521
202	481-500	502-521

FIG. 6 (following)

203	479-498	500-519
204	481-500	502-521
205	481-500	502-521
206	481-500	502-521
207	481-500	502-521
208	481-500	502-521
209	481-500	502-521
210	481-500	502-521
211	481-500	502-521
212	481-500	502-521
213	481-500	502-521
214	481-500	502-521
215	481-500	502-521
216	479-498	500-519
217	481-500	502-521
218	482-500*	502-521
219	454-473	475-493*
220	481-500	502-521
221	480-499	501-520
222	481-500	502-521
223	481-500	502-521
224	481-500	502-521
225	481-500	502-521
226	481-500	502-521
227	483-500*	502-521
228	481-500	502-521
229	481-500	502-521
230	481-500	502-521
231	481-500	502-521
232	481-500	502-521
233	481-500	502-521
234	481-500	502-521
235	481-500	502-521
236	481-500	502-520*
237	482-500*	502-521
238	482-500*	502-521
239	481-500	502-521
240	481-500	502-520*
241	481-500	502-521
242	482-501	503-522
243	481-500	502-521
244	481-500	502-521
245	481-500	502-521
246	481-500	502-521
247	481-500	502-521
248	481-500	502-521
249	481-500	502-521
250	482-500*	502-521
251	464-483	485-503*
252	482-500*	502-521
253	481-500	502-521

FIG. 6 (following)

254	481-500	502-521
255	481-500	502-521
256	482-500*	502-521
257	482-500*	502-521
258	233-252	254-273
259	359-378	380-399
260	414-433	435-454
261	483-502	504-523
262	134-153	155-173*
263	186-204*	206-225
264	332-350*	352-371
265	482-500*	502-521
266	479-498	500-519
267	482-500*	502-521
268	481-500	502-521
269	482-500*	502-521
270	481-500	502-520*
271	481-500	502-520*
272	481-500	502-520*
273	481-500	502-521
274	481-500	502-520*
275	481-500	502-521
276	481-500	502-521
277	481-500	502-521
278	481-500	502-521
279	481-500	502-521
280	481-500	502-521
281	481-500	502-521
282	481-500	502-521
283	485-504	506-525
284	481-500	502-521
285	481-500	502-521
286	481-500	502-521
287	481-500	502-521
288	481-500	502-521
289	481-500	502-521
290	481-500	502-521
291	483-502	504-523
292	481-500	502-521
293	481-500	502-521
294	481-500	502-521
295	481-500	502-521
296	481-500	502-521
297	481-500	502-521
298	481-500	502-521
299	481-500	502-521
300	481-500	502-520*
301	481-500	502-521
302	481-500	502-521
303	481-500	502-521
304	482-500*	502-521

FIG. 6 (following)

305	481-500	502-521
306	481-500	502-521
307	481-500	502-521
308	481-500	502-521
309	481-500	502-520*
310	481-500	502-521
311	481-500	502-521
312	481-500	502-521
313	481-500	502-521
314	235-254	256-275
315	481-500	502-521
316	646-665	667-686
317	481-500	502-521
318	229-248	250-269
319	481-500	502-521
320	481-500	502-521
321	481-500	502-521
322	481-500	502-520*
323	481-500	502-520*
324	481-500	502-521
325	481-500	502-521
326	482-500*	502-521
327	481-500	502-521
328	481-500	502-521
329	481-500	502-520*
330	481-500	502-520*
331	481-500	502-521
332	481-500	502-521
333	481-500	502-521
334	481-500	502-521
335	481-500	502-521
336	481-500	502-520*
337	481-500	502-521
338	481-500	502-521
339	481-500	502-521
340	481-500	502-521
341	481-500	502-521
342	482-500*	502-520*
343	481-500	502-521
344	481-500	502-521
345	482-500*	502-520*
346	481-500	502-521
347	481-500	502-521
348	460-479	481-500
349	481-500	502-521
350	478-497	499-518
351	484-502*	504-523
352	484-502*	504-523
353	483-502	505-523*
354	484-502*	525-543*
355	483-502	504-523

FIG. 6 (following)

356	483-502	504-523
357	480-498*	500-519
358	480-498*	500-519
359	479-498	500-519
360	479-498	500-519
361	479-498	500-519
362	479-498	500-518*
363	479-498	500-519
364	479-498	500-519
365	479-498	500-519
366	412-431	433-452
367	368-387	389-408
368	483-502	504-523
369	484-502*	504-523
370	414-433	435-454
371	418-437	439-458
372	483-502	504-523
373	231-250	252-271
374	408-427	429-447*
375	481-500	502-521
376	278-297	299-318
377	367-385*	387-406
378	437-456	458-477
379	481-500	502-521
380	479-498	500-519
381	479-498	500-519
382	479-498	500-519
383	483-502	504-523
384	483-502	504-523
385	481-500	502-521
386	286-305	307-326
387	477-496	498-517
388	482-500*	502-521
389	481-500	502-521
390	481-500	502-521
391	481-500	502-521
392	224-243	245-263*
393	481-500	502-521
394	33-52	54-73
395	173-192	194-213
396	481-500	502-521
397	327-346	348-366*
398	483-502	504-523
399	221-239*	241-260
400	481-500	502-521
401	365-383*	385-404
402	483-502	504-523
403	483-502	504-523
404	483-502	504-523
405	483-502	504-523
406	484-502*	504-523

FIG. 6 (following)

407	479-498	500-518*
408	482-500*	502-521
409	482-500*	502-521
410	479-498	500-518*
411	481-500	502-520*
412	483-502	504-523
413	483-502	504-523
414	483-502	504-523
415	483-502	504-523
416	483-502	504-523
417	483-502	504-523
418	481-500	502-520*
419	481-500	502-521
420	479-498	500-518*
421	479-498	500-519
422	479-498	500-519
423	481-500	502-520*
424	481-500	502-520*
425	479-498	500-519
426	481-500	502-520*
427	483-502	504-522*
428	483-502	504-523
429	344-363	365-384
430	481-500	502-521
431	481-500	502-521
432	469-488	490-509
433	481-500	502-521
434	481-500	502-521
435	481-500	502-521
436	481-500	-
437	-	502-520*
438	481-500	-
439	481-500	-
440	481-500	-
441	481-500	-
442	481-500	-
443	481-500	-
444	482-500	-
445	481-500	-
446	481-500	-
447	481-500	-
448	481-500	-
449	481-500	-
450	481-500	-
451	481-500	-
452	481-500	-
453	481-500	-
454	481-500	-
455	481-500	-
456	481-500	-
457	481-500	-

FIG. 6 (following)

458	481-500	-
459	481-500	-
460	481-500	-
461	481-500	-
462	481-500	-
463	481-500	-
465	409-428	-
466	481-500	-
467	286-305	-
468	481-500	-
469	481-500	502-521
470	481-500	502-521
471	481-500	502-521
472	481-500	502-521
473	192-211	213-232
474	481-500	502-521
475	481-500	502-521
476	481-500	502-521
477	481-500	502-521
478	481-500	502-521
479	245-264	266-285
480	481-500	502-521
481	481-500	502-521
482	481-500	502-521
483	481-500	502-521
484	481-500	502-521

Fig. 7

SEQ ID NO.	POSITION RANGE OF AMPLIFICATION PRIMERS	COMPLEMENTARY POSITION RANGE OF AMPLIFICATION PRIMERS
1	362-380	792-812
2	310-327	751-771
3	304-321	745-765
4	82-99	540-557
5	308-325	830-847
6	304-321	803-823
7	131-150	561-580
8	287-304	805-825
9	284-303	716-734
10	394-413	826-844
11	270-289	704-721
12	444-462	874-893
13	73-91	577-596
14	139-158	634-652
15	372-392	808-826
16	429-449	865-883
17	233-252	693-712
18	122-141	582-601
19	298-317	772-792
20	296-315	770-790
21	200-217	679-696
22	442-459	921-938
23	228-245	760-777
24	378-396	911-928
25	203-221	736-753
26	37-55	570-587
27	222-241	655-675
28	436-455	880-900
29	476-493	945-962
30	266-283	735-752
31	278-295	613-632
32	418-436	823-842
33	216-235	646-665
34	91-109	510-528
35	137-153	586-604
36	137-153	586-604
37	206-225	727-746
38	400-419	856-876
40	146-165	588-607
41	62-81	504-523
42	210-230	591-610
43	307-326	797-817
44	277-296	767-787
45	1-20	402-421
46	3-21	404-422
47	1-18	355-372

FIG. 7 (following)

48	1-18	356-375
49	108-125	539-556
50	259-276	592-609
51	229-246	630-649
52	325-342	659-676
53	357-377	795-815
54	186-205	621-641
56	1-18	416-435
57	1-18	416-435
58	1-18	416-435
59	185-203	593-610
60	1-18	424-442
61	1-18	424-442
62	1-19	401-420
63	1-18	412-431
64	1-18	412-431
65	1-18	412-431
66	1-18	412-431
67	1-19	403-422
68	1-19	403-422
69	1-19	336-353
70	1-18	406-425
71	1-18	406-425
72	1-18	406-425
73	1-18	406-425
74	1-18	405-424
75	1-18	405-424
76	1-18	405-424
77	1-18	334-352
78	228-247	660-678
79	298-318	806-826
80	132-152	586-603
81	132-152	586-603
82	308-328	779-798
83	122-141	598-618
84	390-409	768-788
85	323-339	800-819
86	411-427	761-777
87	212-230	590-608
88	154-174	746-763
89	124-143	647-664
90	1-18	417-437
91	1-18	417-437
92	1-18	406-426
93	3-24	405-429
94	3-24	405-429
95	1-25	400-420
96	1-25	400-420
97	1-25	400-420
98	1-18	405-427
99	1-21	396-420

FIG. 7 (following)

100	1-21	396-420
101	1-18	423-443
102	1-18	423-443
103	1-18	429-446
104	1-18	429-446
105	1-18	429-446
106	1-25	399-420
107	1-23	398-418
108	1-23	398-418
109	1-18	427-445
110	1-18	427-445
111	1-18	416-436
112	1-18	416-436
113	1-25	396-420
114	1-25	396-420
115	1-25	396-420
116	1-18	416-434
117	1-21	396-420
118	1-19	405-429
119	1-19	405-429
120	1-21	422-439
121	1-21	422-439
122	1-21	422-439
123	1-21	422-439
124	1-21	422-439
125	1-21	413-432
126	1-18	404-423
127	1-21	411-435
128	1-21	411-435
129	1-18	428-449
130	1-18	395-419
131	3-23	398-420
132	1-21	418-442
133	1-21	418-442
134	1-21	418-442
135	1-21	418-442
136	1-24	404-426
137	1-24	404-426
138	1-24	404-426
139	1-24	404-426
140	1-20	396-420
141	459-476	859-878
142	126-143	526-545
143	451-468	853-872
144	388-407	758-775
145	226-245	705-725
146	220-238	636-655
147	478-496	820-837
148	95-112	504-521
149	297-317	742-759
150	416-435	868-886

FIG. 7 (following)

151	139-157	579-599
152	139-157	579-599
153	122-140	562-582
154	472-491	926-945
155	449-468	982-999
156	86-105	615-633
157	285-305	751-770
158	290-310	756-775
159	184-202	616-634
160	113-131	545-563
161	85-102	534-552
162	313-331	792-812
163	252-272	681-701
164	252-272	681-701
165	252-272	681-701
166	252-272	681-701
167	403-422	927-947
168	81-101	513-532
169	154-173	685-705
170	53-70	558-578
171	248-267	684-704
172	447-464	849-867
173	394-411	796-814
174	235-252	637-655
175	478-495	889-908
176	113-132	518-537
177	400-417	800-819
178	430-447	830-849
179	182-199	582-601
180	142-159	542-561
181	415-434	821-840
182	442-460	870-889
183	439-458	946-966
184	113-132	620-640
185	10-29	517-537
186	370-387	812-832
187	257-274	699-719
188	68-86	533-553
189	192-210	740-758
190	20-38	568-586
191	108-126	566-585
192	453-471	911-930
193	62-82	580-600
194	294-314	812-832
195	295-315	813-833
196	6-26	524-544
197	234-254	704-723
198	331-351	801-820
199	213-230	678-698
200	223-243	720-737
201	271-291	768-785

FIG. 7 (following)

202	468-488	965-982
203	311-331	802-820
204	86-106	528-546
205	189-209	621-641
206	266-286	777-795
207	90-109	514-534
208	127-144	571-591
209	336-355	784-802
210	230-249	678-696
211	78-97	526-544
212	283-303	711-731
213	168-188	636-655
214	80-100	535-552
215	90-110	545-562
216	446-463	993-1013
217	406-423	953-973
218	75-92	622-642
219	422-441	982-1001
220	410-429	970-990
221	341-360	901-921
222	324-343	884-904
223	473-491	907-925
224	460-479	889-909
225	376-395	805-825
226	107-127	539-559
227	125-145	558-575
228	191-208	596-613
229	382-400	805-824
230	326-345	728-747
231	148-167	550-569
232	240-257	658-675
233	276-293	692-711
234	136-155	581-598
235	424-444	855-875
236	348-368	784-803
237	105-125	541-560
238	437-456	839-859
239	436-455	838-858
240	384-402	832-849
241	75-94	544-563
242	76-95	545-564
243	280-299	749-768
244	346-365	815-834
245	364-383	833-852
246	363-381	878-893
247	171-189	686-707
248	159-177	674-695
249	17-35	532-553
250	369-386	777-794
251	237-253	567-586
252	221-238	624-641

FIG. 7 (following)

253	390-410	844-861
254	454-474	883-901
255	411-431	840-858
256	345-365	774-792
257	354-372	784-804
258	9-29	439-458
259	9-29	439-458
260	9-29	439-458
261	173-192	645-665
262	1-18	367-384
263	1-18	406-425
264	1-18	406-425
265	88-107	552-572
266	478-498	857-877
267	60-77	585-603
268	190-210	636-654
269	384-402	830-849
270	138-158	658-675
271	378-397	805-825
272	307-325	704-724
273	153-171	550-570
274	240-260	668-688
275	429-446	858-878
276	81-98	510-530
277	302-322	791-811
278	109-129	598-618
279	74-94	583-602
280	423-443	876-896
281	291-311	671-690
282	284-304	712-732
283	365-385	866-884
284	169-189	605-625
285	135-155	596-615
286	450-469	894-914
287	427-446	871-891
288	383-402	888-908
289	126-146	558-577
290	324-341	662-681
291	301-320	701-720
292	190-208	593-611
293	448-465	848-867
294	146-165	546-565
295	354-372	779-798
296	253-271	678-697
297	228-245	645-664
298	222-239	639-658
299	165-182	582-601
300	178-196	637-656
301	162-180	595-612
302	122-140	555-572
303	334-352	830-848

FIG. 7 (following)

304	309-327	805-823
305	203-221	699-717
306	444-462	940-958
307	267-286	703-722
308	342-361	778-797
309	276-295	706-725
310	326-344	779-797
311	301-319	733-753
312	244-262	676-696
313	104-124	594-612
314	99-117	557-577
315	68-86	526-546
316	250-270	800-818
317	250-270	800-818
318	12-32	442-461
319	186-204	623-641
320	87-105	524-542
321	112-130	549-567
322	122-139	602-620
323	368-386	868-888
324	173-191	673-693
325	117-135	617-637
326	181-200	640-658
327	414-433	873-891
328	187-205	637-657
329	181-199	631-651
330	50-68	533-552
331	148-167	651-669
332	12-31	515-533
333	271-291	655-674
334	144-164	528-547
335	375-395	765-783
336	403-423	793-811
337	368-387	800-820
338	328-345	827-845
339	306-323	805-823
340	232-249	731-749
341	50-68	553-572
342	386-405	867-887
343	23-43	522-540
344	99-116	628-647
345	412-429	844-862
346	67-87	513-533
347	230-247	691-710
348	446-463	907-926
349	345-363	729-749
350	478-497	909-927
351	479-498	880-899
352	420-439	788-807
353	420-439	788-807
354	304-322	714-732

FIG. 7 (following)

355	171-189	582-600
356	220-238	624-641
357	230-250	698-717
358	144-164	573-593
359	290-310	719-739
360	156-176	629-649
361	296-316	769-789
362	324-344	797-817
363	412-432	885-905
364	127-147	600-618
365	129-149	602-620
366	163-183	636-654
367	163-183	636-654
368	117-135	592-612
369	87-105	562-582
370	6-26	474-494
371	6-26	474-494
372	359-378	788-808
373	129-147	607-627
374	129-147	607-627
375	100-118	578-598
376	184-203	615-635
377	184-203	615-635
378	184-203	615-635
379	131-150	562-582
380	390-410	903-921
381	76-96	595-613
382	168-188	687-705
383	108-128	566-586
384	384-404	863-883
385	120-139	552-572
386	173-193	692-712
387	418-435	979-1000
388	353-372	809-829
389	348-367	804-824
390	251-270	707-727
391	52-71	508-528
392	46-65	533-553
393	20-39	507-527
394	18-38	505-525
395	18-38	505-525
396	18-38	505-525
397	272-292	704-724
398	209-229	641-661
399	219-237	653-673
400	437-457	908-928
401	279-298	773-793
402	252-271	746-766
403	238-257	660-679
404	172-189	578-597
405	135-152	545-564

FIG. 7 (following)

406	346-366	801-821
407	386-406	847-865
408	335-355	787-807
409	237-257	680-700
410	121-140	565-584
411	339-357	781-801
412	220-238	621-639
413	283-301	686-704
414	272-290	675-693
415	269-287	672-690
416	268-286	671-689
417	219-237	622-640
418	444-464	901-921
419	179-199	689-707
420	114-134	597-615
421	175-195	658-676
422	228-248	711-729
423	251-271	776-795
424	461-481	981-1001
425	343-363	781-799
426	424-442	952-971
427	309-326	777-797
428	455-473	907-927
429	40-59	551-569
430	114-134	562-582
431	115-135	563-583
432	127-147	575-595
433	179-199	627-647
434	321-341	769-789
435	326-346	774-794
436	367-385	797-817
437	184-203	616-633
438	86-106	546-563
439	260-279	755-773
440	255-272	773-790
441	303-322	736-756
442	215-233	617-635
443	479-499	913-932
444	204-222	634-654
445	104-121	506-525
446	370-387	769-793
447	475-495	870-892
448	347-367	764-788
449	111-132	513-537
450	96-113	601-621
451	149-167	577-596
452	312-329	713-731
453	128-145	530-548
454	444-461	855-874
455	76-95	583-603
456	333-353	774-793

FIG. 7 (following)

457	136-156	567-586
458	286-306	714-734
459	152-172	585-602
460	59-78	523-543
461	251-271	771-788
462	119-136	679-696
463	170-188	574-591
465	179-198	611-631
466	83-103	554-574
467	279-298	773-793
468	340-360	788-808
469	177-196	576-595
470	465-484	864-883
471	270-288	527-545
472	325-345	783-800
473	1-20	413-432
474	213-231	613-631
475	158-176	558-576
476	128-146	528-546
477	307-324	700-719
478	474-491	890-909
479	1-19	404-422
480	387-407	833-853
481	454-472	919-939
482	113-133	631-651
483	288-305	753-773
484	174-193	573-592

Fig. 8

SEQ ID NO.	POSITION RANGE OF PROBES
1	489-513
2	489-513
3	489-513
4	489-513
5	449-473
6	489-513
7	489-513
8	489-513
9	489-513
10	489-513
11	489-513
12	489-513
13	489-513
14	489-513
15	489-513
16	489-513
17	489-513
18	489-513
19	489-513
20	489-513
21	489-513
22	489-513
23	489-513
24	489-513
25	489-513
26	489-513
27	489-513
28	489-513
29	489-513
30	489-513
31	489-513
32	489-513
33	489-513
34	489-513
35	220-244
36	274-298
37	488-512
38	468-492
40	414-438
41	489-513
42	491-515
43	489-513
44	489-513
45	318-342
46	330-354
47	265-289
48	285-309

Fig. 8 (following)

49	489-513
50	489-513
51	489-513
52	489-513
53	489-513
54	489-513
56	166-190
57	206-230
58	322-346
59	489-513
60	66-90
61	92-116
62	40-64
63	27-51
64	119-143
65	154-178
66	234-258
67	149-173
68	150-174
69	157-181
70	140-164
71	231-255
72	265-289
73	283-307
74	31-55
75	105-129
76	308-332
77	109-133
78	489-513
79	438-462
80	234-258
81	299-323
82	487-511
83	489-513
84	489-513
85	491-515
86	489-513
87	491-515
88	489-513
89	489-513
90	204-228
91	385-409
92	220-244
93	39-63
94	114-138
95	190-214
96	263-287
97	334-358
98	159-183
99	176-200
100	211-235

Fig. 8 (following)

101	95-119
102	365-389
103	272-296
104	144-168
105	367-391
106	211-235
107	227-251
108	358-382
109	92-116
110	383-407
111	31-55
112	126-150
113	70-94
114	154-178
115	232-256
116	103-127
117	24-48
118	173-197
119	366-390
120	130-154
121	154-178
122	192-216
123	193-217
124	301-325
125	56-80
126	345-369
127	244-268
128	341-365
129	224-248
130	127-151
131	201-225
132	26-50
133	171-195
134	323-347
135	382-406
136	27-51
137	60-84
138	144-168
139	273-297
140	155-179
141	489-513
142	489-513
143	489-513
144	465-489
145	421-445
146	489-513
147	491-515
148	489-513
149	489-513
150	489-513
151	345-369

Fig. 8 (following)

152	461-485
153	489-513
154	489-513
155	467-491
156	488-512
157	489-513
158	489-513
159	491-515
160	491-515
161	489-513
162	489-513
163	369-393
164	449-473
165	461-485
166	479-503
167	489-513
168	489-513
169	489-513
170	489-513
171	489-513
172	489-513
173	489-513
174	489-513
175	485-509
176	489-513
177	489-513
178	489-513
179	489-513
180	489-513
181	489-513
182	489-513
183	489-513
184	489-513
185	489-513
186	489-513
187	489-513
188	489-513
189	489-513
190	489-513
191	489-513
192	473-497
193	489-513
194	489-513
195	489-513
196	489-513
197	489-513
198	489-513
199	489-513
200	489-513
201	489-513
202	489-513

Fig. 8 (following)

203	487-511
204	489-513
205	489-513
206	489-513
207	489-513
208	489-513
209	489-513
210	489-513
211	489-513
212	489-513
213	489-513
214	489-513
215	489-513
216	487-511
217	489-513
218	489-513
219	462-486
220	489-513
221	488-512
222	489-513
223	489-513
224	489-513
225	489-513
226	489-513
227	489-513
228	489-513
229	489-513
230	489-513
231	489-513
232	489-513
233	489-513
234	489-513
235	489-513
236	489-513
237	489-513
238	489-513
239	489-513
240	489-513
241	489-513
242	490-514
243	489-513
244	489-513
245	489-513
246	489-513
247	489-513
248	489-513
249	489-513
250	489-513
251	472-496
252	489-513
253	489-513

Fig. 8 (following)

254	489-513
255	489-513
256	489-513
257	489-513
258	241-265
259	367-391
260	422-446
261	491-515
262	142-166
263	193-217
264	339-363
265	489-513
266	487-511
267	489-513
268	489-513
269	489-513
270	489-513
271	489-513
272	489-513
273	489-513
274	489-513
275	489-513
276	489-513
277	489-513
278	489-513
279	489-513
280	489-513
281	489-513
282	489-513
283	493-517
284	489-513
285	489-513
286	489-513
287	489-513
288	489-513
289	489-513
290	489-513
291	491-515
292	489-513
293	489-513
294	489-513
295	489-513
296	489-513
297	489-513
298	489-513
299	489-513
300	489-513
301	489-513
302	489-513
303	489-513
304	489-513

Fig. 8 (following)

305	489-513
306	489-513
307	489-513
308	489-513
309	489-513
310	489-513
311	489-513
312	489-513
313	489-513
314	243-267
315	489-513
316	654-678
317	489-513
318	237-261
319	489-513
320	489-513
321	489-513
322	489-513
323	489-513
324	489-513
325	489-513
326	489-513
327	489-513
328	489-513
329	489-513
330	489-513
331	489-513
332	489-513
333	489-513
334	489-513
335	489-513
336	489-513
337	489-513
338	489-513
339	489-513
340	489-513
341	489-513
342	489-513
343	489-513
344	489-513
345	489-513
346	489-513
347	489-513
348	468-492
349	489-513
350	486-510
351	491-515
352	491-515
353	491-515
354	491-515
355	491-515

Fig. 8 (following)

356	491-515
357	487-511
358	487-511
359	487-511
360	487-511
361	487-511
362	487-511
363	487-511
364	487-511
365	487-511
366	420-444
367	376-400
368	491-515
369	491-515
370	422-446
371	426-450
372	491-515
373	239-263
374	416-440
375	489-513
376	286-310
377	374-398
378	445-469
379	489-513
380	487-511
381	487-511
382	487-511
383	491-515
384	491-515
385	489-513
386	294-318
387	485-509
388	489-513
389	489-513
390	489-513
391	489-513
392	232-256
393	489-513
394	41-65
395	181-205
396	489-513
397	335-359
398	491-515
399	228-252
400	489-513
401	372-396
402	491-515
403	491-515
404	491-515
405	491-515
406	491-515

Fig. 8 (following)

407	487-511
408	489-513
409	489-513
410	487-511
411	489-513
412	491-515
413	491-515
414	491-515
415	491-515
416	491-515
417	491-515
418	489-513
419	489-513
420	487-511
421	487-511
422	487-511
423	489-513
424	489-513
425	487-511
426	489-513
427	491-515
428	491-515
429	352-376
430	489-513
431	489-513
432	477-501
433	489-513
434	489-513
435	489-513
436	489-513
437	489-513
438	489-513
439	489-513
440	489-513
441	489-513
442	489-513
443	489-513
444	489-513
445	489-513
446	489-513
447	489-513
448	489-513
449	489-513
450	489-513
451	489-513
452	489-513
453	489-513
454	489-513
455	489-513
456	489-513
457	489-513

Fig. 8 (following)

458	489-513
459	489-513
460	489-513
461	489-513
462	489-513
463	489-513
464	489-513
465	417-441
466	489-513
467	294-318
468	489-513
469	489-513
470	489-513
471	489-513
472	489-513
473	200-224
474	489-513
475	489-513
476	489-513
477	489-513
478	489-513
479	253-277
480	489-513
481	489-513
482	489-513
483	489-513
484	489-513

ALLELE FREQUENCY DATA (FRENCH and US)

Seq. ID No.	Protein	Biallelic Marker ID	caucasian FRENCH					caucasian US				
			size	A	C	G	T	size	A	C	G	T
21	MGST-II	12-458/196	no genotyped for this population					180	80,83			19,17
15	MGST-II	12-455/326						93	58,06		41,94	
5	MGST-II	12-426/154						181	58,01		41,99	
9	MGST-II	12-441/233						182		35,44		64,56
437	MGST-II	12-442/133						94		5,85	94,15	
7	MGST-II	12-430/80						93	5,38		94,62	
1	MGST-II	12-421/140						183	79,51		20,49	
436	MGST-II	12-421/135						185			84,59	15,41
13	MGST-II	12-453/429						183		56,28		43,72
12	MGST-II	12-447/58						93		55,38	44,62	
25	MGST-II	12-461/299						183		40,44		59,56
3	MGST-II	12-424/198						176			61,08	38,92
14	MGST-II	12-454/363						188	18,62		81,38	

Figure 9

ALLELE FREQUENCY DATA (US)

Seq. ID No.	Protein	Biallelic Marker ID	caucasian US				
			size	A	C	G	T
37	ME1	12-716-295	189		66,14		33,86
31	ME1	10-428-219	189	66,67		33,33	
38	ME1	12-720-80	190		33,95	66,05	
33	ME1	10-420-284	184		1,36		98,64
41	ME1	12-721-440	94	1,6		98,4	
44	ME1	12-724-225	190		73,16		26,84
42	ME1	12-723-293	92		99,46		0,54
35	ME1	12-713-95	190		32,63		67,37

Figure 10

ALLELE FREQUENCY DATA (FRENCH and US)

Seq. ID No.	Protein	Biallelic Marker ID	Caucasian FRENCH					Caucasian US				
			size	A	C	G	T	size	A	C	G	T
336	UGT1A7	12-148-311	88	47,73		52,27		190	44,47		55,53	
345	UGT1A7	12-156-91	90	50,56		49,44		93	50,54		49,46	
300	UGT1A7	12-121-326	93	30,11		69,89		188	28,99		71,01	
309	UGT1A7	12-128-225	93	50,54	49,46			187	55,35	44,65		
304	UGT1A7	12-124-194	85		19,41		80,59					
326	UGT1A7	12-141-159	92	37,5		62,5						
330	UGT1A7	12-143-453	82	50,61		49,39						
322	UGT1A7	12-139-380	85	17,65		82,35		190	20,79		79,21	
342	UGT1A7	12-153-116	90		62,22		37,78					
323	UGT1A7	12-140-134	89			58,99	41,01	183			56,01	43,99
329	UGT1A7	12-142-321	90	54,44		45,56						

Figure 11

ALLELE FREQUENCY DATA (FRENCH and US)

Seq. ID No.	Protein	Biallelic Marker ID	Caucasian FRENCH					Caucasian US				
			size	A	C	G	T	size	A	C	G	T
380	UGT2B4	12-653-423	6	25			75	177	73,45			26,55
351	UGT2B4	10-470-25	179	56,15			43,85	90	55,56			44,44
356	UGT2B4	10-494-284	6		16,67		83,33	185		22,97		77,03
352	UGT2B4	10-471-84	178	24,44			75,56	92	27,17			72,83
353	UGT2B4	10-471-85	0					188	26,6	73,4		
354	UGT2B4	10-472-202	182		14,29		85,71	93		9,68		90,32
357	UGT2B4	12-637-219	0					187		33,42		66,58
358	UGT2B4	12-639-95	0					187		35,56		64,44
377	UGT2B4	12-652-203	4	50	50			189	57,67	42,33		
369	UGT2B4	12-642-417	0					186	73,66		26,34	
374	UGT2B4	12-648-300	0					91		62,09		37,91

Figure 12

HAPLOTYPE ANALYSIS (MGST-II vs ASTHMA)

297 ALT vs 286 Caucasian US

MARKERS			12-421/135	12-421/140	12-430/80	12-441/233	12-442/133	12-447/58	12-455/326	12-461/299	12-453/429	12-424/198	12-454/363	12-458/196	12-426/154	ESTIMATED FREQUENCIES					
MGST2			lnB		markers in bac																
size (cases / controls)			282 vs 185	281 vs 183	163 vs 93	285 vs 182	172 vs 94	287 vs 93	167 vs 93	287 vs 183	287 vs 183	260 vs 176	277 vs 188	277 vs 180	273 vs 181	haplotype frequencies		p-excess	Odds Ratio	Chi-S	Pvalue (1df)
allelic frequency % (case/controls)			85/84 (G)	81/79 (A)	8/5 (A)	35/35 (C)	8/5 (C)	45/44 (G)	44/41 (G)	63/59 (T)	60/56 (C)	40/38 (T)	21/18 (A)	81/80 (A)	59/58 (A)	cases	controls				
diff freq. all. (cases - controls)			1.0	2.2	3.2	0.3	2.3	1.0	2.4	3.5	4.7	1.7	2.5	0.8	1.3						
pvalue			6.6e-01 1.1	4.0e-01 1.1	1.8e-01 1.6	7.5e-01 1.0	3.2e-01 1.4	7.5e-01 1.0	5.8e-01 1.1	2.7e-01 1.2	1.5e-01 1.2	5.8e-01 1.1	3.4e-01 1.2	7.5e-01 1.1	6.6e-01 1.1						
Test Hardy Weinberg Equilibrium		cases vs	0.00 HW	-0.00 HW	-0.00 HW	0.01 HW	-0.00 HW	-0.00 HW	0.01 HW	0.01 HW	-0.02 HW	0.02 HW	0.00 HW	0.01 HW	0.02 HW						
		controls	0.01 HW	0.00 HW	0.89	0.01 HW	0.88	-0.04 HW	0.02 HW	-0.03 HW	0.00 HW	-0.02 HW	0.00 HW	-0.00 HW	0.00 HW						
haplotype 1		288 vs 180								T	C					0.390	0.310	11.60	1.42	6.16	1.3e-02
haplotype 2		157 vs 93			A								G			0.076	0.025	5.18	3.16	5.54	1.8e-02
haplotype 3		164 vs 94					C						G			0.073	0.025	4.93	3.10	5.28	2.1e-02
haplotype 4		276 vs 93						C					A			0.068	0.025	4.46	2.89	4.89	2.7e-02
haplotype 5	PT2	260 vs 170									C	T				0.216	0.156	7.14	1.49	4.81	2.7e-02
haplotype 6		151 vs 86							G		C	T				0.118	0.011	10.81	12.22	17.23	3.2e-05
haplotype 7		247 vs 162									C	T			G	0.097	0.027	7.13	3.80	14.60	1.3e-04
haplotype 8		166 vs 92						G	G	C						0.112	0.027	8.69	4.53	11.33	7.3e-04
haplotype 9		168 vs 93							G	C	T					0.098	0.022	7.75	4.75	10.38	1.3e-03
haplotype 10		258 vs 165				T					C	T				0.150	0.077	7.99	2.13	10.25	1.3e-03
haplotype 11		265 vs 166								T				A	A	0.251	0.171	9.68	1.63	7.66	5.5e-03
haplotype 12		150 vs 86				T			A			T				0.105	0.034	7.38	3.34	7.59	5.8e-03
haplotype 13		281 vs 175	G							T	C					0.340	0.255	11.36	1.50	7.26	6.9e-03
haplotype 14		277 vs 170								T	C			A		0.322	0.238	11.02	1.52	7.20	6.9e-03
haplotype 15		150 vs 81		A					A			T				0.193	0.098	10.53	2.20	7.07	7.7e-03
haplotype 16		284 vs 176				T				T	C					0.282	0.187	9.29	1.55	6.94	8.2e-03
haplotype 17	PT3	271 vs 88						G		C					G	0.088	0.028	8.12	3.29	6.91	8.2e-03
haplotype 18		144 vs 88							G		C	T	G			0.126	0.000	12.60	100.00	23.52	1.2e-06
haplotype 19		166 vs 92						C	A	T	T					0.101	0.000	10.09	100.00	19.85	8.2e-06
haplotype 20		149 vs 85	G						G		C	T				0.131	0.010	12.20	14.29	19.79	8.6e-06
haplotype 21		146 vs 79							G		T	G		A		0.131	0.009	12.32	16.46	18.98	1.3e-05
haplotype 22		271 vs 88						C		T	T				A	0.099	0.000	9.89	100.00	18.81	1.4e-05
haplotype 23		151 vs 86							G	T	C	T				0.123	0.011	11.29	12.37	18.08	2.1e-05
haplotype 24		151 vs 85						C	A		T	T				0.092	0.000	9.22	100.00	16.66	4.4e-05
haplotype 25		151 vs 86					G		G		T	G				0.130	0.019	11.28	7.72	16.48	4.9e-05
haplotype 26		150 vs 81		A					G		C	T				0.119	0.011	10.91	11.94	16.40	5.1e-05
haplotype 27		143 vs 85			G				G		T	G				0.131	0.019	11.37	7.63	16.31	5.1e-05
haplotype 28		150 vs 86				T			G		C	T				0.114	0.011	10.33	11.04	16.15	5.7e-05
haplotype 29		243 vs 159	G								C	T			G	0.105	0.029	7.81	3.96	16.04	6.0e-05
haplotype 30	PT4	240 vs 161									C	T	G		G	0.101	0.028	7.51	3.88	15.38	8.7e-05

Figure 13

HAPLOTYPE ANALYIS ; PERMUTATION TEST RESULTS

Asthma

PROTEIN MGST2

12-447/68	12-455/326	12-461/299	12-453/429	12-424/198	12-454/363	MARKERS	
markers in bac							
	G		C	T		HAPLOTYPES (ALT vs US)	
	7,52E-01		5,27E-01	7,52E-01		pvalue	ALT+ vs ALT-
	0.8 (44 vs 45)		-2.7 (59 vs 62)	-1 (41 vs 40)		diff all. Freq%	
	5,84E-01		1,47E-01	5,84E-01		pvalue	ALT vs caucasian US
	3.5 (63 vs 60)		4.7 (61 vs 56)	-1.7 (59 vs 61)		diff all. Freq%	
	G		C	T	G	HAPLOTYPES (ALT vs US)	
	7,52E-01		5,27E-01	7,52E-01	4,80E-01	pvalue	ALT+ vs ALT-
	0.8 (44 vs 45)		-2.7 (59 vs 62)	-1 (41 vs 40)	-2,5 (77 vs 80)	diff all. Freq%	
	5,84E-01		1,47E-01	5,84E-01	3,43E-01	pvalue	ALT vs caucasian US
	3.5 (63 vs 60)		4.7 (61 vs 56)	-1.7 (59 vs 61)	-2,5 (79 vs 81)	diff all. Freq%	
C	A	T	T			HAPLOTYPES (ALT vs US)	
4,80E-01	7,52E-01	6,55E-01	5,27E-01			pvalue	ALT+ vs ALT-
-3,1 (52 vs 55)	0,8 (56 vs 55)	1,6 (64 vs 63)	-2,7 (41 vs 38)			diff all. Freq%	
7,52E-01	5,84E-01	2,73E-01	1,47E-01			pvalue	ALT vs caucasian US
-1 (54 vs 55)	-2,4 (56 vs 58)	3,5 (63 vs 60)	4,7 (39 vs 44)			diff all. Freq%	

HAPLOTYPE GCT	sample sizes cases vs controls	haplotype frequencies cases	haplotype frequencies controls	p-excess	odds-ratio	chi-S	P value		PERMUTATIONS Av. Chi-S	PERMUTATIONS Max Chi-S	PERMUTATIONS > iter / nb of iter.
ALT+ vs ALT-	60 vs 91	0.077	0.141	-7,53	0,50	2.96	8.3e-02	*	1.4	14.6	158/1000
ALT+ vs ALT- (1)	60 vs 91	0.077	0.141	-7,53	0,5	2.96	8.3e-02	*	1.4	14.6	158/1000
ALT vs caucasian US	151 vs 86	0.118	0.011	10,81	12,22	17.23	3.2e-05	****	2.2 2.2	19.5 22.6	3/1000 31/10000
ALT vs caucasian US (2)	151 vs 86	0.118	0.011	10,81	12,22	17.23	3.2e-05	****	2.2	19.5	3/1000

HAPLOTYPE GCTG	sample sizes cases vs controls	haplotype frequencies cases	haplotype frequencies controls	p-excess	odds-ratio	chi-S	P value		PERMUTATIONS Av. Chi-S	PERMUTATIONS Max Chi-S	PERMUTATIONS > iter / nb of iter.
ALT+ vs ALT-	56 vs 88	0.088	0.152	-7,46	0,54	2.47	1.1e-01	*	1.4	16.6	182/1000
ALT+ vs ALT- (1)	56 vs 88	0.088	0.152	-7,46	0,54	2.47	1.1e-01	*	1.4	16.6	182/1000
ALT vs caucasian US	144 vs 86	0.126	0.000	12,6	100	23.52	1.2e-06	******	2.8 2.8	20.1 28.7	0/1000 5/10000
ALT vs caucasian US (2)	144 vs 86	0.126	0.000	12,6	100	23.52	1.2e-06	******	2.8	20.1	0/1000

HAPLOTYPE CATT	sample sizes cases vs controls	haplotype frequencies cases	haplotype frequencies controls	p-excess	odds-ratio	chi-S	P value		PERMUTATIONS Av. Chi-S	PERMUTATIONS Max Chi-S	PERMUTATIONS > iter / nb of iter.
ALT+ vs ALT-	64 vs 102	0.139	0.075	7	2,01	3.68	5.4e-02	*	1.5	14.4	114/1000
ALT+ vs ALT- (1)	64 vs 102	0.139	0.075	7	2,01	3.68	5.4e-02	*	1.5	14.4	114/1000
ALT vs caucasian US	166 vs 92	0.101	0	10,09	100	19.85	8.2e-06	*****	3.0 3.0	29.0 29.0	12/1000 76/10000
ALT vs caucasian US (2)	166 vs 92	0.101	0	10,09	100	19.85	8.2e-06	*****	3.0	29.0	12/1000

Figure 14

89 ALT+ vs 208 ALT-

MARKERS			12-421/135	12-421/140	12-430/80	12-441/233	12-442/133	12-447/58	12-455/326	12-461/299	12-453/429	12-424/198	12-454/363	12-458/196	12-426/154	ESTIMATED FREQUENCIES					
MGST2			InB		markers in bac																
size (cases / controls)			88 vs 194	88 vs 195	66 vs 97	87 vs 198	68 vs 104	89 vs 198	65 vs 102	88 vs 199	88 vs 199	80 vs 180	83 vs 194	83 vs 194	85 vs 188	haplotype frequencies		p-excess	Odds Ratio	Chi-S	Pvalue (1df)
allelic frequency % (case/controls)			18/12 (T)	18/18 (G)	91/91 (G)	39/34 (C)	92/91 (G)	47/44 (G)	56/55 (A)	64/62 (T)	40/38 (T)	41/40 (T)	22/20 (A)	22/16 (T)	60/58 (A)						
diff freq. all. (cases - controls)			5.6	0.4	0.4	5.6	1.3	3.1	0.8	1.6	2.7	1.0	2.5	5.5	1.8						
pvalue			7.8e-02	7.5e-01	7.5e-01	1.9e-01	6.6e-01	4.8e-01	7.5e-01	6.6e-01	5.3e-01	7.5e-01	4.8e-01	1.2e-01	6.6e-01						
			1.5	1.0	1.1	1.3	1.2	1.1	1.0	1.1	1.1	1.0	1.2	1.4	1.1						
Test Hardy Weinberg Equilibrium	cases vs		-0.01 HW	0.00 HW	0.83	0.02 HW	0.85	-0.04 HW	-0.02 HW	0.01 HW	-0.01 HW	0.04 HW	-0.00 HW	0.03 HW	-0.00 HW	cases	controls				
	controls		0.00 HW	-0.00 HW	0.00 HW	0.01 HW	0.00 HW	0.01 HW	0.03 HW	0.01 HW	-0.03 HW	0.01 HW	0.00 HW	-0.00 HW	0.03 HW						
haplotype 1		77 vs 170										T			A	0.301	0.180	14.75	1.96	9.11	2.4e-03
haplotype 2		86 vs 198				C					T					0.175	0.096	8.69	1.99	7.00	7.7e-03
haplotype 3		81 vs 190		A										T		0.185	0.108	8.78	1.91	6.20	1.2e-02
haplotype 4		87 vs 198				C				T						0.281	0.196	10.55	1.60	5.03	2.4e-02
haplotype 5	PT2	86 vs 190	T	A												0.186	0.117	7.82	1.72	4.73	2.8e-02
haplotype 6		86 vs 198				C				T	T					0.157	0.049	11.34	3.63	18.68	1.5e-05
haplotype 7		88 vs 197				C		C			T					0.150	0.054	10.15	3.08	14.44	1.4e-04
haplotype 8		79 vs 179				C					T	T				0.128	0.046	8.59	3.04	11.15	8.2e-04
haplotype 9		81 vs 190		A							C			T		0.134	0.053	8.51	2.74	10.33	1 3e-03
haplotype 10		77 vs 170									T	T			A	0.159	0.069	9.69	2.55	9.80	1.7e-03
haplotype 11		77 vs 170								T		T			A	0.301	0.180	14.74	1.96	9.08	2.6e-03
haplotype 12		81 vs 189		A				G						T		0.124	0.052	7.67	2.61	8.83	2.9e-03
haplotype 13		84 vs 188								T	T				A	0.193	0.105	9.87	2.04	7.90	4.7e-03
haplotype 14		75 vs 166		A								T			A	0.217	0.122	10.88	2.00	7.34	6.5e-03
haplotype 15		86 vs 189	T	A				C								0.114	0.051	6.71	2.41	7.29	6.9e-03
haplotype 16		83 vs 187				C					T				A	0.164	0.087	8.40	2.05	6.86	8.6e-03
haplotype 17		59 vs 91				C			A			T				0.189	0.087	11.24	2.46	6.81	8.6e-03
haplotype 18	PT3	73 vs 167										T	G		A	0.283	0.179	12.74	1.82	6.68	9.6e-03
haplotype 19		83 vs 187				C				T	T				A	0.141	0.028	11.64	5.75	25.13	5.2e-07
haplotype 20		86 vs 197				C		C		T	T					0.154	0.043	11.62	4.04	20.84	4.8e-06
haplotype 21		83 vs 186				C		C			T				A	0.140	0.047	9.80	3.32	14.32	1.5e-04
haplotype 22		64 vs 98					G			T	T				A	0.147	0.039	11.27	4.26	12.11	4.8e-04
haplotype 23		61 vs 95			G			G	A	T						0.203	0.072	14.08	3.26	11.72	5.9e-04
haplotype 24		56 vs 85		A					A			T			A	0.239	0.092	16.23	3.10	11.45	7.0e-04
haplotype 25		79 vs 179				C				T	T	T				0.130	0.048	8.67	2.99	11.05	8.6e-04
haplotype 26		85 vs 194		A		C				T	T					0.113	0.040	7.65	3.07	10.91	9.1e-04
haplotype 27		59 vs 87		A			G					T			A	0.207	0.080	13.88	3.02	10.06	1.5e-03
haplotype 28		81 vs 183						C			T			A	A	0.121	0.047	7.76	2.77	9.41	2.1e-03
haplotype 29		77 vs 170								T	T	T			A	0.159	0.071	9.53	2.49	9.39	2.2e-03
haplotype 30		56 vs 83		A	G							T			A	0.208	0.082	13.70	2.93	9.17	2.4e-03
haplotype 31	PT4	64 vs 99	G					G	A	T						0.173	0.067	11.40	2.92	9.07	2.6e-03

Fig. 15

Zyflo secondary effects

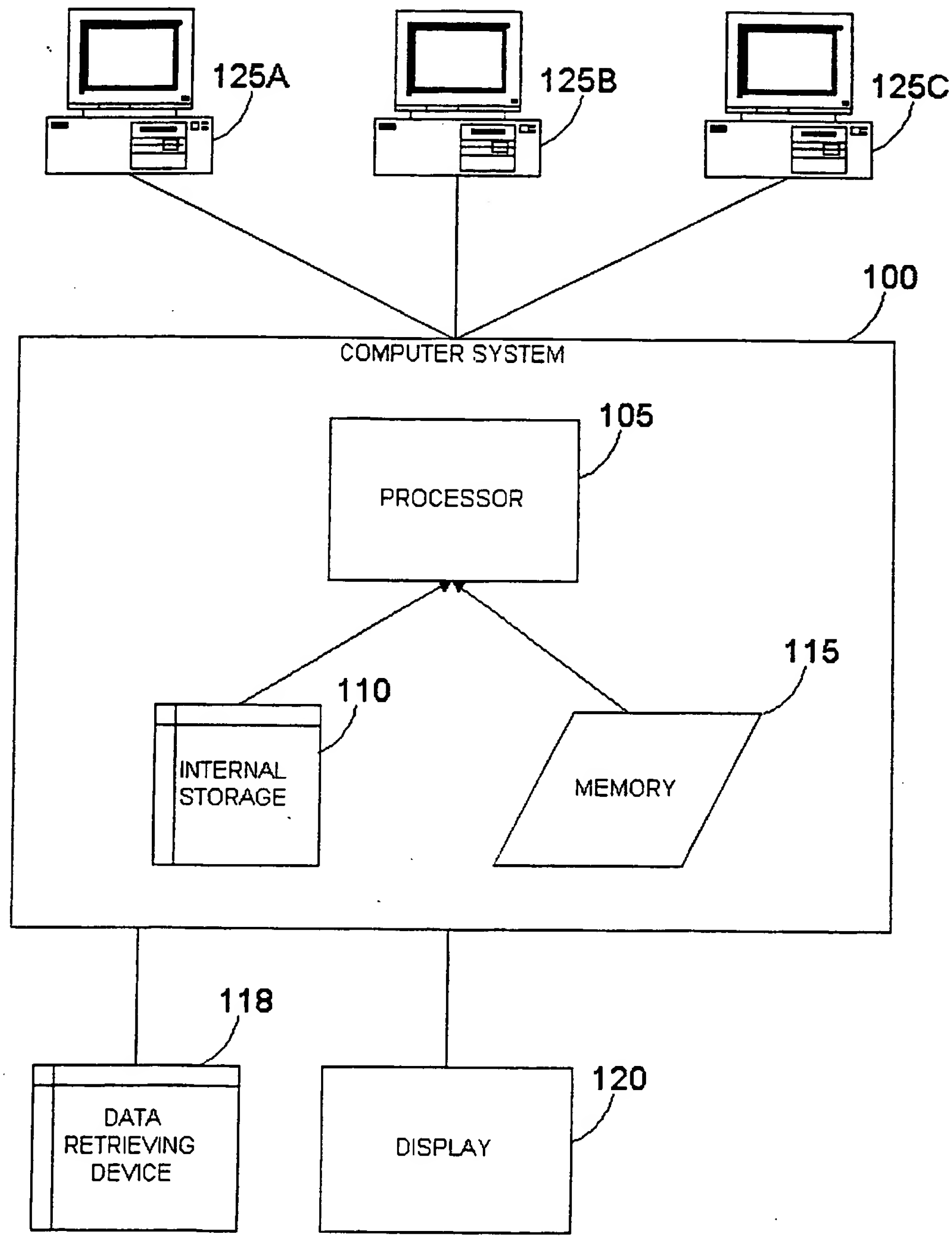
HAPLOTYPE ANALYSIS ; PERMUTATION TEST RESULT

PROTEIN MGST2	12-441/233	12-461/299	12-453/429	12-426/154		
	markers in bac				MARKERS	
	C	T	T		HAPLOTYPES (ALT+ vs ALT-)	
	1,92E-01	6,55E-01	5,27E-01		pvalue	ALT+ vs ALT-
	-5.6 (40 vs 34)	1.6 (64 vs 63)	-2.7 (41 vs 38)		diff all. Freq %	
	7,52E-01	2,73E-01	1,47E-01		pvalue	ALT vs caucasian US
	-0.3 (36 vs 35)	3.5 (63 vs 60)	4.7 (39 vs 44)		diff all. Freq %	
	C	T	T	A	HAPLOTYPES (ALT+ vs ALT-)	
	1,92E-01	6,55E-01	5,27E-01	6,55E-01	pvalue	ALT+ vs ALT-
	-5.6 (40 vs 34)	1.6 (64 vs 63)	-2.7 (41 vs 38)	1.8 (61 vs 59)	diff all. Freq %	
	7,52E-01	2,73E-01	1,47E-01	6,55E-01	pvalue	ALT vs caucasian US
	-0.3 (36 vs 35)	3.5 (63 vs 60)	4.7 (39 vs 44)	1.3 (59 vs 58)	diff all. Freq %	

HAPLOTYPE CTT	sample sizes cases vs controls	haplotype frequencies		p-excess	odds-ratio	chi-S	P value		PERMUTATIONS		
		cases	controls						Av. Chi-S	Max Chi-S	> Iter / nb of Iter.
ALT+ vs ALT-	86 vs 198	0.157	0.049	11,34	3,63	18.68	**1.5e-05**	*****	1.9 1.9	18.9 25.4	1/1000 12/10000
ALT+ vs ALT- (1)	86 vs 104	0.157	0.088	7,54	1,93	4.26	3.8e-02	*	1.1	16.5	52/1000
ALT+ vs ALT- (2)	86 vs 94	0.157	0.042	11,91	4,19	13.36	2.5e-04	****	1.5	15.4	3/1000
ALT vs caucasian US	284 vs 176	0.092	0.071	2,2	1,32	1.18	2.7e-01	*	2.1	20.9	479/1000
ALT vs caucasian US (2)	284 vs 94	0.092	0.047	4,67	2,04	3.77	5.1e-02	*	1.9	17.3	158/1000
ALT vs caucasian US (3)	284 vs 82	0.092	0.116	-2,79	0,77	0.88	3.4e-01		1.8	17.7	498/1000

HAPLOTYPE CTTA	sample sizes cases vs controls	haplotype frequencies		p-excess	odds-ratio	chi-S	P value		PERMUTATIONS		
		cases	controls						Av. Chi-S	Max Chi-S	> Iter / nb of Iter.
ALT+ vs ALT-	83 vs 187	0.141	0.028	11,64	5,75	25.13	**5.2e-07**	******	2.6 2.5	25.2 35	1/1000 7/10000
ALT+ vs ALT- (1)	83 vs 98	0.141	0.066	8,03	2,33	5.61	1.7e-02	**	1.7	17.4	59/1000
ALT+ vs ALT- (2)	83 vs 89	0.141	0.034	11,03	4,6	12.42	4.1e-04	***	1.7	18.3	3/1000
ALT vs caucasian US	270 vs 167	0.082	0.058	2,61	1,46	1.85	1.7e-01	*	2.7	25.9	438/1000
ALT vs caucasian US (2)	270 vs 89	0.082	0.023	6,12	3,89	7.61	5.5e-03	**	2.7	30.3	92/1000
ALT vs caucasian US (3)	270 vs 78	0.082	0.110	-3,06	0,73	1.11	2.7e-01	*	2.3	17.8	499/1000

Figure 16


125A
125B
125C
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COMPUTER SYSTEM
105
PROCESSOR
115
110
INTERNAL STORAGE
MEMORY
118
120
DATA RETRIEVING DEVICE
DISPLAY

FIG.17

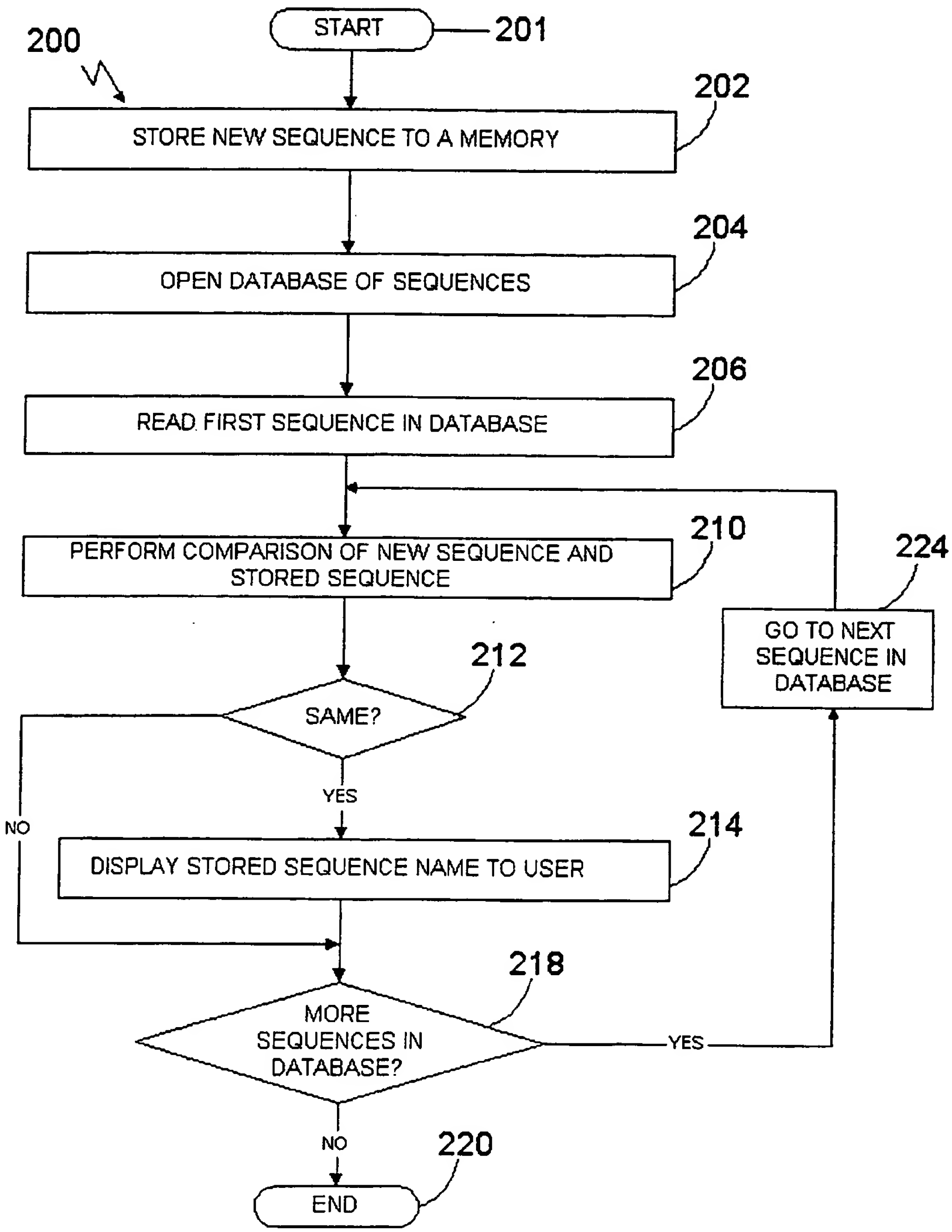
200
START
201
STORE NEW SEQUENCE TO A MEMORY
202
OPEN DATABASE OF SEQUENCES
204
READ FIRST SEQUENCE IN DATABASE
206
PERFORM COMPARISON OF NEW SEQUENCE AND STORED SEQUENCE
210
224
GO TO NEXT SEQUENCE IN DATABASE
212
SAME?
YES
NO
DISPLAY STORED SEQUENCE NAME TO USER
214
218
MORE SEQUENCES IN DATABASE?
YES
NO
220
END

FIG.18

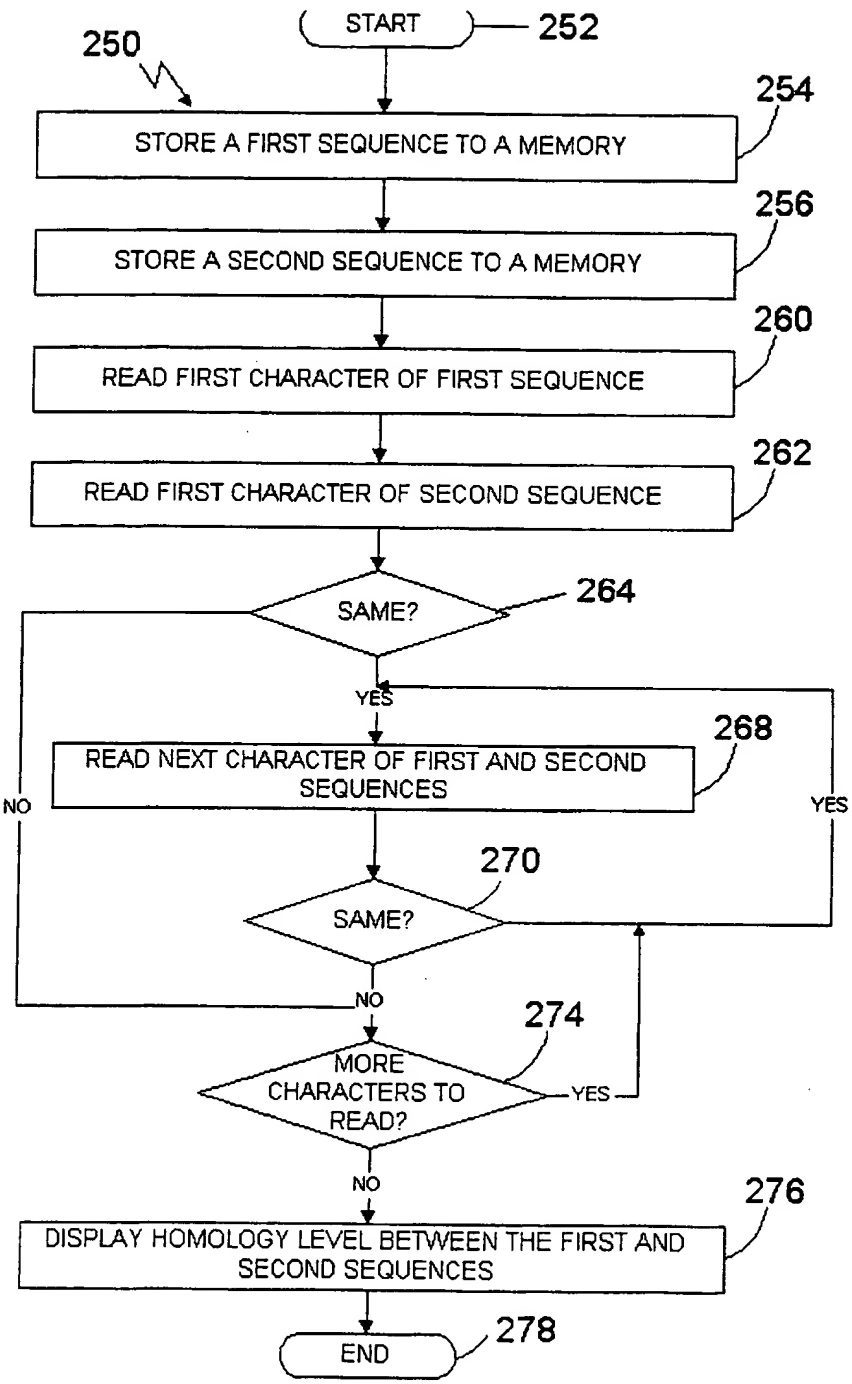
START
252
250
254
STORE A FIRST SEQUENCE TO A MEMORY
256
STORE A SECOND SEQUENCE TO A MEMORY
260
READ FIRST CHARACTER OF FIRST SEQUENCE
262
READ FIRST CHARACTER OF SECOND SEQUENCE
264
SAME?
YES
NO
268
READ NEXT CHARACTER OF FIRST AND SECOND SEQUENCES
YES
270
SAME?
NO
274
MORE CHARACTERS TO READ?
YES
NO
276
DISPLAY HOMOLOGY LEVEL BETWEEN THE FIRST AND SECOND SEQUENCES
278
END

FIG.19

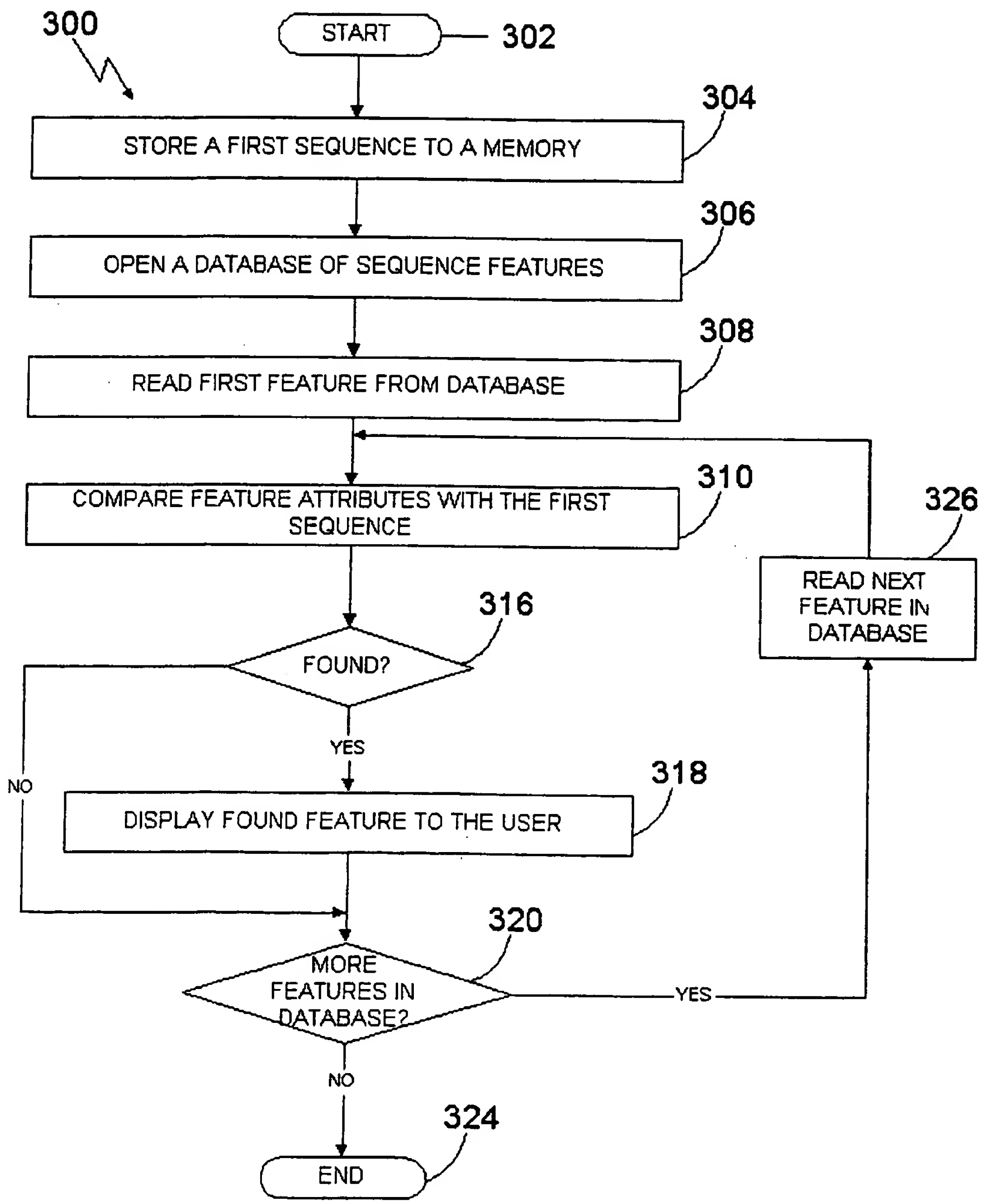
300
START
302
STORE A FIRST SEQUENCE TO A MEMORY
304
OPEN A DATABASE OF SEQUENCE FEATURES
306
READ FIRST FEATURE FROM DATABASE
308
COMPARE FEATURE ATTRIBUTES WITH THE FIRST SEQUENCE
310
326
READ NEXT FEATURE IN DATABASE
316
FOUND?
YES
NO
318
DISPLAY FOUND FEATURE TO THE USER
320
MORE FEATURES IN DATABASE?
YES
NO
324
END

FIG.20

SEQUENCE LISTING

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<120> BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM

<130> 62.WO1

<150> US 60/126,269
<151> 1999-03-25

<150> US 60/131,961
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<220>
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agggttttac agactactcc ctaggcttga aagcgtgggg tgaataccac cgggagtaca 360
cgagataatt gtaagaggtg tgtagacttg gttttaaata acattgaact acatgatgag 420
aagtcattct catttcaatt atctttgaat ccttatggtt aagtcaagtg gaaagtattg 480

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ccaatgttta taattattgt gattaagaaa ataatgttga aagcagggcc ttatagtata    900
ctgtggttac atttccttct tgtgcaattt tttttcccta gggttaataa ttgctcttta    960
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gtgctgaaac tggcaactgc tagttcagca actccaaggc aggcaatgca gaaacatggc    120
gtggggggga tggggaattc ctctcttacc aaccctgcct catttcagtt tttgcttcag    180
aagcttgggc ttctcaccac tttctccatc tggctagctg gtctactcta agccctactg    240
tggggccact catccagggc tcacagaggg ccccatggta aggccaccag ctcttgattc    300
agcttccgca caatgtggga acttaggaca gctcaggaaa cctaactcag ggccttcctt    360
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cttgtaccag gagagaaacg cccattagta atttccaagc atgcacacat gttataggtt    480
ctgagggctc aggaacagtt rcatgaggtc cagagttcga nttatgaagc tgaggaattt    540
nactaatgta ttcattcgtt gaatatttca gtgtattttg caagttggca ctgtgtgagt    600
gctacacttg gctctacagt ggttagcaaa tctgnacaca gtcctcatgg atcttacata    660
agaggaaaaa actgacaacc aaatgatcac acaaatgagt aactacacag tatgcaatgc    720
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tccacaaaag gagggtcatg gtgctatctt cacgagaata taagcaccac agtggttttc 780
tttattttgt tcattgatgt acctagaatg gggcctcaca catattaagt gctaaataag 840
tatttgttga atgaatgaat aaataaatgc atgaaagcta tgagattact tctgagaggt 900
cagggatgaa ttcctgaggc agtgttattt tggctgatgt taaagagaaa aaaaaattct 960
tagttcgaat tctgctagat aaatttatat taaccaaac 999

<210> 3
<211> 993
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-424-198 : polymorphic base G or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-424-198.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-424-198.mis2, potential complement

<220>
<221> primer_bind
<222> 304..321
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 745..765
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-424-198 potential probe

<220>
<221> misc_feature
<222> 515,535,629
<223> n=a, g, c or t

<400> 3
aatctgctgg tctctagaca atgttcccct tccctctggt gctactggct tccagtgctg 60
aaactggcaa ctgctagttc agcaactcca aggcaggcaa tgcagaaaca tggcgtgggg 120
gggatgggga attcctctct taccaaccct gcctcatttc agtttttgct tcagaagctt 180
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cgcacaatgt gggaacttag gacagctcag gaaacctaac tcagggcctt ccttctcctt 360
accatactac tttactctgc tatggctgtg taaaagactg aatgggacag agatcttgta 420
ccaggagaga aacgcccatt agtaatttcc aagcatgcac acatgttata ggttctgagg 480
gctcaggaac agttgcatga kgtccagagt tcganttatg aagctgagga atttnactaa 540
tgtattcatt cgttgaatat ttcagtgtat tttgcaagtt ggcactgtgt gagtgctaca 600
cttggctcta cagtggttag caaatctgna cacagtcctc atggatctta cataagagga 660
aaaaactgac aaccaaatga tcacacaaat gagtaactac acagtatgca atgctccaca 720
aaaggagggt catggtgcta tcttcacgag aatataagca ccacagtggt tttctttatt 780
ttgttcattg atgtacctag aatggggcct cacacatatt aagtgctaaa taagtatttg 840
ttgaatgaat gaataaataa atgcatgaaa gctatgagat tacttctgag aggtcaggga 900
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gaattctgct agataaattt atattaacca aac 993

<210> 4
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-425-57 : polymorphic base G or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-425-57.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-425-57.mis2, potential complement

<220>
<221> primer_bind
<222> 540..557
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 82..99
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-425-57 potential probe

<400> 4
atctggtgga ggtcctggtt tctgagaaac aactcaagaa cttatgtgaa gacgttgtct 60
ttagtttcta tagggaaccg aacgtcttgt aactctgtct tatttgggtg actattattt 120
aaactattat tatcttctcg cttagcggga ctgaaggata gcaaggtgct tggaatttcc 180
cttgaaggaa ctcaagagtt tttatttccg tgcttgaggt ggctagcagg tccctaagag 240
tgttccttgc tctgtctcca tgccagaagt ttattatggg gtgaaaagag gaagttaagg 300
acaggaggca agacctactg aaggctcaaa aactgacaga ggaggaagta tggatgtgga 360
agtgaaagaa gtccacagag ctcatcacaa gatgaaggtg gtcccaggca tcagagttga 420
ttatctaatg aaataaagga gaagaaagtc atactgtttt ataacaggga aacgtcggca 480
ggtaggagcc atcatcccca ragttttctt gtacctgctg ggcaaggtgt cagagccctg 540
gcaatggaaa gtgattggcc cacagggagt aagaatttac cgacaacaat ataggtttga 600
aaaggaaagt tttattagat tgagagaaag ctgcagaaga gtgcagcggg ctgcctcagc 660
gagaggactg agcgcgccgg ggaggatttt ccttaggggt atttatggac cttaaagcaa 720
gagcttaggg gtaatttggt ccatattagc cacatatgtc atgataaatg attacatttg 780
tagacatttt ggtgtcgtaa tgtcagcaag ggttgcacaa tgagttttgt catgcatgca 840
ttccggagat gtatagaggt agagaaagtc tagttacata taaattttgg ggaaagaagc 900
ctggaaccgg ccttagatat agggaagatc aattatttct aaactcctca gataaggagt 960
tctgcctctg gatggtcggc ttcatggcca ccaggtggtc t 1001

<210> 5
<211> 961
<212> DNA
<213> Homo Sapiens

<220>
<221> allele

<222> 461
<223> 12-426-154 : polymorphic base A or G

<220>
<221> misc_binding
<222> 441..460
<223> 12-426-154.mis1, potential

<220>
<221> misc_binding
<222> 462..481
<223> 12-426-154.mis2, potential complement

<220>
<221> primer_bind
<222> 308..325
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 830..847
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 449..473
<223> 12-426-154 potential probe

<220>
<221> misc_feature
<222> 705,761..762
<223> n=a, g, c or t

<400> 5
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tccctagcta gcaaaatcag tgactcctgg gaacttgtaa aaaatgcaga ttctcaagcc     60
ccgcttcaga tttactgaat cagaaacact gtgtatgttt taacaagctc tgctggtgct    120
ttcagtgcag gctaaagttt gagaactaca gatacaaagg agggctctgt atctgcaaca    180
acaactatgt aatgatgact agtccccact cttctgaagc tacccatggc aaaattagaa    240
acataattct tcaaaaacca ctggcactga tttagtgcac agaacacctg tggataactc    300
aattcctttt gtccttccct gtgtcaaggc caaaggatct aatgtgatat aagcattcca    360
gaggtggaag ggagtggtag ctactcaaga cccagtattt ttacaggtga tcttcaatgt    420
gatctgtcag taaatatcaa tggctttcag actgtaaact rcagctcaca gttcatgatc    480
taggatatat acatgtgggt ttaaaacaga aagaaaagtt tctgatatgc tctggtaatt    540
tctgttgtat ttcattttaa aaatgttggt tgtgacccac taagttgttt ccaataacct    600
tgtgtgttgc aatctgagaa gttaaaaatg ctaccttaga tcagaaaatt ttcacccagt    660
ctattgataa agttcaggga tacttgtgaa attatataaa agttntgtat atatttacat    720
attatatgtt tctctgcaag aggcttcata gctttttgca nnacacttaa aggaataggt    780
aacttttgag aagctaggac acattgatct agatcccaca aaatgggcag aggatgggat    840
taggatttct gctgctaggt gacccctgta gccccctgaa aactcctgtg gataagatta    900
ggaaggctcc tcaggctatt ttcttcaccc catataagac cctcaagggt cttttttttt    960
t                                                                    961
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<210> 6
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-429-198 : polymorphic base C or T

<220>

<221> misc_binding
<222> 481..500
<223> 12-429-198.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-429-198.mis2, potential complement

<220>
<221> primer_bind
<222> 304..321
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 803..823
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-429-198 potential probe

<220>
<221> misc_feature
<222> 44,561..562,954
<223> n=a, g, c or t

<400> 6
ggtcaggagt tcaagaccag cctggccaat atggtgaaac cccngtccgt actaaaaata 60
aaaaaattag ctgggcgtgg tggcaggcac ctgtagtctc agctactcag gaggctgagg 120
caggagaatc gcttgaaccc aggaggcgga ggttgcagtg agttgacagt gtaccactgc 180
actccagcat gggcgacaga ccaagattct gtcttaaaaa acaaaacaaa acaaaacaaa 240
aaactgggag gggaaaatat ttttttattt tctaatatgt tagaaccctt tctcaatgtg 300
taactctcct cattcttctc cctctcatct ttaaccaaaa ttgtaaatgt tctacatgtg 360
catcatgtta gtctatcagg tgttatttag ataattggtg cctttgactt acattcttgt 420
aaacgttgct ttagttcata aactcataat attcccagac ctgaagcctg tcttaaaatt 480
gataatgtaa atcatctagg yctgaatgcc taaagtgatg gggagctcac cacctcttgt 540
ttctggtcat aggtaggtga nngatccctt ctgcagcaag aagtcagggg caggcctgtg 600
acactagctc tgattcctgc aaatgaccaa atgaggggca gggcctggtg gtctcccagt 660
cccagctgag gctcccatga cctgcaccct cctgccctcc caactctcag gttctcccaa 720
cagccctccc ccagctaatt tcataaaagg cactaaaaac ttttgatcag tcacaaaatc 780
atgggaagag aaagaaatac aagaagagag aaagaaggga aagtggcgtg aatcattaac 840
aaaggcacca catccctgat actgtactgt tctgggtgct tttttctcaa tgaattctca 900
caaaatcctg ttggtattag tgattcatat ttcttacata tagaaactga gtcngcaaag 960
aggttattac ttaacttgcc caagatcgta cagctaataa g 1001

<210> 7
<211> 996
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-430-80 : polymorphic base T or C

<220>
<221> misc_binding
<222> 502..521
<223> 12-430-80.mis1, potential complement

<220>
<221> misc_binding
<222> 482..500
<223> 12-430-80.mis2

<220>
<221> primer_bind
<222> 561..580
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 131..150
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-430-80 potential probe

<220>
<221> misc_feature
<222> 918,971,978
<223> n=a, g, c or t

<400> 7
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actttaaaat ggttctgcga aatatatatg tgaagcattt atggcaaagt gttaatgatt    120
acatctaatt ggtaagtgta taggtattcg ttgtattatt atttctactt tcctggttgt    180
ttaaaaatgt ttataataaa gagttaaagg atctgaagag aagttaaaac ctaaaatcag    240
attcttggta gccctgaaga ttttctgtgt tgagcattgt taagagatcc agtggtattg    300
atggatccac agtcatccat gctggcctgg cagctgtcct gggtgtggca cagatgcctg    360
ggccccacat gtgtgagagc tgcagtaatt acctccacct gttgcatgaa atgaggcagg    420
tgtctgtgcc agctactcca gaggacacta gtggaggaat ttaatgtcct tagtacttaa    480
aagagaattg aggacaaaat yggatttaca aaaagaggaa acaaatcaaa aagaaaatta    540
aaaggtaaag actggttacc caaagaggta gctctgttcc attttcagat aatttttctt    600
gttccacttt tcttttaggg gttggaggtg ggtggggtat ggccaaaaaa gtcattaata    660
aacaaaatca ggtcatttga ggttcaccct ttttctccag acacaatctt ccttgaaaag    720
aatggtcaga ggcagaaaca gctcattgaa tgctatggaa tgttccttaa tcaccagtga    780
aatacgtctt tctcactggg ggcagatgtc tagtgacttt ctagaaaaat gtttattctc    840
tcctctttct tcccccatca ccatacttac tgcactagga ttttataaag gtcagtaaga    900
ttacatgtaa gaactcantt tgaaaagaga aaggtattcc attcatccag tgccaaacga    960
gtataagtaa ngaatatngt ggcttgaatt gattgg                              996
```

<210> 8
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-433-215 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-433-215.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-433-215.mis2, potential complement

<220>
<221> primer_bind
<222> 287..304
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 805..825
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-433-215 potential probe

<220>
<221> misc_feature
<222> 92,202
<223> n=a, g, c or t

<400> 8
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agctgtgggg gcactcccag ccattgtctc ctcagctgag gcctcagaca ttgaagagca    180
gagacatgcc agtcctaccg tngccctact gacccacata actcattaga gcctaattaa    240
atggttgtta taaacccota aactttgggg tactttgtca cacctgagta gtcaccagaa    300
caacctcatt gcaaggtaac aactcagctt cccagggttc atcatttggc tccagtgata    360
ccacccccatg ccctgcaagt gtggcacttc agacaggagc cagggacacc aggagtatgg   420
ctggtggccc ttaggtggca ggattgcaga ggccccaccg gaagtcagct ggccacagca    480
gagccaaggt agagtgcatg rttgaaaatt caggagacag gatgagctcc agaaaattgg    540
gcgctgcact ggacgtgcct gataaagcaa agagggagag aaaagaggag ttaaggattt    600
ccacatttct ggtttctgaa cagctagata cattaatgat ggggcaattt actgccacag    660
aatttagacc aaaggagggg gctaggtttg aagtgcctgt gagtccatta gaaatgacaa    720
gaagtgggag cccaggtcac caaagatggt caaggtcatt gatcttgaga ccacagggcc    780
ccaagaaggc ttaagggtct gtccctgatt cttgtttcct gtgtgagaaa tattttgcag    840
gtgtcaggct gggactcttg accagctgaa ttacgtattt ccagaacagg gtgttaaaga    900
agacagaagc gaccccagga aaaagcgtgg cttccacaag agctgccata tacaaacaag    960
catgccccac aacgctggca ggagagatat catcagattt a                       1001
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<210> 9
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-441-233 : polymorphic base G or A

<220>
<221> misc_binding
<222> 502..521
<223> 12-441-233.mis1, potential complement

<220>
<221> misc_binding
<222> 482..500
<223> 12-441-233.mis2

<220>
<221> primer_bind
<222> 716..734

<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 284..303
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-441-233 potential probe

<220>
<221> misc_feature
<222> 661,929,990
<223> n=a, g, c or t

<400> 9
gaagaactta gacaatgcct gaaatgcaaa ggcgacactg gagtcttctt tctctaacgt 60
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ttttttgtga gccacatctg atatttctga tatccccagg aaggagtggc ctggaggtca 180
ctggttcagg ctccctttgg gcgaaatcct gggagtgatg ctctaaaaat ccacctttcc 240
catcatccct actcatcaga aagacaaata taaaatccca gagaggtgga ggagctaaaa 300
aagcaattgc tccaccttac aaatttggat agaaaggaga tgtagtttat ttcatatggg 360
caaagtagtc ctcttccaaa gtcctgtaca attgttctct gcaattgacg cacatctgcc 420
ctaagcgaaa tctgtcagaa ggaatcaaca aggctccttg cctcccctcc caatccccct 480
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tcccctcctc cctccgtgtc ctagacgctg gctgccttct gtgcactccc aggcagatca 600
ctacggaaga gtcggagcct gtggggttgg actggccaca ctcagtcctg agaaggcgag 660
nttgccatgg aaagctgggg gcagaggtgt ttttggagag gaggcggcag gcaaacattg 720
cctttgactt gctctccgcg tacccggggt tgtagagctg ctcaggaagg ggcaggatgt 780
aaggccagag gtgcctggtg ggtgagaagc ccaggcaggg gctgggcgcc ctctccgaag 840
aggtggcagc agggtgaccc tgaactcccc aaatggggag tgatgccact ggggaaactg 900
agtggatcaa agagatgaaa ccaaaaaana agcaaacaaa caaatgagaa gacacaaaac 960
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<210> 10
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-441-343 : polymorphic base G or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-441-343.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-441-343.mis2, potential complement

<220>
<221> primer_bind
<222> 826..844
<223> upstream amplification primer, complement

<220>
<221> primer_bind

<222> 394..413
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-441-343 potential probe

<220>
<221> misc_feature
<222> 3,771
<223> n=a, g, c or t

<400> 10
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gacaatgcct gaaatgcaaa ggcgacactg gagtcttctt tctctaacgt gtagcgttga    180
atgaatatct gcctggaacc aagagggctg ctctgatgtt tgggagtcgg tttttgtga    240
gccacatctg atatttctga tatccccagg aaggagtggc ctggaggtca ctggttcagg    300
ctccctttgg gcgaaatcct gggagtgatg ctctaaaaat ccacctttcc catcatccct    360
actcatcaga aagacaaata taaaatccca gagaggtgga ggagctaaaa aagcaattgc    420
tccaccttac aaatttggat agaaaggaga tgtagtttat ttcatatggg caaagtagtc    480
ctcttccaaa gtcctgtaca rttgttctct gcaattgacg cacatctgcc ctaagcgaaa    540
tctgtcagaa ggaatcaaca aggctccttg cctcccctcc caatcccccct tttggaggac    600
ttgtggcttc agtgtcgtcc taagtgagag tggcgtgtgc ttttttcctg tcccctcctc    660
cctccgtgtc ctagacgctg gctgccttct gtgcactccc aggcagatca ctacggaaga    720
gtcggagcct gtggggttgg actggccaca ctcagtcctg agaaggcgag nttgccatgg    780
aaagctgggg gcagaggtgt ttttggagag gaggcggcag gcaaacattg cctttgactt    840
gctctccgcg tacccggggt tgtagagctg ctcaggaagg ggcaggatgt aaggccagag    900
gtgcctggtg ggtgagaagc ccaggcaggg gctgggcgcc ctctccgaag aggtggcagc    960
agggtgaccc tgaactcccc aaatggggag tgatgccact g                        1001
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<210> 11
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-442-221 : polymorphic base T or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-442-221.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-442-221.mis2, potential complement

<220>
<221> primer_bind
<222> 704..721
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 270..289
<223> downstream amplification primer

<220>

<221> misc_binding
<222> 489..513
<223> 12-442-221 potential probe

<220>
<221> misc_feature
<222> 180,531..532,822
<223> n=a, g, c or t

<400> 11
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agaggacata aacactgatt ttttcccccc attcatttaa ctatttgcac acagagacan 180
gaagccagaa atctgactgg gaagaaattc ctaccctttt gccagcatgc taagcttctg 240
ggttctcttt ccctgagtgg ccctagtgat ctggcttgtg gcacaactgc ctttgggggc 300
caagccgcat cataaaggaa aagtatttct ttttgttctg gccaaagcaa aatacgcgta 360
ataaaacata gatattaacc aggctgctta gcatccaata tcaaactggc aaggcttaaa 420
tttgccctca ggtgggccct gtcatcttta atctaacctc cgactaggag tttcaacatg 480
tggtctctgg gcaagatggt ygccctgagt aatagaaaag aaagagaaag nngagagaga 540
gaaaaacatt gcctgtggca gggcggggaa ggtgaaatga tcagggaggc agagaaagaa 600
ccacccattg cagcgacact aaaaagttca ggtggctgct gtcggtggag caaggatctt 660
ttccagtaat cctaccagct ctcaaatttc ccttgttagg gaggaaaaag ctccccatgt 720
cccaggatcc tgtacattcc taattctgtc acccatagcc atcagcaaag tacaagggag 780
attaatccaa agagaatagc agttaacatc ccatagtgcc gnaacctgtt cttagccgag 840
agggacttta ccgaagaggg gcctctaacc cgctaaatct tagaagggac tctaactctc 900
ctaagtcggg cctctaacca gaggtcagtc aagcatcctt gccttttatt aagggggagc 960
ctttaaccac ctctatctta ggagagactc taactccact a 1001

<210> 12
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-447-58 : polymorphic base G or C

<220>
<221> misc_binding
<222> 482..500
<223> 12-447-58.mis1

<220>
<221> misc_binding
<222> 502..521
<223> 12-447-58.mis2, potential complement

<220>
<221> primer_bind
<222> 444..462
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 874..893
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-447-58 potential probe

<220>
<221> misc_feature
<222> 44,894
<223> n=a, g, c or t

<400> 12
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tgggctgtag ttttctgact cctgatctat gtaatctcca attngcgcaa catcagtttg     60
tctctctctc tctcttttttt ttttttttt tcagacaggg tctcactctg tggcccaggc    120
tggagtgcag tggcatgatc ttagcttatt gcagctttga tctcccaggc tcaaacgatc    180
ctcctgcctc agcctcctga gtagctggga ctacaggtgg gtgccactgg gcccagatag    240
ttttttattt tttgtagaga tagagttttg ccatgttgcc taggctggtt tcaaactcct    300
ggactcaagt tatctgccca ccttggcctc ccaaggtgct gggattacaa acgttagcca    360
ctgcccccag ctgtctccat tttttaaatt aaaatacata atgttctagt aaatattctt    420
gtgggcaatt cattggacct gtcttagatt acatgcccag agtaaattct agaaatgaaa    480
ttcctggtct tctccgaaga sggaattgag tggggaaaaa aaagaaaatg aaaaaagaaa    540
taaacacaag atattcttgg tcaaattgtg tctgcccttt ctcctccagt gagctacgat    600
gaagccacag taatccacat tcccagggga acacaggtgg tctgcctctc catgtgctca    660
gagtgccaat tcttggtaag gagatatagg gactggagtg aaacattgga ataatgactc    720
atattcatgt tttataaaca aatttaaaat attggatcag gttatttatc tggaaaccct    780
gaagtttggc tgtttaaagg gctattttaa atataggcaa cagaaaacaa aatacaaagt    840
cttatttctg acactttaaa atgttggcaa agtgtcttcc ttgttagtat ggtnggtgag    900
tatccccacc tgtcataaaa tggcaaatag gctgggtgca gtggctcatg cctgtaatcc    960
cagcactttg ggaggtcaag ttgggaggat catttgagtc c                       1001
```

<210> 13
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-453-429 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-453-429.mis1, potential

<220>
<221> misc_binding
<222> 502..520
<223> 12-453-429.mis2, complement

<220>
<221> primer_bind
<222> 73..91
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 577..596
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-453-429 potential probe

<400> 13
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aatcatgatt tacccctgga tgggaatcag ggtcaccttc aaagagcata tggacatgtg     60
aaggagcata aacacaatca caaaattggg gctcccacca tcggttgcag aggcagtcgg    120
cagtgtctgc tacaagtgac atcaagtagc atctatcaag tggcattact ttaacaaata    180
```

```
ttaacaatag ggtcctcatc tcagtttaga agaaaaatcc aaaatcaaag tagactgaag    240
ataaggtaaa cggtgatgtt tgccacacta gtggtgaggt tttcatagtt ttacccaaac    300
cagtttttat ttttagtgct tggttggggt cactgaaact tccaggttgt cctaacctgt    360
taaaatcttt taaaacatta tttgtgactg tttctctttg gacagtgctt tttgttaatc    420
acaaaaaaca gggtagaagg taataacaca tgcaaaggga tgtgtagcaa tcaaagggaa    480
atgttatcct tcctaggaga yaggatttat gggattcctg gatctttttt gtgtctgatt    540
gttaaggtct tgacagcctt tcaattgagg aatacggtcg tgtctgttaa actaattgta    600
gctgttcact ccactatata attttacaac atttcagctt caaatagaat ggcttcaata    660
aacataaagc agactgacac atcccagatt tctgcagttt attttacacc aagaaattac    720
atttagagat ttccagacac atactataaa tgaaaattca acaggaagtt tctttcattt    780
cctctagatc tgacctatat ttcaaaaata tatgagtggg ctataaccag gaacttcttc    840
tcttgctccc attattcaca ccgttttctg aagagttttt ttctcgtccg cgactctaat    900
ggccattaag ggaattgcag acattggaag actatacaac cctaagtgaa atgagtgaaa    960
tgataaatgt tatccacaag atggccaaat tgtatggttc t                       1001
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<210> 14
<211> 929
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-454-363 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-454-363.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-454-363.mis2, potential complement

<220>
<221> primer_bind
<222> 139..158
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 634..652
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-454-363 potential probe

<220>
<221> misc_feature
<222> 674..679,881..882,892..893
<223> n=a, g, c or t

<400> 14

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atcccagatg attactaatt taaaactact ttacatttta tttagtaatg tgtttggaac     60
agttacattt tgtagctact tacaatttta ctttaactga aataataaga caaggccata    120
aatattggcc tccctggctg gggagttgtg tgggtttcct ttccaggcag ttgaggtttt    180
ccatggagcc tactctacag tgtcagcagg agtataacat agaaggcttc caggtcaggt    240
ggcccagagt caaatcaaag ccccatccct ttttagcaaa tttctcagcc ttacttagct    300
gtgccggcct gcctctttct aaaatgagga aaataataat acccacttca ctggtttatt    360
gagaggatta aatgaggaca tgtgttattt cacaccatta ttgcttctgt tgttattatt    420
```

```
ttaaaatcta ggttggtgat tgcatcagtt tcttagggct gctctaaaga aagtaccaca     480
agctgagtga cttacatagc rgaaaagtgt tttcttacag gttaagaggc tggaagtctg     540
aaatcaaggt gtcagcaggg ccatgctccc actgaaaccc atagcgggga atcctttctt     600
gcttctaagt ttctagtgtt tccttggctt gtagatgtgt cacttcagtc acacggccat     660
cttcttcttt cttnnnnnnc ttcttcttct tcttcttctt cttcttcttc ttcttcttct     720
tcttcttctt cttcttcctt cttcttcttc ttcttcttct tcttcttctt cttcttcttc     780
ttcttcttct tcttcttctt cttcttcttc ttcttcttct tcttcttctt cttcttcttc     840
ttcttcttct tcttcttctt cttcttcttc tttgagatgg nntcgctgct gnngctcagg     900
ctggagtgca atggcgtgat cttggctca                                       929
```

<210> 15
<211> 827
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-455-326 : polymorphic base T or C

<220>
<221> misc_binding
<222> 502..520
<223> 12-455-326.mis1, complement

<220>
<221> misc_binding
<222> 481..500
<223> 12-455-326.mis2, potential

<220>
<221> primer_bind
<222> 808..826
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 372..392
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-455-326 potential probe

<220>
<221> misc_feature
<222> 798..799
<223> n=a, g, c or t

<400> 15

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cttagaggaa attgacagga agaggaattg agaagaattc tatagaatgg gtaatgaaca     120
atggatcagg aacaatagca gaataataag gcctgcagaa ctacctggaa acctgaactc     180
tgggtcacac acagggtgca aacttaagaa aactccccac agcttttaaa acagctcagg     240
aaatctgtga gttaaaggaa agcctaacac aaatacagct ttaccttaag catctttgtc     300
caccctcgcc ctataattcc tcagctttga gagaaagcct tccctgcaga ctgctactgt     360
agatttcaat ttgttttgtt tttagagatg cccatacctg acttagcatt atcctaggga     420
aaggcctgag gctgtccaca agagatcccc aggcggcttc tgtgagggtc tgcacagaga     480
atcttgcaca gcaggctctt ycttatagga ggtgtgaggt tgtcatataa agctgaaggc     540
ccaacataag tctgcctcac agttatcctt ctagaatatt cctgataggg tcagaatttt     600
atgaattttt tcttaaagaa atagagacgg ggtcgcacta tgttgaccag gctggtctcg     660
aacttctggc ctcaagcgat cctcccatct cagcctccca aagtgctagg attacagatg     720
```

tgagccacca cgccctgcca gaattttgca aatttactaa gcatccacca ccgtgtatcc 780
tgtgtaggac acgggccnng ggaggtccct attaaccaag atagcag 827

<210> 16
<211> 884
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-455-383 : polymorphic base G or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-455-383.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-455-383.mis2, potential complement

<220>
<221> primer_bind
<222> 865..883
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 429..449
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-455-383 potential probe

<220>
<221> misc_feature
<222> 855..856
<223> n=a, g, c or t

<400> 16
tgatttctgg tacaggggtc tgtgtaatca gcacatggcg gggactgtct cacatgcttc 60
ataagccgta atatttctag cttgaagaaa aaaataataa ttcagagaac tctgtttctt 120
agaggaaatt gacaggaaga ggaattgaga agaattctat agaatgggta atgaacaatg 180
gatcaggaac aatagcagaa taataaggcc tgcagaacta cctggaaacc tgaactctgg 240
gtcacacaca gggtgcaaac ttaagaaaac tccccacagc ttttaaaaca gctcaggaaa 300
tctgtgagtt aaaggaaagc ctaacacaaa tacagcttta ccttaagcat ctttgtccac 360
cctcgcccta taattcctca gctttgagag aaagccttcc ctgcagactg ctactgtaga 420
tttcaatttg ttttgttttt agagatgccc atacctgact tagcattatc ctagggaaag 480
gcctgaggct gtccacaaga ratccccagg cggcttctgt gagggtctgc acagagaatc 540
ttgcacagca ggctctttct tataggaggt gtgaggttgt catataaagc tgaaggccca 600
acataagtct gcctcacagt tatccttcta gaatattcct gatagggtca gaattttatg 660
aatttttttct taaagaaata gagacggggt cgcactatgt tgaccaggct ggtctcgaac 720
ttctggcctc aagcgatcct cccatctcag cctcccaaag tgctaggatt acagatgtga 780
gccaccacgc cctgccagaa ttttgcaaat ttactaagca tccaccaccg tgtatcctgt 840
gtaggacacg ggccnnggga ggtccctatt aaccaagata gcag 884

<210> 17
<211> 1001
<212> DNA

<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-456-269 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-456-269.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-456-269.mis2, potential complement

<220>
<221> primer_bind
<222> 233..252
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 693..712
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-456-269 potential probe

<220>
<221> misc_feature
<222> 20,447
<223> n=a, g, c or t

<400> 17
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atatacctac ctgatgggct gcagcagata ttggcactca gacaagccaa ttttaggcat 120
cagagccctg tagccgtggt aacctcaccc ctgtgctgga cgggaggcag gtcggctaag 180
cagaggtgct ggaagtgtgt gtggtaccag gactgggccg caggagctgc acagcctcac 240
agcacattag ccaatggccc catgccaacc cccttggctg ggttttctgg aacaggtacc 300
tccttaccat tccaagaaaa agtctcctcc tgcccccсaa aagtgggggg caggtgatcc 360
aaaagatcac taagcaaatg cctgtttgtc ctttggaata ctcaaccctg atcagtggtg 420
aatactcagt caccaactat gtggaangag gcacaaccat ggcagacaac agatatggaa 480
agagcaggaa ttcttctagc rggaattctt atatcaaatg caatggtggc catgccccca 540
acagctctgc agttggaaaa atgaagcctt caagtaaggc caaagtccta ctgtttgagg 600
gcaattcatc tgggccaaat ccctcaggag cagggccatg cgggggttac aactgttcat 660
gcaacacaac agattgggct taagctggcc agggcagtga cgggcttttc atcttaattg 720
tagttgtctg tgtcccaaga aaatgttatc agcttttcag aaaaactttc aagagactcg 780
agcaagtcaa acccaagctg ccctccttgt ctgcatatcc tgctctgttt tcccatttgg 840
gaaatgaaac cagcagcagc tgagagggag aaggttctac actcactggt tttctccact 900
cctaccactc cctccttccc cctcctctct gtcaccctga agaaatctcc ttctggaata 960
aggtgtcatt catccttgtc acctccagta tagttatgtc a 1001
```

<210> 18
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele

<222> 501
<223> 12-456-380 : polymorphic base G or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-456-380.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-456-380.mis2, potential complement

<220>
<221> primer_bind
<222> 122..141
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 582..601
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-456-380 potential probe

<220>
<221> misc_feature
<222> 336
<223> n=a, g, c or t

<400> 18
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tttaggcatc agagccctgt agccgtggta acctcacccc tgtgctggac gggaggcagg     60
tcggctaagc agaggtgctg gaagtgtgtg tggtaccagg actgggccgc aggagctgca    120
cagcctcaca gcacattagc caatggcccc atgccaaccc ccttggctgg gttttctgga    180
acaggtacct ccttaccatt ccaagaaaaa gtctcctcct gccccccaaa agtgggggc     240
aggtgatcca aaagatcact aagcaaatgc ctgtttgtcc tttggaatac tcaaccctga    300
tcagtggtga atactcagtc accaactatg tggaangagg cacaaccatg gcagacaaca    360
gatatggaaa gagcaggaat tcttctagca ggaattctta tatcaaatgc aatggtggcc    420
atgccccaa cagctctgca gttggaaaaa tgaagccttc aagtaaggcc aaagtcctac     480
tgtttgaggg caattcatct kggccaaatc cctcaggagc agggccatgc gggggttaca    540
actgttcatg caacacaaca gattgggctt aagctggcca gggcagtgac gggcttttca    600
tcttaattgt agttgtctgt gtcccaagaa aatgttatca gcttttcaga aaaactttca    660
agagactcga gcaagtcaaa cccaagctgc cctccttgtc tgcatatcct gctctgtttt    720
cccatttggg aaatgaaacc agcagcagct gagagggaga aggttctaca ctcactggtt    780
ttctccactc ctaccactcc ctccttcccc ctcctctctg tcaccctgaa gaaatctcct    840
tctggaataa ggtgtcattc atccttgtca cctccagtat agttatgtca gatgcagtga    900
ggtgctggat ttagattaca agaagcggga ggattcttgc aaagagagga caacatttgc    960
ttaactatgc caagggtccc cttgtccccc gaccaagagg g                       1001
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<210> 19
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-457-204 : polymorphic base A or G

<220>

<221> misc_binding
<222> 481..500
<223> 12-457-204.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-457-204.mis2, potential complement

<220>
<221> primer_bind
<222> 298..317
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 772..792
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-457-204 potential probe

<400> 19
ttgagggcaa ttcatctggg ccaaatccct caggagcagg gccatgcggg ggttacaact 60
gttcatgcaa cacaacagat tgggcttaag ctggccaggg cagtgacggg cttttcatct 120
taattgtagt tgtctgtgtc ccaagaaaat gttatcagct tttcagaaaa actttcaaga 180
gactcgagca agtcaaaccc aagctgccct ccttgtctgc atatcctgct ctgttttccc 240
atttgggaaa tgaaaccagc agcagctgag agggagaagg ttctacactc actggttttc 300
tccactccta ccactccctc cttccccctc ctctctgtca ccctgaagaa atctccttct 360
ggaataaggt gtcattcatc cttgtcacct ccagtatagt tatgtcagat gcagtgaggt 420
gctggattta gattacaaga agcgggagga ttcttgcaaa gagaggacaa catttgctta 480
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ctgaacttta ggcaggattc ttcctaacct ccctttttttt tttagagcat ttcttgtcat 600
tgtacatttt ttctctgccc ctttgagatg tatgtaaatc tcttcaaaag cctcctgcca 660
gttttacaat ccaggaatgt ctttctcaag gacctgggag ccctcccttt gaaatgtaat 720
catcaaagga gatggcaccc ctgtctccca gtctttgtgg agagtttttg tgggagtcta 780
acttcagcag gacaccttcc tccaagtcat aaaaccatcc cttgtcaaaa gatagaagtt 840
tattagcaaa cacaaatggc ctacgacctc ttcacaacat cctctggcat gtttcactag 900
cctttaaaag cctttaaaaa ctttgcaccc tctgcatcag cagcattgag ttcacactga 960
gttctagtcc ctctctcctg ttgcaataac ttcggataaa c 1001

<210> 20
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-457-206 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-457-206.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-457-206.mis2, potential complement

<220>
<221> primer_bind
<222> 296..315
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 770..790
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-457-206 potential probe

<400> 20
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gagggcaatt catctgggcc aaatccctca ggagcagggc catgcggggg ttacaactgt     60
tcatgcaaca caacagattg ggcttaagct ggccagggca gtgacgggct tttcatctta    120
attgtagttg tctgtgtccc aagaaaatgt tatcagcttt tcagaaaaac tttcaagaga    180
ctcgagcaag tcaaacccaa gctgccctcc ttgtctgcat atcctgctct gttttcccat    240
ttgggaaatg aaaccagcag cagctgagag ggagaaggtt ctacactcac tggttttctc    300
cactcctacc actccctcct tccccctcct ctctgtcacc ctgaagaaat ctccttctgg    360
aataaggtgt cattcatcct tgtcacctcc agtatagtta tgtcagatgc agtgaggtgc    420
tggatttaga ttacaagaag cgggaggatt cttgcaaaga gaggacaaca tttgcttaac    480
tatgccaagg gtccccttgt yccccgacca agagggcctt catgctccct cagcttgact    540
gaactttagg caggattctt cctaacctcc cttttttttt tagagcattt cttgtcattg    600
tacatttttt ctctgcccct ttgagatgta tgtaaatctc ttcaaaagcc tcctgccagt    660
tttacaatcc aggaatgtct ttctcaagga cctgggagcc ctccctttga aatgtaatca    720
tcaaaggaga tggcacccct gtctcccagt ctttgtggag agtttttgtg ggagtctaac    780
ttcagcagga caccttcctc caagtcataa aaccatccct tgtcaaaaga tagaagttta    840
ttagcaaaca caaatggcct acgacctctt cacaacatcc tctggcatgt ttcactagcc    900
tttaaaagcc tttaaaaact ttgcaccctc tgcatcagca gcattgagtt cacactgagt    960
tctagtccct ctctcctgtt gcaataactt cggataaact t                       1001
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<210> 21
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-458-196 : polymorphic base T or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-458-196.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-458-196.mis2, potential complement

<220>
<221> primer_bind
<222> 679..696
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 200..217
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-458-196 potential probe

<220>
<221> misc_feature
<222> 33,792
<223> n=a, g, c or t

<400> 21
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catgctgtgg agggaaggcg agggcacttc ccgccgtcat ctccagaacc gccacagcct    120
tgggaggggg gctgagagag atcagtgctg actgcctgag aagaggcctt ccacaagctg    180
cctttctggt gtccccatgt tcttccttcc ttccttccag aggccgtgag agggagggcc    240
cgtgtcagcc tgctctgccg gtttcccgac tgctgaacct gtctgtggga agctgggttt    300
gactatgtga tgctgaggct ctgagaggag ggctaccctt ttccccaccc tcggccccca    360
ttcctatgag tagaagcctg cccagctgcg gtggtggggt ttgaggaggc taggacttag    420
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acttctcctt atgtaaagat wgtggctgac gaccagcttc ttagaggaag caagtctagg    540
agaagggctc atacctggtc cgtgagggcc tatgggggat cagggcataa gaccacctga    600
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aggttttaca tatatagtca ctgagaaatc ctgagaggat tgaaaaatag catctatttt    720
acagctttaa attgtgccct gagctgagcg tggtggctca tgcctgtaat cccagcactt    780
tgggaggctg anggtgggag gattgcttga gttcagttca ggaccagcct gggcaacagc    840
aagacctcat ctctactaaa aataaaaaaa ttagctgggc atggtggtgt gcacctgtag    900
tcccaattac tcaggaggct gaggtgggag gattgcttga gcctgggagg ttgaggctgc    960
agtgagctgt gattgtgcca ctgcactcca gcttgggtga c                       1001
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<210> 22
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-458-438 : polymorphic base T or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-458-438.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-458-438.mis2, potential complement

<220>
<221> primer_bind
<222> 921..938
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 442..459
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513

<223> 12-458-438 potential probe

<220>
<221> misc_feature
<222> 275
<223> n=a, g, c or t

<400> 22
aaaataggga gggggagcag tctcagctgt cttcagctgc tagggagatt tttttccccc 60
tcctgagcta ctgtttcccc caacccgagc ctttctctct tattgtaccc accctttctg 120
atgaagtcat caaagcaaag attgcataac tgatgcatag gcctatcttg tgttatactg 180
ggagacaggc caatgtttcc attaatagac aagagcacca ccacgctgcc aaatggagct 240
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ggcatgctgt ggagggaagg cgagggcact tcccgccgtc atctccagaa ccgccacagc 360
cttgggaggg gggctgagag agatcagtgc tgactgcctg agaagaggcc ttccacaagc 420
tgcctttctg gtgtccccat gttcttcctt ccttccttcc agaggccgtg agagggaggg 480
cccgtgtcag cctgctctgc yggtttcccg actgctgaac ctgtctgtgg gaagctgggt 540
ttgactatgt gatgctgagg ctctgagagg agggctaccc ttttccccac cctcggcccc 600
cattcctatg agtagaagcc tgcccagctg cggtggtggg gtttgaggag gctaggactt 660
agagcaggga aaaacaagga agcagaatga aaaacagaaa cacttagaaa tctgggattg 720
gtacttctcc ttatgtaaag attgtggctg acgaccagct tcttagagga agcaagtcta 780
ggagaagggc tcatacctgg tccgtgaggg cctatggggg atcagggcat aagaccacct 840
gaccctgggc cttgcatcca caagaacctt gagtttagat ttttagacat attctttgaa 900
caaggtttta catatatagt cactgagaaa tcctgagagg attgaaaaat agcatctatt 960
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<210> 23
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-460-274 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-460-274.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-460-274.mis2, potential complement

<220>
<221> primer_bind
<222> 228..245
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 760..777
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-460-274 potential probe

<220>
<221> misc_feature

<222> 873
<223> n=a, g, c or t

<400> 23
gacataattg ccctctgcct ccttaggaaa acaccagacc tctgagaagg aggtgattaa 60
accgttcagt cacttgacaa agataatcta attaattaat gaaaggattt aacacccatg 120
tctggagcat ttgcaatgtg ctagacaccc ttctgcatat gccgtgacag ctctgacatg 180
acaaacaagg cctgtggaga aacgcagact aggtaacaga ataaacaaga atgtgtaagg 240
tggtgacaaa tgctatgatg aaaattaaca aagggaagta ttaaaccaga gaagtattca 300
atagaagtgt ggctgggtag ctacccttgg ttgggtggcc agggaagaca tctttgagga 360
agtgactttt atgctgagac caaaaaccag ctaagagaag ataaggggag gggaatccca 420
ggtaaggagg aactgtgaat gcaaaggtcc cgaggtagga cagaacaaaa tgcaaaggcc 480
ctgaggtagg atagaacaaa rcagtctcgg cctcccaaag tgctaggatt acaggcatga 540
gccaccactc ctggctacac tggaaggctt taagcagggc aaagccttat gtgatctgac 600
ttgaaaggcc actctcctac ccatgaagaa caggcaagag tagaggcaga agcacaaatg 660
aattagatga cagcagggat gctggtggcc actatgtagt gtacactcaa ccgtgtgcct 720
ggagctcctt aaagcccttt atctgcatta tccattaatc cacacaacct ctctatagag 780
taatttctag aatttccata ttacatatac agaaaataaa gtctagaaaa gtaatgtgcc 840
tccagctggt aaggtttttt tttttttaac aancctcttt ttataactat ataagtcaat 900
aatagtcatc ataagaaaca ttttttaatg agcaaaaaga aaaaattaaa tcacttgaga 960
tcacatcatc ctgtgataat tactattaac attttggctt a 1001

<210> 24
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-461-124 : polymorphic base A or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-461-124.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-461-124.mis2, potential complement

<220>
<221> primer_bind
<222> 378..396
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 911..928
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-461-124 potential probe

<220>
<221> misc_feature
<222> 850
<223> n=a, g, c or t

<400> 24

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ctggattaag ttatcatgac aattagtagt agtagatcat tggaaaaact aacataagta     120
tatatacatt ttgtgaaatc attattttaa aaagtaaaat tttattgaaa atatatctta     180
ataagatagg actagttttt cttccaaata cttcttggtg tgtttttttg tttgtttgct     240
ttttggttaa tatttctaat tactagaatg agacaggttt ctatatgaat tctattccta     300
cttttatttt ttatagacac aagcaaggaa tattgttgac ataagtagaa atgaatcttg     360
taattgcaat tttacttaat tttctgaatg ccttccaagt tctcaatcaa caatcacagt     420
gatctgacat ccaaaattat ttttaaaatg ttgatactac cagctaaaaa cttgatgaga     480
ttctccttta atacagttga magcagagaa ttagaaacca cctggcttgc aaaaaggtct     540
gttacccaaa catttgagtc attgtctatt tcactattaa catcattatt tcaaattctc     600
ctttggttgc tgcactggag gttttgcttt atttgtttgc tggtttgggg tttttgttgt     660
tgttgttgtt ttctgtcttt ttaactatat aggacagggg ttggcaaact aaggccagtt     720
tgtactgatc aaatcttgcc tagcttgctt tcatgcagcc ctcaggttaa gaatggtttt     780
catattttg gtttgttttt ttttttaaaa ggaagtacta cttcttattg atcaaataaa     840
ttctgctttn cttattatca ttattttgta tttgctcaag gaaagctact taaagactaa     900
gtaaagaaca gagttgggag aggtaaagta ccaacttctt gaccacatgt aaggagttct     960
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<210> 25
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-461-299 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-461-299.mis1, potential

<220>
<221> misc_binding
<222> 502..520
<223> 12-461-299.mis2, complement

<220>
<221> primer_bind
<222> 203..221
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 736..753
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-461-299 potential probe

<220>
<221> misc_feature
<222> 675,831,997
<223> n=a, g, c or t

<400> 25
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ttgcttttttg gttaatattt ctaattacta gaatgagaca ggtttctata tgaattctat    120
tcctactttt atttttata gacacaagca aggaatattg ttgacataag tagaaatgaa     180
tcttgtaatt gcaattttac ttaattttct gaatgccttc caagttctca atcaacaatc    240
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acagtgatct gacatccaaa attattttta aaatgttgat actaccagct aaaaacttga     300
tgagattctc ctttaataca gttgaaagca gagaattaga aaccacctgg cttgcaaaaa     360
ggtctgttac ccaaacattt gagtcattgt ctatttcact attaacatca ttatttcaaa     420
ttctcctttg gttgctgcac tggaggtttt gctttatttg tttgctggtt tggggttttt     480
gttgttgttg ttgttttctg yctttttaac tatataggac aggggttggc aaactaaggc     540
cagtttgtac tgatcaaatc ttgcctagct tgctttcatg cagccctcag gttaagaatg     600
gttttcatat ttttggtttg tttttttttt taaaaggaag tactacttct tattgatcaa     660
ataaattctg ctttncttat tatcattatt ttgtatttgc tcaaggaaag ctacttaaag     720
actaagtaaa gaacagagtt gggagaggta aagtaccaac ttcttgacca catgtaagga     780
gttcttagac tggccttcct gtgtgtatac ttaggtctca attcaccacc natgataagg     840
cctgctttgg catatactct aaactcaggg atgatctcaa aattatatct tctttttttt     900
tttttttgag acggagtctc actctgtcac ccaggctgga gtgcagtggt gtgatctcag     960
ctcactgcaa gctccccctc ccgggttcat gccattnctc c                         1001
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<210> 26
<211> 985
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-461-465 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-461-465.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-461-465.mis2, potential complement

<220>
<221> primer_bind
<222> 37..55
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 570..587
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-461-465 potential probe

<220>
<221> misc_feature
<222> 509,665,831
<223> n=a, g, c or t

<400> 26

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agctaaaaac ttgatgagat tctcctttaa tacagttgaa agcagagaat tagaaaccac     180
ctggcttgca aaaaggtctg ttacccaaac atttgagtca ttgtctattt cactattaac     240
atcattattt caaattctcc tttggttgct gcactggagg ttttgcttta tttgtttgct     300
ggtttggggt tttgttgtt gttgttgttt tctgtctttt taactatata ggacaggggt     360
tggcaaacta aggccagttt gtactgatca aatcttgcct agcttgcttt catgcagccc     420
tcaggttaag aatggttttc atatttttgg tttgtttttt tttttaaaag gaagtactac     480
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ttcttattga tcaaataaat yctgctttnc ttattatcat tattttgtat ttgctcaagg 540
aaagctactt aaagactaag taaagaacag agttgggaga ggtaaagtac caacttcttg 600
accacatgta aggagttctt agactggcct tcctgtgtgt atacttaggt ctcaattcac 660
caccnatgat aaggcctgct ttggcatata ctctaaactc agggatgatc tcaaaattat 720
atcttctttt tttttttttt tgagacggag tctcactctg tcacccaggc tggagtgcag 780
tggtgtgatc tcagctcact gcaagctccc cctcccgggt tcatgccatt nctcctacct 840
cagcctcccg agtagctggg actacaggca cctgccacca tacctggcta atttttttgt 900
atttttagta gagacggggt ttcactgtgt tagccaggat ggtctcgatc tcctgacctc 960
gtgatccgcc cgcctcggcc tccca 985

<210> 27
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-462-280 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-462-280.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-462-280.mis2, potential complement

<220>
<221> primer_bind
<222> 222..241
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 655..675
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-462-280 potential probe

<220>
<221> misc_feature
<222> 174
<223> n=a, g, c or t

<400> 27
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ctgaggagca tccatgactg aggaagggcg agtcccctat aatgcccttg ctanggggag 180
catcagacat ccctagactt acaagtccct cgtgtaataa ggtgaactat ggaaagctat 240
gatttgagga aagttccctc tgattgaaag agttcttcaa atatgaagaa tgtaacactt 300
atggggcacc tactcattgc aaaacactct actaggggct ttcacctgta tgtttaactc 360
attttgttga tttttttttt tttaagccca aatttctgag aggttaagga acttgtctgg 420
tggtggcgtc tctgggattc tgacttttcc actgaccata acatgcatct ggtctaaatt 480
gagcggacca cccaggagga ygttggaata aaaagaaatg ggaagggggt ggggagagga 540
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caaaatatgc atcatttttt ttaatatgtt gtctggtacc caaaattggg atgcctctgt 660
ggtatcaact ttgacattta aagaaagggc ataagattag atcattcaac cataagtgga 720

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aggaagaaac aaaataaaat aaaaccttac aattcccttt gaagttgatc aggtgtcaag    780
gcagtgattt ggttttcttt tacaaacttt ctttttccag aaaaattttt actgtgggtt    840
tggagaggtg tttacaataa attcatagca gagctccaaa agggcccacc ccatctaata    900
tcctctgtct cagcagatta ttgaagaaga ttggattaaa aggtttgttt tgtgatgtgt    960
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<210> 28
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-464-66 : polymorphic base G or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-464-66.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-464-66.mis2, potential complement

<220>
<221> primer_bind
<222> 436..455
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 880..900
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-464-66 potential probe

<220>
<221> misc_feature
<222> 121,163..164
<223> n=a, g, c or t

<400> 28
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gggccatttc catagctggt gaagaaattt tctttcccac agtcttcctc ctctcttttt    120
ncatactttt ccctcttttg ctttctggcc atatgccttc ttnnttgctt tcctcccctt    180
ccacctctaa ctcacagcaa ttctcttccc tctaccaacc agcctgttcc aaaaaaaaaa    240
aaaaaaaaaa aaaaggtccc cttttattcc ttagggtagc acttgttttt gtttttttaac   300
atccaaatcc ttcttggagc cccttcgtat tctctctctg aggaagacgg agggggcttc    360
cctcatcctc ccttgttacc tagcaacttg tcttcttcct gacaagtcac caccctgcca    420
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cccagacgcc tctcccccag taagctggcc acactgctcc tccagggatc tcagagagat    600
ggcagcttgt caagttcctg agtcgctggg tatgtactgg gaatttcaga tttaatccct    660
aattacatcc agctcatcac ctttgtaata ggagccataa tcatcttttc attgttgtct    720
ttgagtcact ggggctgtgt ggaacactat atccatattc atgcatgtgt tttctatttt    780
gctactacat cctcttcctt agacttcaaa atgaaggggg attttctttt ctcctgcaaa    840
agcctttatg aaagaaggtg tttgcttaac actttcaagc ttccccattg acatcctttg    900
ttctttctct acacattcat ggattaacta ctttgggtcc agccgtggta accaacttca    960
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<210> 29
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-465-26 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-465-26.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-465-26.mis2, potential complement

<220>
<221> primer_bind
<222> 476..493
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 945..962
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-465-26 potential probe

<220>
<221> misc_feature
<222> 556,630,796
<223> n=a, g, c or t

<400> 29
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gttcttttgt tctactaaat taccacaaaa cttcctgctt catttgtatt tatgaggtat 180
atgagttgtg gaacgtggac tggtttgaaa gcaatatttc tgcacagaca aattctaggg 240
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gaagaaggcc atatactcca gaggcgatag gatcactgaa aaaaactaaa tgtgtggctt 420
gcaagaagag gaggtggcct ccttctaaga tgtcccttgt cattctgaag aagacttcct 480
cccaaaccaa ctctttccca ytgggcagtc agcttgatct cttgaggttg aggaaggccc 540
tgctattaat tgtccntagg agaaagagca tatccactga gctatgagtc aatgatctgt 600
cttagggtgg gatttattat tttcattatn ttgtgtgttt gattttcttg ttagagttct 660
ttccttagga ctgtttgttg cttttaacga ggtggatggg ggtggtagtg tgctgagcag 720
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tatgttctag tagctaggag agtcccagca tgtgctctta gaggccattt tggagagggt 900
gaaatagaga aactagaaac attattcatc tcagagactc tctggacctg agagagaaca 960
gtaactgtat tcaggcctaa tccctcagat ggctgccttg g 1001

<210> 30
<211> 1001

<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-465-234 : polymorphic base G or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-465-234.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-465-234.mis2, potential complement

<220>
<221> primer_bind
<222> 266..283
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 735..752
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-465-234 potential probe

<220>
<221> misc_feature
<222> 346,420,586,869..870,876..877
<223> n=a, g, c or t

<400> 30
gcaatatttc tgcacagaca aattctaggg ttggcttttt gcatactata ataactctag 60
acaaatcatg gaaattgtga cttccccagg aagatgggga ctggggggag tgaagtatgg 120
aggaagggaa aggaggcttg gagaggaaag gaagaaggcc atatactcca gaggcgatag 180
gatcactgaa aaaaactaaa tgtgtggctt gcaagaagag gaggtggcct ccttctaaga 240
tgtccccttgt cattctgaag aagacttcct cccaaaccaa ctctttccca ttgggcagtc 300
agcttgatct cttgaggttg aggaaggccc tgctattaat tgtccntagg agaaagagca 360
tatccactga gctatgagtc aatgatctgt cttagggtgg gatttattat tttcattatn 420
ttgtgtgttt gattttcttg ttagagttct ttccttagga ctgtttgttg cttttaacga 480
ggtggatggg ggtggtagtg kgctgagcag agcagtgctg atgctgacaa caacaccaca 540
gcaaacagca aacaggacat gcaaagcagg aggcaaactc gtcttnccca accaacattt 600
agctgaggac tagtcagggt gtgtggctat tatgttctag tagctaggag agtcccagca 660
tgtgctctta gaggccattt tggagagggt gaaatagaga aactagaaac attattcatc 720
tcagagactc tctggacctg agagagaaca gtaactgtat tcaggcctaa tccctcagat 780
ggctgccttg gcggccactc tctttaccat gaaaattgcc ccccagatgg aaacctcttg 840
aacttggaaa aacctcttta tttccaaann cagaannaaa aaaaaatcac tatgtatttc 900
ttcttaagaa aaaaaaattg ttattcaact actgtgtccc attttcccaa taaacattaa 960
ttgaactgct agtgggcacc attcatccat ttaacaaata c 1001

<210> 31
<211> 1000
<212> DNA
<213> Homo Sapiens

<220>

<221> allele
<222> 501
<223> 10-428-219 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 10-428-219.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-428-219.mis2, potential complement

<220>
<221> primer_bind
<222> 278..295
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 613..632
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-428-219 potential probe

<220>
<221> misc_feature
<222> 203,238,334,348,369,374..376,645,675
<223> n=a, g, c or t

<400> 31
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actcttttat atcataaagt aaaactactt tacagatgag gaaactatct atttgatgta     60
cacaataatt tctctaaatt ctttcagcta gtcagtgggt tgttgagcta gaatctgagg    120
aatccagatc ccatcctttc attgattatg tcactaagat aagtcacaga atcttctttt    180
agggaagttt tcaagaatag tangtaagct gctatcttaa aatattgatg tcagtagncc    240
tgggaatttt accacgtatg caagcatggg ataagacaac cacaggtttc tcttctgtac    300
cagttaacct gttttatgat tatttcaagt tgtngaataa aagcttgnaa aattggcagg    360
atctgtttng aggnnnttac tcaaggatat ttattacttg tttcaggaac agcatctgtt    420
gcagttgcag gtctcccttgc agctcttcga ataaccaaga acaaactgtc tgatcaaaca    480
atactattcc aaggagctgg rgaggtattt gccttgtgta atacttatgt tctcctaaac    540
taacatataa ttagtgttaa ttgctcatta actcaagatt tgacgtattc tttcaaattt    600
ttagtatatt atgactgtag gctttatgga agattcccaa attanagtac tgagacatat    660
taattattca taggnataat ttagtacaga agtaatgaga tatttttcac agttttaaat    720
ttgtggtatt atcaaatgtt gccgtaggta tttgttatgc atatctaagg tgccatacag    780
gaaaactttc caatgtatgt gtatatatgc aagcttttat gtatttaagc tggtttatct    840
gatactggct tttagtatac tccagtgtta caaaaacaag tttttaaaat ttgactcaca    900
attcagtgtg tatgtatgta actacatatg tgtttttaag aaaaaacatt ttgaattagg    960
gatttgtagt atattattac tgttcacatg caaaaatccc                          1000
```

<210> 32
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-429-84 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 10-429-84.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-429-84.mis2, potential complement

<220>
<221> primer_bind
<222> 418..436
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 823..842
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-429-84 potential probe

<220>
<221> misc_feature
<222> 222
<223> n=a, g, c or t

<400> 32
taattataaa atttaccaaa taccaaggaa gttgattcct ttaatcttgc aataaatttc 60
acagcacttt tggtatccaa attagaagag taagtagatg cttggaaaca cagatctttt 120
atttttcatc agtttcattc tgttgcctaa ttggtcaagt tcccatccaa atgaccaagc 180
ttctttcttc aaattcaatt agagtagctt gaacctaaca antaaacaat acagttcaat 240
gagcaaggtt gaccagttca ttattttgaa ttcagtattt tttcttggag caaatcttgg 300
ttgtattaac aggattaaat acactgacaa tcaaggatat caccagttta tctgtggcca 360
aatagcaagc cacataatag tggctctgtt gtagtaaaaa gggtaaataa ttgttatttg 420
gcttaaccta aatgtgacaa aaatattttg ttcccactaa caaagacaaa atggggtgaa 480
atgtaaccct taataagata ycatgtagaa caactttaaa atttttttctt ttcatcactg 540
aggctgccct agggattgca cacctgattg tgatggcctt ggaaaaagaa ggtttaccaa 600
aagagaaagc catcaaaaag atatggctgg ttgattcaaa aggattaata gttaaggtaa 660
gaatttgtca tttttaacca gaataaagat aactatgcca ttctggatgg ccatctcaaa 720
gacaactctg tttctaccac ctccctttac actatattaa aagagtagcc attaaataca 780
aatgatcatg tcatacagaa tactgatact cttctgaata aagaaaacta tgacttagga 840
acagattcca tctgcaatgt gagtcggctc cttacacccc tttgaattga cagtccattt 900
gaattagttt agttttcttt ctttctttcc ttcctttctt tcctttctct ttctttcttt 960
ctttttcttt ctttccttcc ttccttcctt tccttccttt t 1001

<210> 33
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-420-284 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 10-420-284.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-420-284.mis2, potential complement

<220>
<221> primer_bind
<222> 216..235
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 646..665
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-420-284 potential probe

<220>
<221> misc_feature
<222> 42,308,413
<223> n=a, g, c or t

<400> 33
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agcctatcgg ttgaaccact gcagagaata gagtgatggt cnttagggca tcctgtactt     60
tgcatgctcc tcctggaagt aaagagtaag acagagaata gtaataatca cccattccag    120
aactggttgc acaacatcac aaaagcttgt ccagacttat tagcaagtta ataaaaaact    180
agacttcttt ctaagtactt ataatttagg ctgtggggta gttctgttat gatacatttg    240
ttttaaaata ttctgcttct ttttaaagtg agttgtatgt gtctttgttg tagggacgtg    300
caattttntg ccagtggcag tccttttgat ccagtcactc ttccaaatgg acagacccta    360
tatcctggcc aaggcaacaa ttcctatgtg ttccctggag ttgctcttgg tgnttgtggc    420
gtgtggattg aggcagatca cagataatat tttcctcact actgctgagg tattgtaaaa    480
tcctctaagt ttaccaaggg yttaaaatac caagtgtgct cagcctaggt tgtctaatgt    540
tttatttatc tagcatctca gcttactctc tgaaagaagt aaagtctgaa gaacttccca    600
gtggagtata aggggtgggt agcatgttca tactgactca caaacgaaag gttcttcttc    660
agtagtcatt agaaaaattg tgtttttgat ttcttaagag gaacattttt gtgtcttcac    720
acatcagatc aagttctgtg acagtgatgg gacaattaaa aatattgttt ccagggctgg    780
gtgtggtggc tcatgcccct aatcccagca ctttgggagg ctgaggcagg cagatcactt    840
gagcccagga gttcgaggcc agcttggcca acatggtgaa acttcatctc tactaaaaat    900
acaaacatta gccgggcatg gtggtgtgtg cctgtgatcc cccctgactc aagaggctga    960
ggcaggagaa ttgcttgaat ccaggaggca gaggttgcag t                        1001
```

<210> 34
<211> 821
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-423-411 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 10-423-411.mis1, potential

<220>
<221> misc_binding
<222> 502..521

<223> 10-423-411.mis2, potential complement

<220>
<221> primer_bind
<222> 91..109
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 510..528
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-423-411 potential probe

<220>
<221> misc_feature
<222> 5,804
<223> n=a, g, c or t

<400> 34
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cctangattc tattcccatc tttttcacca attatgtgat ctcaaccacc accacaccac     60
tctgggctta tttctttgtt gatagaagtg gggatgaaat taggtaatca tattaatgtc    120
actggttttt gtatagacca ttatatgtaa ccgttcactt agttattggc gtacccacca    180
cattgtatcg tgtgaagtat aaacactttt tttctttctt tttttcataa ggttatagct    240
cagcaagtgt cagataaaca cttggaagag ggtcggcttt atcctccttt gaataccatt    300
agagatgttt ctctgaaaat tgcagaaaag gtaaaaccac tcttgttcaa gcttcattat    360
ttttccttcc ttttcttgct aaatatgcat ttttaaatat taaaaatctg cttccttgaa    420
atgtatatct gtatcaactt actatgtcag aagtcagaga aatgaggcac actgacactg    480
tagagcttag gagctacatt ygcttctcag agaagaatgg aagtattggg gccgaataat    540
taatttccct ctctatcgtt cttttttttct cctaaaattt aaataattca ttagggcttc    600
ctgtcagcca gatttctccc atttcacctt tttaaagttg ttcttttcta tatcacatta    660
gtgataatta accaaaatat tacagatatg ttagagtaac atttagacct tgaaccacct    720
tccatatcca tgtcactatg atgtgtggca tcataaatga cagatcacaa ctgataatac    780
tgggcggaag gcaaaataaa gagntcaaag aacttgaaag c                        821
```

<210> 35
<211> 732
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 232
<223> 12-713-95 : polymorphic base C or T

<220>
<221> misc_binding
<222> 213..231
<223> 12-713-95.mis1

<220>
<221> misc_binding
<222> 233..252
<223> 12-713-95.mis2, potential complement

<220>
<221> primer_bind
<222> 137..153
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 586..604
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 220..244
<223> 12-713-95 potential probe

<220>
<221> misc_feature
<222> 154
<223> n=a, g, c or t

<400> 35
ggtctcttct gtgaccccat tattgtcctg tgcatttatc tcaagatcag attcattatt 60
aaatctatcc agacaattcc tctatcatgt ccttgatcca tttctataac cataacccag 120
tttctataat cataacccaa cttcaccatt ttantatctt tacaccatct cggtaacttc 180
tgattttctt taggatcata ttaataagta ttcaggaact tacctttacc cygctattga 240
ctgttttcac ctacatataa atccctttgt gatctggccc atgcacttca ccttcctgtc 300
tgccatcctc cacccctccg tgtatccttt acaccattgt ataaataaat agttttagtt 360
ggctgcacat gtcattgttc tgtcacactt cttctctgta taaactgctc cttcttcccc 420
cagtgctttt gcttatttaa ttcatgctta tctttcataa ctcaggttaa atatctagac 480
tggattagag aagttttctg tatagtatcc tagcatggat acaccaaaat agcatgtatc 540
acactgtatt gtaattatat gtatttattt gacttagcat taagtcatca agatattaga 600
ggtcagggcc tcattctttt ctctcttcct ttataatata tgttgttact gtgatacttc 660
tttttaataa ctttaatttt aagttcagga gtacatgtgc aggtttgtta cataggtgac 720
cttgtatgat gg 732

<210> 36
<211> 786
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 286
<223> 12-713-149 : polymorphic base G or C

<220>
<221> misc_binding
<222> 266..285
<223> 12-713-149.mis1, potential

<220>
<221> misc_binding
<222> 287..306
<223> 12-713-149.mis2, potential complement

<220>
<221> primer_bind
<222> 137..153
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 586..604
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 274..298

<223> 12-713-149 potential probe

<220>
<221> misc_feature
<222> 154
<223> n=a, g, c or t

<400> 36
ggtctcttct gtgaccccat tattgtcctg tgcatttatc tcaagatcag attcattatt 60
aaatctatcc agacaattcc tctatcatgt ccttgatcca tttctataac cataacccag 120
tttctataat cataacccaa cttcaccatt ttantatctt tacaccatct cggtaacttc 180
tgattttctt taggatcata ttaataagta ttcaggaact tacctttacc ctgctattga 240
ctgttttcac ctacatataa atccctttgt gatctggccc atgcasttca ccttcctgtc 300
tgccatcctc cacccctccg tgtatccttt acaccattgt ataaataaat agttttagtt 360
ggctgcacat gtcattgttc tgtcacactt cttctctgta taaactgctc cttcttcccc 420
cagtgctttt gcttatttaa ttcatgctta tctttcataa ctcaggttaa atatctagac 480
tggattagag aagttttctg tatagtatcc tagcatggat acaccaaaat agcatgtatc 540
acactgtatt gtaattatat gtatttattt gacttagcat taagtcatca agatattaga 600
ggtcagggcc tcattctttt ctctcttcct ttataatata tgttgttact gtgatacttc 660
tttttaataa ctttaatttt aagttcagga gtacatgtgc aggtttgtta cataggtgac 720
cttgtatgat gggggtttgt tgtacagatt atttcatcac ccaggaacta agcatagtac 780
tcgtta 786

<210> 37
<211> 902
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 500
<223> 12-716-295 : polymorphic base C or T

<220>
<221> misc_binding
<222> 477..499
<223> 12-716-295.mis1

<220>
<221> misc_binding
<222> 501..520
<223> 12-716-295.mis2, potential complement

<220>
<221> primer_bind
<222> 206..225
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 727..746
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 488..512
<223> 12-716-295 potential probe

<220>
<221> misc_feature
<222> 67,139,690,834
<223> n=a, g, c or t

<400> 37
caatgtgtac tacaaaaata aaatgcatgc aatttagagt cactattgca ataattatga 60
actgtgntaa gtcatatatt atgaaaaagc cactcttcta tacattactt aaggtgaaaa 120
tctatgcaaa aaatatggnt agtgtatgta gagaatatat catgacatga ttagaatgat 180
attttcccca tgcaagatat attcactaga gtcattaaac agatgaaaga gaatttaaac 240
tagaaagaga ggtatagata tccacttact aaataagaag ttattcagaa atagtagctc 300
aagctatctc tctcttgggt tcttttgaag taaactgccc agaagtttgg atctggggaa 360
ctctaagctc ccttccaact ctgagattct atgattttaa gggtttctat aagatttaac 420
cagttgaagc atcaaagttg aagtatcatc agcaatcact gtatttgtat tattattttt 480
atttacatcg aattggacay ttacggtcag atagacagaa aatattctaa aatatcctat 540
ttggtacctt aatttcatat ggttatgcta gatcacttaa aactcaaaat gtgttaagtt 600
catacattat atttaaagat atatttcata atatttcctg agaacacaat gaaaacacta 660
atcttccatt tatagaatta attaataaan atcagaaaga tatttttagc actatcaaaa 720
atttaacttg aacatgattc ttgtacatgg cctggtacta ccttgattta aatttcattg 780
cagagaaggg aatacatgta gaaaattgaa atttcataaa actgtaaatt tttnacaata 840
aattattcca taataagttt tactttaaga tttaaaacta agctttttat aagtcagaca 900
ga 902

<210> 38
<211> 981
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 480
<223> 12-720-80 : polymorphic base G or C

<220>
<221> misc_binding
<222> 461..479
<223> 12-720-80.mis1

<220>
<221> misc_binding
<222> 481..500
<223> 12-720-80.mis2, potential complement

<220>
<221> primer_bind
<222> 400..419
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 856..876
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 468..492
<223> 12-720-80 potential probe

<220>
<221> misc_feature
<222> 191,218,225,437,480,694,772,775
<223> n=a, g, c or t

<400> 38
ctgcaggaaa catttggcaa tgtctggaag ctttgagttg tcttaactag ggtagcgggg 60
ttggaaggga gtaaagggag gggctactga catctagcag atagaggcag cggaatgatt 120
ctactaaata tcctgtagtg cactggacag cccctgcgac aaggaattat ccagcctaaa 180
atgtcaatag ntgctgaggt tgagaaatac tgcagtanga taagnaccct cctggaagac 240

```
agggatcaca tctcacaaat ctttattttc cttatagcac ttaatacagt acttacacaa    300
tgcatgtgca gtgcaagact ttaaagtggt tttagaaaac tcaaaggaat ttatgaaact    360
ttattcttta ttttgtgcat atataatttt gatttttacc ttgtattata ctccattcct    420
acaagctctt gtgaaancag atgacaacgt tgaaaataat gatgataact acaataaaas    480
gaagtactta ctccatgaca ggaactttac taagtgttta atattgtttt tacaaaatat    540
attctgtcaa taatcttatt gtttttcatt tccattatgc taattgcttt attcttctgt    600
taaagttact tcagtgggtg gtactttact tttgcagatg aatcagatgg ttgtcttaag    660
tgatagcgtt ggtttataaa acttaattgc tttngtagcc tgacaagact gaaatatact    720
catagaattg cttataaaga aagtttacac attagataca aatttccaag tnganttggt    780
aactaactca atgtactatg gaagccaaat attatcttta gtttttaata gatatttgta    840
gatttgtgac cctaaggatt gtaaggattg ttggcattaa caaacttgcc tctttttgtc    900
actatacttg aatacaaata gtttatatag cattttgttt agggtctatt agaaaatgag    960
ctgatagata tcattgattt g                                              981
```

<210> 39
<211> 872
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 372
<223> 12-721-227 : polymorphic base C or T

<220>
<221> misc_binding
<222> 352..371
<223> 12-721-227.mis1, potential

<220>
<221> misc_binding
<222> 373..392
<223> 12-721-227.mis2, potential complement

<220>
<221> primer_bind
<222> 146..165
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 588..607
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 360..384
<223> 12-721-227 potential probe

<220>
<221> misc_feature
<222> 756,794,799
<223> n=a, g, c or t

<400> 39

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aaattaatga gttaaatgat gagtttatta taaaattatg gtcaacaccc tacaattata     60
tgttataata ttttgtataa tatgtagagc aatactaatc aaacaaatag ttatactagt    120
aactttacct ccttctcctt tccatcttac ctctgcctaa atgtccctgg tcagaagtcc    180
ttagtcaccg acgggattta actccaaact cctttttttga cattgataat gctccagtcc   240
ttatttctgt acccagaccc tctgctcccc caggtcagga cacttgggcc tgctgagtcc    300
agctcacaca caactctgcc tttggtctga ctctgttttt tgtctgaaat gcctacctac    360
tttctgtttg tytaactcca ggctttcctg taggtttgcc tttcaagcca ctgtgcacta    420
taaggccttc cagaactgct cttcctctgg atttcttagc acccacattt caccattagc    480
```

```
ctaagccgtc ttctctttca gcgttctctt tttcttcccg tactctgtta ccttactaaa     540
ttatacatct ctcaaggaca ataacacttt tcttaagctt ctccgtagtg ttatgcttgt     600
tcagtgcata tatgtttgct gatggcaaag aataatattt tggaaataat ttcatgattt     660
aaaaatctaa aagatattaa gatatactga aaaataagta tttgattatt taaaatgtta     720
caaaagagga aggtttccta ctccctctct gcatcncaca ttttcatgga acaaaggcct     780
aggtataagc tgantttang atttgccccc atctagaaat ttaatcaaag tcttagagct     840
ggagagaaca tcagggttac tgagtctccc tc                                   872
```

<210> 40
<211> 926
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 426
<223> 12-721-281 : polymorphic base A or C

<220>
<221> misc_binding
<222> 406..425
<223> 12-721-281.mis1, potential

<220>
<221> misc_binding
<222> 427..446
<223> 12-721-281.mis2, potential complement

<220>
<221> primer_bind
<222> 146..165
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 588..607
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 414..438
<223> 12-721-281 potential probe

<220>
<221> misc_feature
<222> 756,794,799,893
<223> n=a, g, c or t

<400> 40

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aaattaatga gttaaatgat gagtttatta taaaattatg gtcaacaccc tacaattata      60
tgttataata ttttgtataa tatgtagagc aatactaatc aaacaaatag ttatactagt     120
aactttacct ccttctcctt tccatcttac ctctgcctaa atgtccctgg tcagaagtcc     180
ttagtcaccg acgggattta actccaaact cctttttgga cattgataat gctccagtcc     240
ttatttctgt acccagaccc tctgctcccc caggtcagga cacttgggcc tgctgagtcc     300
agctcacaca caactctgcc tttggtctga ctctgttttt tgtctgaaat gcctacctac     360
tttctgtttg tctaactcca ggctttcctg taggtttgcc tttcaagcca ctgtgcacta     420
taaggmcttc cagaactgct cttcctctgg atttcttagc acccacattt caccattagc     480
ctaagccgtc ttctctttca gcgttctctt tttcttcccg tactctgtta ccttactaaa     540
ttatacatct ctcaaggaca ataacacttt tcttaagctt ctccgtagtg ttatgcttgt     600
tcagtgcata tatgtttgct gatggcaaag aataatattt tggaaataat ttcatgattt     660
aaaaatctaa aagatattaa gatatactga aaaataagta tttgattatt taaaatgtta     720
caaaagagga aggtttccta ctccctctct gcatcncaca ttttcatgga acaaaggcct     780
aggtataagc tgantttang atttgccccc atctagaaat ttaatcaaag tcttagagct     840
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ggagagaaca tcagggttac tgagtctccc tctctgcctt agggttcaat acnaaaattt 900
aacactgttt gatttggaac taggga 926

<210> 41
<211> 1000
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-721-440 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-721-440.mis1, potential

<220>
<221> misc_binding
<222> 502..520
<223> 12-721-440.mis2, complement

<220>
<221> primer_bind
<222> 62..81
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 504..523
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-721-440 potential probe

<220>
<221> misc_feature
<222> 672,710,715,809
<223> n=a, g, c or t

<400> 41
tagagcaata ctaatcaaac aaatagttat actagtaact ttacctcctt ctcctttcca 60
tcttacctct gcctaaatgt ccctggtcag aagtccttag tcaccgacgg gatttaactc 120
caaactcctt ttttgacatt gataatgctc cagtccttat ttctgtaccc agaccctctg 180
ctcccccagg tcaggacact tgggcctgct gagtccagct cacacacaac tctgcctttg 240
gtctgactct gttttttgtc tgaaatgcct acctactttc tgtttgtcta actccaggct 300
ttcctgtagg tttgcctttc aagccactgt gcactataag gccttccaga actgctcttc 360
ctctggattt cttagcaccc acatttcacc attagcctaa gccgtcttct ctttcagcgt 420
tctctttttc ttcccgtact ctgttacctt actaaattat acatctctca aggacaataa 480
cacttttctt aagcttctcc rtagtgttat gcttgttcag tgcatatatg tttgctgatg 540
gcaaagaata atattttgga aataatttca tgatttaaaa atctaaaaga tattaagata 600
tactgaaaaa taagtatttg attatttaaa atgttacaaa agaggaaggt ttcctactcc 660
ctctctgcat cncacatttt catggaacaa aggcctaggt ataagctgan tttangattt 720
gcccccatct agaaatttaa tcaaagtctt agagctggag agaacatcag ggttactgag 780
tctccctctc tgccttaggg ttcaatacna aaatttaaca ctgtttgatt tggaactagg 840
gaatggtttg gggacagtaa atgttgaggc taattaggtg atttagataa tccagagtct 900
gtgtaaaatt aaaatcctat ttgtagtgag actctgaact agctttctca gccttttgct 960
ctacctcctg cacaagaata tgactcagag ctgggagtaa 1000

<210> 42

<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 12-723-293 : polymorphic base C or T

<220>
<221> misc_binding
<222> 484..502
<223> 12-723-293.mis1

<220>
<221> misc_binding
<222> 504..523
<223> 12-723-293.mis2, potential complement

<220>
<221> primer_bind
<222> 210..230
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 591..610
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 12-723-293 potential probe

<220>
<221> misc_feature
<222> 312,379
<223> n=a, g, c or t

<400> 42
ctcattagtt ctcagacatt tgaatagtcc ttctccagtg catagttact tgggtaaagg 60
gctgtagttc cctgtggata aagattaggg ggattattac cctgtattct tgtcatggtg 120
ttataaggtt ctttcttctg ggaactaggc ctcttcttca gtttatgggt tctgggtcta 180
aaaattaact caggttcgga agctgagcaa gagattgtga cttcattggg gcagctacac 240
tcaactttgt ggtcattcat ctttggtttc ttttgatagt aaatattgag tagtagcttt 300
gttagctctc cngttttgcc tctagggatg caagattccg ttaattatct caaaaacatt 360
ttgtgggtta gccacacanc accccacttt tgccactctt atgataattg tgtccatctg 420
gcttctgatt gttaagcatt ctcacctggt cttagcatcc ttattgctat cagtcaggct 480
ggttatatat catccttttc ttytgtcact cctgaccttc aggggagaac caccactgaa 540
atttttagta atgttgatgt cttctcattg gcatattcct tatggctttg ggaaatggtg 600
tgttttctgg gccttcctgt ggaatatgtt catcttatgg attttctggc ttttacatgt 660
gtctatatac cagactgccc agttctctga gcctcgcaat cccctcttct gtcatttgcc 720
acagcattcc tggcatttca gtcatattag tatcagccat taatttgtcc atgtttctag 780
gaaccatcct agcaatgagt ttgcaccatc ttctgggatt cttgccacat gttaaatcct 840
gtatctcagg agagtgcctg caaatcagta agctctccct tttcctaggt tccagccctt 900
ttaatcaaac accctcagaa tttaattcta catgtattct cctggctaat acaaatactg 960
gtcttgtggc tcctttgggg taaagtctct ttcttccttt a 1001

<210> 43
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-724-195 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-724-195.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-724-195.mis2, potential complement

<220>
<221> primer_bind
<222> 307..326
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 797..817
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-724-195 potential probe

<220>
<221> misc_feature
<222> 244,249,631,669
<223> n=a, g, c or t

<400> 43
tcacctgagg tcaggagttc gagaccagcc tggccaacat ggtgaaaccc tgtctctact 60
aaaaatacaa aaattagcta ggcgtggtgg caggcgcttg taatcccagc tacttgggag 120
gctgaggcag gagaatcact tgaacccagg tggtggaggt tgcagtgagc cgtgattgca 180
ccaccgcact ccagcctggg caacagagcg agaatccatc tcaaaaaaaa aaaaaaaaag 240
aaanaagana aagcatgaag tatgtggagg catacatgaa aagagacaaa tgacatgtta 300
tttttacatt ttaataggca accaagtata acaataatgt gaagcaagac tttctaatta 360
tgtgcacagg ccatctgatg gacggcaaag gtggaacatg gggagatgag tatgtgaaag 420
agggaacatc atggcctctg agctgaaggc agcatgggta caggctcaaa tcctcagaga 480
agctttggct ctaaaggact yatctgtgct tcaacatacc actgtattct cctatttcta 540
gtttgtacca ttccttatgc ctaaaatgcc ttcatataag ggatgcagaa atttagaaaa 600
tgcttttata aactccatgt gcaaacttac naatagagaa ttaaaggtct cctcaaagca 660
tgttccagnt aaatacctca tctccaacct caatcatgtc atttacttct gtagtttgaa 720
tcactaaatc tgtgactttt tctccattta gcctgaatca aactgtttat ttctaaaagc 780
cagcaacttc tatgaacact aagggtcaca tattcagcag aaaagagaat tgtatattat 840
tttactgaag aatattacag tcataaaatt ttagatctag aaatgtcctc agagatgatt 900
tagcaataac taatgaccag gaaggttaaa aaacacccaa ggttccagaa aaatatatgg 960
tagtgagtgt tgccatctaa gagaaaagcc agagggacta a 1001

<210> 44
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-724-225 : polymorphic base C or T

<220>
<221> misc_binding
<222> 482..500
<223> 12-724-225.mis1

<220>
<221> misc_binding
<222> 502..521
<223> 12-724-225.mis2, potential complement

<220>
<221> primer_bind
<222> 277..296
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 767..787
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-724-225 potential probe

<220>
<221> misc_feature
<222> 214,219,601,639
<223> n=a, g, c or t

<400> 44
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tggccaacat ggtgaaaccc tgtctctact aaaaatacaa aaattagcta ggcgtggtgg     60
caggcgcttg taatcccagc tacttgggag gctgaggcag gagaatcact tgaacccagg    120
tggtggaggt tgcagtgagc cgtgattgca ccaccgcact ccagcctggg caacagagcg    180
agaatccatc tcaaaaaaaa aaaaaaaaag aaanaagana aagcatgaag tatgtggagg    240
catacatgaa aagagacaaa tgacatgtta tttttacatt ttaataggca accaagtata    300
acaataatgt gaagcaagac tttctaatta tgtgcacagg ccatctgatg gacggcaaag    360
gtggaacatg gggagatgag tatgtgaaag agggaacatc atggcctctg agctgaaggc    420
agcatgggta caggctcaaa tcctcagaga agctttggct ctaaaggact tatctgtgct    480
tcaacatacc actgtattct yctatttcta gtttgtacca ttccttatgc ctaaaatgcc    540
ttcatataag ggatgcagaa atttagaaaa tgcttttata aactccatgt gcaaacttac    600
naatagagaa ttaaaggtct cctcaaagca tgttccagnt aaatacctca tctccaacct    660
caatcatgtc atttacttct gtagtttgaa tcactaaatc tgtgactttt tctccattta    720
gcctgaatca aactgtttat ttctaaaagc cagcaacttc tatgaacact aagggtcaca    780
tattcagcag aaaagagaat tgtatattat tttactgaag aatattacag tcataaaatt    840
ttagatctag aaatgtcctc agagatgatt tagcaataac taatgaccag gaaggttaaa    900
aaacacccaa ggttccagaa aaatatatgg tagtgagtgt tgccatctaa gagaaaagcc    960
agagggacta agtccaatag ccacgtacgg tagagcagac c                       1001
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<210> 45
<211> 421
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 330
<223> 10-153-329 : polymorphic base G or T

<220>
<221> misc_binding
<222> 310..329

<223> 10-153-329.mis1, potential

<220>
<221> misc_binding
<222> 331..349
<223> 10-153-329.mis2, complement

<220>
<221> primer_bind
<222> 1..20
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 402..421
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 318..342
<223> 10-153-329 potential probe

<400> 45
agagtcaccc tbggtcttag gtagtaggtg gagctgaggg ataatggccc aaggccaaga 60
gttgatcctt ccaactttgt tcagtgatcc agctttcata tcaggtgatc aggacaacca 120
ggccaatctg atagggggcg gtgtttataa aaaggccact cacctagagc cagaagctcc 180
acaccagcca ttacaaccct gccaatctca agcacctgcc tctacaggta cctttcttgg 240
gaccaattta caatctctgg gatccccaac tatagaacct ggaagctagt ggggacagaa 300
agacggggag cctgggctag gtgtaggggk cctgagttcc gggctttgct acccagctct 360
tgacttctgt ttcccgattt taaatgagca gtttggacta agccattttt aaggagagcg 420
a 421

<210> 46
<211> 428
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 342
<223> 10-95-342 : polymorphic base A or G

<220>
<221> misc_binding
<222> 322..341
<223> 10-95-342.mis1, potential

<220>
<221> misc_binding
<222> 343..361
<223> 10-95-342.mis2, complement

<220>
<221> primer_bind
<222> 3..21
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 404..422
<223> downstream amplification primer, complement

<220>

<221> misc_binding
<222> 330..354
<223> 10-95-342 potential probe

<220>
<221> misc_feature
<222> 192,253..254,424..425
<223> n=a, g, c or t

<400> 46
rwtccctcct tttttccctg cagttggtac agatggcatt gtcccagtct gttcccttct 60
cggccacaga gcttctcctg gcctctgcca tcttctgcct ggtattctgg gtgctcaagg 120
gtttgaggcc tcgggtcccc aaaggcctga aaagtccacc agagccatgg ggctggccct 180
tgctcgggca tntgctgacc ctggggaaga acccgcacct ggcactgtca aggatgagcc 240
agcgctacgg ggnngtcctg cagatccgca ttggctccac gcccgtgctg gtgctgagcc 300
gcctggacac catccggcag gccctggtgc ggcagggcga cratttcaag ggccggcctg 360
acctctacac ctccaccctc atcactgatg gccagagctt gaccttcagc acagactctg 420
gagnnata 428

<210> 47
<211> 373
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 277
<223> 10-100-277 : polymorphic base C or T

<220>
<221> misc_binding
<222> 258..276
<223> 10-100-277.mis1

<220>
<221> misc_binding
<222> 278..297
<223> 10-100-277.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 355..372
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 265..289
<223> 10-100-277 potential probe

<400> 47
tagggatgga gatggcggtg ggcaggctgt ctggatgggg tggaggtagg agcaacacat 60
gccccagctt tccagccctg agcctcacag tgccctcttc cctcctcagc acaacaaggg 120
acacaacgct gaatggcttc tacatcccca agaaatgctg tgtcttcgta aaccagtggc 180
aggtcaacca tgacccgtga gtacataccc ctcacgaaaa aatgtgtgca ggttcagcag 240
tcaggaaggc tgtttgtccc tgctaggaac tgtttayata atgaaaggag gggacctcaa 300
ttgctatagt ctgctctaag tgacgatatt tacaaaagtt tcacaaactt tagtgcacag 360
gaatcaacta ggg 373

<210> 48
<211> 375
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 297
<223> 10-102-294 : polymorphic base C or T

<220>
<221> misc_binding
<222> 278..296
<223> 10-102-294.mis1

<220>
<221> misc_binding
<222> 298..317
<223> 10-102-294.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 356..375
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 285..309
<223> 10-102-294 potential probe

<220>
<221> misc_feature
<222> 30,218
<223> n=a, g, c or t

<400> 48
agagwgctgt gggaggaccc ctctgagttn cggcctgagc ggttcctcac cgccgatggc 60
actgccatta acaagccctt gagtgagaag atgatgctgt ttggcatggg caagcgccgg 120
tgtatcgggg aagtcctggc caagtgggag atcttcctct tcctggccat cctgctacag 180
caactggagt tcagcgtgcc gccgggcgtg aaagtcgncc tgaccccat ctacgggctg 240
accatgaagc acgcccgctg tgaacatgtc caggcgcggc tgcgcttctc catcaaytga 300
agaagacacc accattctga ggccagggag cgagtggggg ccagccacgg ggactcagcc 360
cttgtttctc ttcct 375

<210> 49
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-413-394 : polymorphic base A or G

<220>
<221> misc_binding
<222> 482..500
<223> 10-413-394.mis1

<220>
<221> misc_binding
<222> 502..520
<223> 10-413-394.mis2, complement

<220>
<221> primer_bind
<222> 108..125
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 539..556
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-413-394 potential probe

<400> 49
tgtgatttgt gtaccaattg cctgggtcat tgcgtggcac atcacaggcc atctataagt 60
ggcagctata acaatcacca tcacatttat gtacaaaatt cagaaatatc gaatctatgt 120
gtggcaaata tgaacattaa aaaatacaat gaaaatgtca gtctgaatca tacatagtat 180
ttggagcaaa tagcgactta ttttgctgct atttgcattt cctttcccag ttctcaaaag 240
tctatggtcc tgtgttcacc gtgtattttg gcatgaatcc catagtggtg tttcatggat 300
atgaggcagt gaaggaagcc ctgattgata atggagagga gttttctgga agaggcaatt 360
ccccaatatc tcaaagaatt actaaaggac ttggtaggtg cacatatttc tgtgtcagct 420
ttggtaactg gggtgagggg gatggaaaac agagccctaa aaagcttctc agcagagctt 480
agcctatctg catggctgcc ragtgttgca gcactttctt ccttggctgt gaattctccc 540
agtttctgcc ccttttttta ttaggaatca tttccagcaa tggaaagaga tggaaggaga 600
tccggcgttt ctccctcaca accttgcgga attttgggat ggggaagagg agcattgagg 660
accgtgttca agaggaagct cactgccttg tggaggagtt gagaaaaacc aagggtgggt 720
gactctactc tgcgtcattg accttaacag ttacctgtct tcactagtga cgtccttgga 780
aacatttcag ggtggccag gtcttcattg cgcatcctgg ttgtcagccc tcaggtggtg 840
gagggagatt tgaagcacag agacaaggga ggttttgtgt atctgtgctt tgcctgtata 900
aatgtgttgg ttcatagggt gtaggaataa aaggtcattt aatcctattt tctgctcaat 960
tttgtttcct tgttttcaaa tcagaaatta taaataaggg t 1001

<210> 50
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-414-243 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 10-414-243.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-414-243.mis2, potential complement

<220>
<221> primer_bind
<222> 259..276

<223> upstream amplification primer

<220>
<221> primer_bind
<222> 592..609
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-414-243 potential probe

<220>
<221> misc_feature
<222> 981
<223> n=a, g, c or t

<400> 50
atgaaaatgt cagtctgaat catacatagt atttggagca aatagcgact tattttgctg 60
ctatttgcat ttcctttccc agttctcaaa agtctatggt cctgtgttca ccgtgtattt 120
tggcatgaat cccatagtgg tgtttcatgg atatgaggca gtgaaggaag ccctgattga 180
taatggagag gagtttctg gaagaggcaa ttccccaata tctcaaagaa ttactaaagg 240
acttggtagg tgcacatatt tctgtgtcag ctttggtaac tggggtgagg gggatggaaa 300
acagagccct aaaaagcttc tcagcagagc ttagcctatc tgcatggctg ccaagtgttg 360
cagcactttc ttccttggct gtgaattctc ccagtttctg cccctttttt tattaggaat 420
catttccagc aatggaaaga gatggaagga gatccggcgt ttctccctca caaccttgcg 480
gaattttggg atggggaaga rgagcattga ggaccgtgtt caagaggaag ctcactgcct 540
tgtggaggag ttgagaaaaa ccaagggtgg gtgactctac tctgcgtcat tgaccttaac 600
agttacctgt cttcactagt gacgtccttg gaaacatttc aggggtggcc aggtcttcat 660
tgcgcatcct ggttgtcagc cctcaggtgg tggagggaga tttgaagcac agagacaagg 720
gaggttttgt gtatctgtgc tttgcctgta taaatgtgtt ggttcatagg gtgtaggaat 780
aaaaggtcat ttaatcctat tttctgctca attttgtttc cttgttttca aatcagaaat 840
tataaataag ggtcttgagt tcatttttga agagttaaag aaggtttccc ccatagcata 900
aatctgcatt acctccacca gaacatttca ccagagaaca cttggaaagt ggacatggtg 960
aaagtgacct catcacactt natgaaatat gaaccaagtt a 1001

<210> 51
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-416-273 : polymorphic base A or T

<220>
<221> misc_binding
<222> 482..500
<223> 10-416-273.mis1

<220>
<221> misc_binding
<222> 502..520
<223> 10-416-273.mis2, complement

<220>
<221> primer_bind
<222> 229..246
<223> upstream amplification primer

<220>
<221> primer_bind

<222> 630..649
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-416-273 potential probe

<220>
<221> misc_feature
<222> 619,997
<223> n=a, g, c or t

<400> 51
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aaataatgta ttacttaaat ttgtattgtc atatatgcta atttatagaa atgtacttat     60
gcactgtaat gactagtttg taggagagtg gtatgtatct atattatggt aattcttttt    120
atatggctgg ttgtacttct ggacatgtaa ctcatgtttg taatgttgct gggattttta    180
tatcatgtta atgtggccat gaattgctat gacaaatgtt ccatatatct tcgtttccat    240
cagttctttc ttgtgtcttg tcagctaaag tccaggaaga gattgatcat gtaattggca    300
gacacaggag cccctgcatg caggatagga gccacatgcc ttacactgat gctgtagtgc    360
acgagatcca gagatacagt gaccttgtcc ccaccggtgt gccccatgca gtgaccactg    420
atactaagtt cagaaactac ctcatcccca aggtaagctt gtttctctta cactatattt    480
ctgtacttct gaaatttcca wagtgctggt ttggttccaa ccctctaaca acacaagatg    540
agagaagtgc aaaactcata catgtggcag cttgatggac tttctgctat tttgtttggg    600
gctataaaga tttataaang ctaggtctcc ttaataggct gctcttaggt gttacacttt    660
caaataattg ttgaaaatat cagtgtgtca atttcccaaa acactcttct gagattttta    720
tcaaagtgac attcattgtg tagttcgata tggaaagact taacatgttc atgcattgaa    780
ttttttaatt catgaatatg gttatgctcc caacttattg agctttattc tattttctca    840
gtaatgtctt attttcagtg cagtggttta caactctttt attaggtttt tcctagataa    900
ttaatatttt gttgtgttat aattttttaa ttttttttta tttctttgta attggtataa    960
gtaattgtat tcaattatac tattctgatg accttanatc t                       1001
```

<210> 52
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-418-177 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 10-418-177.mis1, potential

<220>
<221> misc_binding
<222> 502..520
<223> 10-418-177.mis2, complement

<220>
<221> primer_bind
<222> 325..342
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 659..676
<223> downstream amplification primer, complement

<220>

<221> misc_binding
<222> 489..513
<223> 10-418-177 potential probe

<220>
<221> misc_feature
<222> 68,174,203,619,885,890,897,907,918
<223> n=a, g, c or t

<400> 52
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ggttgtcatc ccagatgaca tcatattaaa atagattaca tgtttattta caaaagttct     60
atgaacanga tactctggac atttcaagtg tcaacagaga cttccatttt aaaccataat    120
ctacataatc aaaatacaag atgtgtcaaa tttgaagtga tgaaatagag cggncaaatg    180
aggccagaaa agggcatcca aancttgatg atctggagaa cacattcaga aggttgcaca    240
caagtatcca agatgtaaga cttcaaatgt gattggaaag ctctttagca agcttccacc    300
actggcctta agctcatcca tgtaaattac tgtgtctggc tggacctgag tttcctcatc    360
tatagatcaa cgttatggcg ctacgtgatg tccactactt ctcctcactt ctggacttct    420
ttataaatca gattatctgt tttgttactt ccagggcaca accataatgg cattactgac    480
ttccgtgcta catgatgaca ragaatttcc taatccaaat atctttgacc ctggccactt    540
tctagataag aatggcaact ttaagaaaag tgactacttc atgcctttct cagcaggtaa    600
tagaaactcg tttccattnt gtatttaaag gaaagagaga actttttgga attagttgga    660
atttacatgg cacctcctct ggggctggta gaattgctat ttgtccatga tcaagagcac    720
cactcttaac acccatgtgc tccaccctca caatacacca tcattattgg gccagatagc    780
ggggcttgca ggagttaact ctgttgttcc caattgagaa aatgaacatc ttggtttgac    840
tgaactctgc cactagatac atcactaagg cacccaagag ctccntcctn agaaggntaa    900
aattcantct gatctttncc ttacctgcct tgacaaatgt atctaagtcc acaactgcat    960
tgagtgtctt ctacatggtg tctgtcacct cccaggctga g                        1001
```

<210> 53
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-665-315 : polymorphic base T or C

<220>
<221> misc_binding
<222> 502..521
<223> 12-665-315.mis1, potential complement

<220>
<221> misc_binding
<222> 482..500
<223> 12-665-315.mis2

<220>
<221> primer_bind
<222> 795..815
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 357..377
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-665-315 potential probe

<220>
<221> misc_feature
<222> 175,181..182,195,215,227,238,245,652,747
<223> n=a, g, c or t

<400> 53
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tatcagctaa agtccaggaa gagattgaac gtgtgattgg cagaaaccgg agcccctgca     60
tgcaagacag gagccacatg ccctacacag atgctgtggt gcacgaggtc cagagataca    120
ttgaccttct ccccaccagc ctgccccatg cagtgacctg tgacattaaa ttcangaaac    180
nntatctcat tcccnaaggt aagtttgttt ctccntacac tgcaacntcc atgttttncg    240
aagtnccccca aattcatagt atcattttta aacctctacc atcaccgggt gagagaagtg   300
cataactcat atgtatggca gtttaactgg actttctctt gtttccagtt tggggctata    360
aaggtttgta acaggtccta gtgtctggca gtgtgtgttc tccagattta ttatctttct    420
tcaagattgg tttggctact cttaggtgct tatatttcca aataattttt aaaggtatta    480
gtttgtcaat ttcccaaaac yttgggctgg aatttctggc agggtgacac taaatttata    540
ggctagtttg gaaagaactg aatcttgaca cgttgaggct ttccattcct gaatataatt    600
atgcttccaa tttgtttggg gtttctttta tttaaccagg aatgttgtga antttgttgt    660
catggctttc gagtctttgg ttttccctag ataattaata tttttgttgt agaacataaa    720
tagtttttat cattctgatg atgttanatc tgtcaacttt gctaaattta ctagtcacta    780
ttcgtaattt atttctggat tcattgtaat ttctgtgtat attatactgt atctgagtta    840
atattgtttt atttcttatt ttccatttct catgggctta atgtctcttt atcgcattca    900
ttattgcatt agctagaatt tctaggagag cattgaatag aattggtgac agtggggatc    960
cttgtttctc atttctaatc tgcaggaagc agtggaagtt t                       1001
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<210> 54
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-666-324 : polymorphic base A or C

<220>
<221> misc_binding
<222> 482..500
<223> 12-666-324.mis1

<220>
<221> misc_binding
<222> 502..521
<223> 12-666-324.mis2, potential complement

<220>
<221> primer_bind
<222> 186..205
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 621..641
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-666-324 potential probe

<400> 54
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gcatactttt ccatttttaa gatccaccat aatttattta caacctccag taaagttttg     60
tttcaaatct tttatgaata atcataaaat aagcattcat atatatagta attaatatat    120
accttcagtg atatccatta atactcaaga agtgaaactg tttgaaggat ggaggtgttt    180
```

atatacattt ctatgaatat cgtcccattg gctttaaaag agagtaaaca aattcacacg 240
ctcctttatg cccacattca ttcattcatt aagtagtcat taatttatct agtatctatt 300
gagccaatat cttctaaaca gtgtttcagg tgtctggaat tcattagtga gccaaataaa 360
gttctctgct catataaaac atgtatttta gggatgaaac ataaacaata aaaataaatg 420
cagagaatta gcaaagttgt tagccacttc tactttccag tcagattgcc cttgttcaac 480
tgttggctct gacacttaaa magctgtgtg accttgaaca agatacttaa cagatcatca 540
gtgcaattgt ttggttgttc aaattggtat aataataata tggtaggcta aataatgtct 600
tgacataaag agattaagct ggtgggtttc atgtaatcac aagggtcttt acattagtgt 660
taaatatagt gaaccccaag tttatcttca aagaatcagt atgtcagtat gtgcatctat 720
cttattgttt gattctccat tttaaagttt aacttcttaa ttctctttgc ccccttgctt 780
ccagtttcag taaacaactt tcttaccagt cctaataaat agttcacatc tgttcccctg 840
gtcacctgct ttgaccctag tcacccctgg tcacctgctc tatcctgact catcctgagc 900
caccagttct gtaaccgccc ttcccaccaa actacttacc ccaccactct ggctcatact 960
cctgctgttt tttaaaagag ccaattggaa ttagcttaga c 1001

<210> 55
<211> 436
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 155
<223> 10-72-155 : polymorphic base A or G

<220>
<221> misc_binding
<222> 135..154
<223> 10-72-155.mis1, potential

<220>
<221> misc_binding
<222> 156..175
<223> 10-72-155.mis2, potential complement

<220>
<221> primer_bind
<222> 1..20
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 417..436
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 143..167
<223> 10-72-155 potential probe

<400> 55
gtggctgaat aaaagcatac aaatacaatg aaaatatcad kctaaatcag gcttagcaaa 60
tggacaaaat agtaacttcr tttgctgtta wctctrtcta ctttcctagc tctcaaargt 120
ctatggccct gtgttcactc tgtattttgg cctgraaccc atrgtggtgc tgcatggata 180
tgaaghrgtg aaggaagccc tgattgatct tggagaggag ttttctggaa gaggcawttt 240
cccactggct gaaagagcta acagaggatt tggtaggtgt gcawgtgcct gtttcagcat 300
ctgtcttggg gatggggagg atggaaaaca gagacttdca gagctcctcg ggcagagctt 360
ggcccatcca catggctgcc cagtgtcagc ttcctctttc ttgcctgggt ctccctccta 420
gtttcgtttc tcttcc 436

<210> 56
<211> 678
<212> DNA

<213> Homo Sapiens

<220>
<221> allele
<222> 178
<223> 10-76-177 : polymorphic base A or T

<220>
<221> misc_binding
<222> 158..177
<223> 10-76-177.mis1, potential

<220>
<221> misc_binding
<222> 179..198
<223> 10-76-177.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 416..435
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 166..190
<223> 10-76-177 potential probe

<220>
<221> misc_feature
<222> 549,635,642,655,661
<223> n=a, g, c or t

<400> 56
ttacgcatga ggagtaactg ctctctgtgt ttgctatttt caggaaaacg gatttgtgtg 60
gggagaagcc ctggccggca tggagctgtt tttattcctg acctccattt tacagaactt 120
taacctgaaa tctctggttg acccaaagaa ccttgacacc actccagttg tcaatggwtt 180
tgcctctgtg ccgcccttct accagctgtg cttcattcct gtctgaagaa gagcagatgg 240
cctggctgct gctgtgcagt ccctgcagct ctctttcctc tggggcatta tccatctttc 300
actatctgta atgccttttc tcacctgtca tctcacattt tcccttccct gaagatctag 360
tgaacattcg acctccatta cggagagttt cctatgtttc actgtgcaaa tatatctgct 420
attctccata ctctgtaaca gttgcattga ctgtcacata atgctcatac ttatctaatg 480
ttgagttatt aatatgttat tattaaatag agaaatatga tttgtgtatt ataattcaaa 540
ggcatttcnt tttctgcatg ttctaaataa aaagcattat tatttgctga gtcagtttat 600
tagaccttcc ttcttttatg cataatgtag gtcangaaat tnaaagaaaa tagangttcc 660
naggaggcca tgctggtt 678

<210> 57
<211> 718
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 218
<223> 10-76-217 : polymorphic base C or T

<220>
<221> misc_binding

<222> 198..217
<223> 10-76-217.mis1, potential

<220>
<221> misc_binding
<222> 219..238
<223> 10-76-217.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 416..435
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 206..230
<223> 10-76-217 potential probe

<220>
<221> misc_feature
<222> 549,635,642,655,661,708
<223> n=a, g, c or t

<400> 57
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ttacgcatga ggagtaactg ctctctgtgt ttgctatttt caggaaaacg gatttgtgtg     60
gggagaagcc ctggccggca tggagctgtt tttattcctg acctccattt tacagaactt    120
taacctgaaa tctctggttg acccaaagaa ccttgacacc actccagttg tcaatggatt    180
tgcctctgtg ccgcccttct accagctgtg cttcattyct gtctgaagaa gagcagatgg    240
cctggctgct gctgtgcagt ccctgcagct ctctttcctc tggggcatta tccatctttc    300
actatctgta atgccttttc tcacctgtca tctcacattt tcccttccct gaagatctag    360
tgaacattcg acctccatta cggagagttt cctatgtttc actgtgcaaa tatatctgct    420
attctccata ctctgtaaca gttgcattga ctgtcacata atgctcatac ttatctaatg    480
ttgagttatt aatatgttat tattaaatag agaaatatga tttgtgtatt ataattcaaa    540
ggcatttcnt tttctgcatg ttctaaataa aaagcattat tatttgctga gtcagtttat    600
tagaccttcc ttcttttatg cataatgtag gtcangaaat tnaaagaaaa tagangttcc    660
naggaggcca tgctggttct caaaatgata aggacagaaa ggacaaanga ggaagagg      718
```

<210> 58
<211> 834
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 334
<223> 10-76-333 : polymorphic base G or C

<220>
<221> misc_binding
<222> 315..333
<223> 10-76-333.mis1

<220>
<221> misc_binding
<222> 335..354
<223> 10-76-333.mis2, potential complement

<220>

<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 416..435
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 322..346
<223> 10-76-333 potential probe

<220>
<221> misc_feature
<222> 549,635,642,655,661,708,751
<223> n=a, g, c or t

<400> 58
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ttacgcatga ggagtaactg ctctctgtgt ttgctatttt caggaaaacg gatttgtgtg     60
gggagaagcc ctggccggca tggagctgtt tttattcctg acctccattt tacagaactt    120
taacctgaaa tctctggttg acccaaagaa ccttgacacc actccagttg tcaatggatt    180
tgcctctgtg ccgcccttct accagctgtg cttcattcct gtctgaagaa gagcagatgg    240
cctggctgct gctgtgcagt ccctgcagct ctctttcctc tggggcatta tccatctttc    300
actatctgta atgccttttc tcacctgtca tctsacattt tcccttccct gaagatctag    360
tgaacattcg acctccatta cggagagttt cctatgtttc actgtgcaaa tatatctgct    420
attctccata ctctgtaaca gttgcattga ctgtcacata atgctcatac ttatctaatg    480
ttgagttatt aatatgttat tattaaatag agaaatatga tttgtgtatt ataattcaaa    540
ggcatttcnt tttctgcatg ttctaaataa aaagcattat tatttgctga gtcagtttat    600
tagaccttcc ttcttttatg cataatgtag gtcangaaat tnaaagaaaa tagangttcc    660
naggaggcca tgctggttct caaaatgata aggacagaaa ggacaaanga ggaagagggt    720
agggaagcta ttttgggtga gtgttagagt ntacttgagg attggatttg aaagtgagaa    780
actgtgtcca ggggcagctc taacctctag ggaaatattc agaggatcag tcaa          834
```

<210> 59
<211> 995
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-77-316 : polymorphic base A or T

<220>
<221> misc_binding
<222> 481..500
<223> 10-77-316.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-77-316.mis2, potential complement

<220>
<221> primer_bind
<222> 185..203
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 593..610

<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-77-316 potential probe

<220>
<221> misc_feature
<222> 427,513,520,533,539,586,629,762..765,774..776,813
<223> n=a, g, c or t

<400> 59
acctgaaatc tctggttgac ccaaagaacc ttgacaccac tccagttgtc aatggatttg 60
cctctgtgcc gcccttctac cagctgtgct tcattcctgt ctgaagaaga gcagatggcc 120
tggctgctgc tgtgcagtcc ctgcagctct ctttcctctg gggcattatc catctttcac 180
tatctgtaat gccttttctc acctgtcatc tcacattttc ccttccctga agatctagtg 240
aacattcgac ctccattacg gagagtttcc tatgtttcac tgtgcaaata tatctgctat 300
tctccatact ctgtaacagt tgcattgact gtcacataat gctcatactt atctaatgtt 360
gagttattaa tatgttatta ttaaatagag aaatatgatt tgtgtattat aattcaaagg 420
catttcnttt tctgcatgtt ctaaataaaa agcattatta tttgctgagt cagtttatta 480
gaccttcctt cttttatgca waatgtaggt cangaaattn aaagaaaata gangttccna 540
ggaggccatg ctggttctca aaatgataag gacagaaagg acaaangagg aagagggtag 600
ggaagctatt ttgggtgagt gttagagtnt acttgaggat tggatttgaa agtgagaaac 660
tgtgtccagg ggcagctcta acctctaggg aaatattcag aggatcagtc aaagggtgga 720
atggacatta aatgctagaa ttcttatatc cacattggtg tnnnntcctt tttnnnacaa 780
agtcttgctc tgtcacccag gctggagtgc agnggtgtga tctcagctct ctataacctc 840
cgcctcccag gttcaagtga ttctcctgcc tcagcctcct gagtagctgg gattacaggt 900
gcatgccacc acacctggct aatttttgt attttagta cagacgggtt ttcaccgtgt 960
tagccaggat ggtcttaatc tcctgacctt gtgat 995

<210> 60
<211> 442
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 78
<223> 10-155-78 : polymorphic base C or T

<220>
<221> misc_binding
<222> 58..77
<223> 10-155-78.mis1, potential

<220>
<221> misc_binding
<222> 79..98
<223> 10-155-78.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 424..442
<223> downstream amplification primer, complement

<220>
<221> misc_binding

<222> 66..90
<223> 10-155-78 potential probe

<400> 60
accgagctta ttttacccaa aataaggtag tatatttctg ttagagttta gagtttcatg 60
agtcagggac caagttaytg cttttctttg ccctgtataa aggcttctcc aaggcctttg 120
acttacctaa gtactaaatg ttataaaacc aaactcttct gacctctcaa tctagtcaac 180
tggggctgta attattaatg aaattaatgt ttattttgaa aataatttac tagactgaat 240
tacgaaatcc tgaatcattg tacactatca gtaaatattg gtggacccaa ctgaactgaa 300
tgttttgctt gaaatgaaac ctttgagatg cagggcttat gggttctagt cccagctcta 360
gcactagcag acagcatgtt cttggctaag atactgaatc ttcaaggctc agcttcctca 420
ttccggaaat gggtcaattt ta 442

<210> 61
<211> 442
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 104
<223> 10-155-104 : polymorphic base G or C

<220>
<221> misc_binding
<222> 84..103
<223> 10-155-104.mis1, potential

<220>
<221> misc_binding
<222> 105..124
<223> 10-155-104.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 424..442
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 92..116
<223> 10-155-104 potential probe

<400> 61
accgagctta ttttacccaa aataaggtag tatatttctg ttagagttta gagtttcatg 60
agtcagggac caagttattg cttttctttg ccctgtataa aggsttctcc aaggcctttg 120
acttacctaa gtactaaatg ttataaaacc aaactcttct gacctctcaa tctagtcaac 180
tggggctgta attattaatg aaattaatgt ttattttgaa aataatttac tagactgaat 240
tacgaaatcc tgaatcattg tacactatca gtaaatattg gtggacccaa ctgaactgaa 300
tgttttgctt gaaatgaaac ctttgagatg cagggcttat gggttctagt cccagctcta 360
gcactagcag acagcatgtt cttggctaag atactgaatc ttcaaggctc agcttcctca 420
ttccggaaat gggtcaattt ta 442

<210> 62
<211> 772
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 52
<223> 10-156-52 : polymorphic base A or G

<220>
<221> misc_binding
<222> 32..51
<223> 10-156-52.mis1, potential

<220>
<221> misc_binding
<222> 53..71
<223> 10-156-52.mis2, complement

<220>
<221> primer_bind
<222> 1..19
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 401..420
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 40..64
<223> 10-156-52 potential probe

<400> 62
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ttcaaggctc agcytcctca ttccggaaat gggtcaattt tattgtaagc araggtaatt     60
gagagattca aaagggacat gaggtgtaac aattctctgt aaattgttag aatccctgtt    120
aaaaatgacc agtaaagctt tgtgcaactg tgtcttgaca taactttatt tttcttaata    180
aaagaaatgg aaataacctc actagggaat ttagaacaaa tatgatgata tctttaaaga    240
aaatggcttt gcacaagtat tgacattaat gatctagtaa agtgtatctt tctagttgta    300
tttagatcct caactcagta tgtcagctcc tgttaaggtc tatacattgt ggtggttctg    360
tgctgtgggt ccatttagtg atttccctac ctcccatctt ctattgcatc cacaactgtg    420
gttctgtcca taatttcctt tgctttctgt gcattattac atcatatctg aaaatgagaa    480
accaaaaaca atagaaagca gccatgtctg gaggtgactg gggggtcgag aagccctagt    540
ttctcaaacc cttagcacca aatttttccc tcagttacac tgagcgtttc acttctgcag    600
tgatggagaa gggagatccc ttatttcttc tcatgagcat ctctggtgct gtttccctta    660
gagacaaata aggggttcta tttaatgtga agcctgtttt atgaacagaa taaatgtggt    720
gtatattcag aataactaat gtttggaagt ttgttttatt ttgctaaaat tg            772
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<210> 63
<211> 431
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 39
<223> 10-157-39 : polymorphic base C or T

<220>
<221> misc_binding
<222> 20..38
<223> 10-157-39.mis1

<220>
<221> misc_binding
<222> 40..59

<223> 10-157-39.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 412..431
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 27..51
<223> 10-157-39 potential probe

<400> 63
ctgtgggkcc atttagtgat ttccctacct cccatcttyt attgcatcca caactgtggt 60
tctgtccata atttcctttg ctttctgtgc attattacat catatctgaa aatgagaaac 120
caaaaacaat agaaagcagc catgtctgga ggtgactggg gggtcgagaa gccctagttt 180
ctcaaaccct tagcaccaaa tttttccctc agttacactg agcgtttcac ttctgcagtg 240
atggagaagg gagatccctt atttcttctc atgagcatct ctggtgctgt ttcccttaga 300
gacaaataag gggttctatt taatgtgaag cctgttttat gaacagaata aatgtggtgt 360
atattcagaa taactaatgt ttggaagttt gttttatttt gctwaaaatt ggttctcaag 420
gcagctctgg t 431

<210> 64
<211> 431
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 131
<223> 10-157-131 : polymorphic base A or G

<220>
<221> misc_binding
<222> 111..130
<223> 10-157-131.mis1, potential

<220>
<221> misc_binding
<222> 132..150
<223> 10-157-131.mis2, complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 412..431
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 119..143
<223> 10-157-131 potential probe

<400> 64

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tctgtccata atttcctttg ctttctgtgc attattacat catatctgaa aatgagaaac    120
caaaaacaat rgaaagcagc catgtctgga ggtgactggg gggtcgagaa gccctagttt    180
ctcaaaccct tagcaccaaa tttttccctc agttacactg agcgtttcac ttctgcagtg    240
atggagaagg gagatccctt atttcttctc atgagcatct ctggtgctgt ttcccttaga    300
gacaaataag gggttctatt taatgtgaag cctgttttat gaacagaata aatgtggtgt    360
atattcagaa taactaatgt ttggaagttt gttttatttt gctwaaaatt ggttctcaag    420
gcagctctgg t                                                         431
```

<210> 65
<211> 431
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 166
<223> 10-157-166 : polymorphic base A or G

<220>
<221> misc_binding
<222> 146..165
<223> 10-157-166.mis1, potential

<220>
<221> misc_binding
<222> 167..186
<223> 10-157-166.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 412..431
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 154..178
<223> 10-157-166 potential probe

<400> 65

```
ctgtgggkcc atttagtgat ttccctacct cccatcttyt attgcatcca caactgtggt     60
tctgtccata atttcctttg ctttctgtgc attattacat catatctgaa aatgagaaac    120
caaaaacaat agaaagcagc catgtctgga ggtgactggg gggtcragaa gccctagttt    180
ctcaaaccct tagcaccaaa tttttccctc agttacactg agcgtttcac ttctgcagtg    240
atggagaagg gagatccctt atttcttctc atgagcatct ctggtgctgt ttcccttaga    300
gacaaataag gggttctatt taatgtgaag cctgttttat gaacagaata aatgtggtgt    360
atattcagaa taactaatgt ttggaagttt gttttatttt gctwaaaatt ggttctcaag    420
gcagctctgg t                                                         431
```

<210> 66
<211> 431
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 246
<223> 10-157-246 : polymorphic base A or G

<220>
<221> misc_binding
<222> 226..245
<223> 10-157-246.mis1, potential

<220>
<221> misc_binding
<222> 247..266
<223> 10-157-246.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 412..431
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 234..258
<223> 10-157-246 potential probe

<400> 66
ctgtgggkcc atttagtgat ttccctacct cccatcttyt attgcatcca caactgtggt 60
tctgtccata atttcctttg ctttctgtgc attattacat catatctgaa aatgagaaac 120
caaaaacaat agaaagcagc catgtctgga ggtgactggg gggtcgagaa gccctagttt 180
ctcaaaccct tagcaccaaa tttttccctc agttacactg agcgtttcac ttctgcagtg 240
atggaraagg gagatcccttt atttcttctc atgagcatct ctggtgctgt ttcccttaga 300
gacaaataag gggttctatt taatgtgaag cctgttttat gaacagaata aatgtggtgt 360
atattcagaa taactaatgt ttggaagttt gttttatttt gctwaaaatt ggttctcaag 420
gcagctctgg t 431

<210> 67
<211> 581
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 161
<223> 10-159-161 : polymorphic base A or T

<220>
<221> misc_binding
<222> 142..160
<223> 10-159-161.mis1

<220>
<221> misc_binding
<222> 162..181
<223> 10-159-161.mis2, potential complement

<220>
<221> primer_bind
<222> 1..19
<223> upstream amplification primer

<220>
<221> primer_bind

<222> 403..422
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 149..173
<223> 10-159-161 potential probe

<400> 67
aggaattttt tttagggggt ttaatggtaa aggtgtttat atctgctaag gtaatttact 60
tgatatatgt ttggttattt aagatatatg agttatgtta gctatttcat gtttaggctg 120
ctgtattttt agtaggctat attaaatatt tgaaaggatt wcattataaa gaacaaagtc 180
tcctaatctt tgatatagca ttgacatact ttttaaatat acaaggcata gaatatggcc 240
atttctgtta aatcatatat tcccaactgg ttattaatct aagaattcag aattttgagt 300
aattgctttt gcatcagatt atttacttca gtgctctcaa ttatgatggt gcattagaac 360
catctgggtt aacatttgtt ttttattacc aatacctagg ctccaaccaa gtacagtgaa 420
actggaatgt acagagtgga caatggaacg aaggagaaca agaccaaagg acattttatt 480
tttatctgta tcagtgggtc aaagtccttt cagaaggagc atatagtgga cctaggtgat 540
tggtcrmttt atccatcaaa gaggcacaca ccgaattagc a 581

<210> 68
<211> 581
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 162
<223> 10-159-162 : polymorphic base A or C

<220>
<221> misc_binding
<222> 142..161
<223> 10-159-162.mis1, potential

<220>
<221> misc_binding
<222> 163..182
<223> 10-159-162.mis2, potential complement

<220>
<221> primer_bind
<222> 1..19
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 403..422
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 150..174
<223> 10-159-162 potential probe

<400> 68
aggaattttt tttagggggt ttaatggtaa aggtgtttat atctgctaag gtaatttact 60
tgatatatgt ttggttattt aagatatatg agttatgtta gctatttcat gtttaggctg 120
ctgtattttt agtaggctat attaaatatt tgaaaggatt tmattataaa gaacaaagtc 180
tcctaatctt tgatatagca ttgacatact ttttaaatat acaaggcata gaatatggcc 240
atttctgtta aatcatatat tcccaactgg ttattaatct aagaattcag aattttgagt 300
aattgctttt gcatcagatt atttacttca gtgctctcaa ttatgatggt gcattagaac 360
catctgggtt aacatttgtt ttttattacc aatacctagg ctccaaccaa gtacagtgaa 420

actggaatgt acagagtgga caatggaacg aaggagaaca agaccaaagg acattttatt 480
tttatctgta tcagtgggtc aaagtccttt cagaaggagc atatagtgga cctaggtgat 540
tggtcrmttt atccatcaaa gaggcacaca ccgaattagc a 581

<210> 69
<211> 353
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 169
<223> 10-83-169 : polymorphic base C or T

<220>
<221> misc_binding
<222> 150..168
<223> 10-83-169.mis1

<220>
<221> misc_binding
<222> 170..189
<223> 10-83-169.mis2, potential complement

<220>
<221> primer_bind
<222> 1..19
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 336..353
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 157..181
<223> 10-83-169 potential probe

<400> 69
aagtcatact gcttcttact aggtctgtct gggtgggaat gtaacttctt tggacctcaa 60
ttttcttatc tattgataaa agagattgga ctaggtgatt tccatcactt cttcccactc 120
tttgacttct ttataactta gtttgtctgt tttgctattt tcagggcayg accataataa 180
catccctgac ttctgtgctg cacaatgaca aagaattccc caacccagag atgtttgacc 240
ctggccactt tctggataag agtggcaact ttaagaaaag tgactacttc atgcctttct 300
cagcaggtaa tagatattca tttccatctg tccttcaggg cacatgatac ctt 353

<210> 70
<211> 425
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 152
<223> 10-84-152 : polymorphic base C or T

<220>
<221> misc_binding
<222> 132..151
<223> 10-84-152.mis1, potential

<220>

<221> misc_binding
<222> 153..172
<223> 10-84-152.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 406..425
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 140..164
<223> 10-84-152 potential probe

<220>
<221> misc_feature
<222> 413
<223> n=a, g, c or t

<400> 70
```
gaacaaatcc cctatgtctc ttattttcag gaaaacggat gtgtatggga gagggcctgg    60
cccgcatgga gctgttttta ttcctgacca ccattttgca gaactttaac ctgaaatctc   120
aggttgaccc aaaggatatt gacatcaccc cyattgccaa tgcatttggt cgtgtgccac   180
ccttgtacca gctctgcttc attcctgtct gaagaagggc agatagtttg gctgctcctg   240
tgctgtcacc tgcaattctc ccttatcagg gccattggcc tctcccttct ctctgtgagg   300
gatattttct ctgacttgtc aatccacatc ttcccattcc ctcaagatcc aatgaacatc   360
caacctccat taaagagagt ttcttgggtc acttcctaaa tatatctgct atnctccata   420
ctctg                                                               425
```

<210> 71
<211> 425
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 243
<223> 10-84-243 : polymorphic base C or T

<220>
<221> misc_binding
<222> 224..242
<223> 10-84-243.mis1

<220>
<221> misc_binding
<222> 244..263
<223> 10-84-243.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 406..425
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 231..255
<223> 10-84-243 potential probe

<220>
<221> misc_feature
<222> 413
<223> n=a, g, c or t

<400> 71
gaacaaatcc cctatgtctc ttattttcag gaaaacggat gtgtatggga gagggcctgg 60
cccgcatgga gctgttttta ttcctgacca ccattttgca gaactttaac ctgaaatctc 120
aggttgaccc aaaggatatt gacatcaccc ccattgccaa tgcatttggt cgtgtgccac 180
ccttgtacca gctctgcttc attcctgtct gaagaagggc agatagtttg gctgctcctg 240
tgytgtcacc tgcaattctc ccttatcagg gccattggcc tctcccttct ctctgtgagg 300
gatattttct ctgacttgtc aatccacatc ttcccattcc ctcaagatcc aatgaacatc 360
caacctccat taaagagagt ttcttgggtc acttcctaaa tatatctgct atnctccata 420
ctctg 425

<210> 72
<211> 425
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 277
<223> 10-84-277 : polymorphic base A or G

<220>
<221> misc_binding
<222> 257..276
<223> 10-84-277.mis1, potential

<220>
<221> misc_binding
<222> 278..297
<223> 10-84-277.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 406..425
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 265..289
<223> 10-84-277 potential probe

<220>
<221> misc_feature
<222> 413
<223> n=a, g, c or t

<400> 72
gaacaaatcc cctatgtctc ttattttcag gaaaacggat gtgtatggga gagggcctgg 60

```
cccgcatgga gctgttttta ttcctgacca ccattttgca gaactttaac ctgaaatctc    120
aggttgaccc aaaggatatt gacatcaccc ccattgccaa tgcatttggt cgtgtgccac    180
ccttgtacca gctctgcttc attcctgtct gaagaagggc agatagtttg gctgctcctg    240
tgctgtcacc tgcaattctc ccttatcagg gccattrgcc tctcccttct ctctgtgagg    300
gatattttct ctgacttgtc aatccacatc ttcccattcc ctcaagatcc aatgaacatc    360
caacctccat taaagagagt ttcttgggtc acttcctaaa tatatctgct atnctccata    420
ctctg                                                                425
```

<210> 73
<211> 425
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 295
<223> 10-84-295 : polymorphic base A or G

<220>
<221> misc_binding
<222> 275..294
<223> 10-84-295.mis1, potential

<220>
<221> misc_binding
<222> 296..314
<223> 10-84-295.mis2, complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 406..425
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 283..307
<223> 10-84-295 potential probe

<220>
<221> misc_feature
<222> 413
<223> n=a, g, c or t

<400> 73

```
gaacaaatcc cctatgtctc ttattttcag gaaaacggat gtgtatggga gagggcctgg     60
cccgcatgga gctgttttta ttcctgacca ccattttgca gaactttaac ctgaaatctc    120
aggttgaccc aaaggatatt gacatcaccc ccattgccaa tgcatttggt cgtgtgccac    180
ccttgtacca gctctgcttc attcctgtct gaagaagggc agatagtttg gctgctcctg    240
tgctgtcacc tgcaattctc ccttatcagg gccattggcc tctcccttct ctctrtgagg    300
gatattttct ctgacttgtc aatccacatc ttcccattcc ctcaagatcc aatgaacatc    360
caacctccat taaagagagt ttcttgggtc acttcctaaa tatatctgct atnctccata    420
ctctg                                                                425
```

<210> 74
<211> 424
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 43
<223> 10-85-43 : polymorphic base C or T

<220>
<221> misc_binding
<222> 24..42
<223> 10-85-43.mis1

<220>
<221> misc_binding
<222> 44..63
<223> 10-85-43.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 405..424
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 31..55
<223> 10-85-43 potential probe

<400> 74
```
gtttcttggg tcacttccta aatatatctg ctattctcca taytctgtat cacttgtatt    60
gaccaccaca tatgctaata cctatctact gctgagttgt cagtatgtta tcactagaaa   120
acaaagaaaa atgattaata aatgacaatt cagagccatt tattctctgc atgctctaga   180
taaaaatgat tattatttac tgggtcagtt cttagatttc tttcttttga gtaaaatgaa   240
agtaagaaat gaaagaaaat agaatgtgaa gaggctgtgc tggccctcat agtgttaagc   300
acaaaaaggg agaaaggtaa gagggtagga aagctgtttt agctaaatgc cacctagagt   360
tattggaggt ctgaatttgg aaaaaaaaac tatgtccagg agcagctgta acvtgtaggg   420
aaat                                                                424
```

<210> 75
<211> 424
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 117
<223> 10-85-117 : polymorphic base G or T

<220>
<221> misc_binding
<222> 97..116
<223> 10-85-117.mis1, potential

<220>
<221> misc_binding
<222> 118..136
<223> 10-85-117.mis2, complement

<220>
<221> primer_bind
<222> 1..18

<223> upstream amplification primer

<220>
<221> primer_bind
<222> 405..424
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 105..129
<223> 10-85-117 potential probe

<400> 75
```
gtttcttggg tcacttccta aatatatctg ctattctcca tactctgtat cacttgtatt     60
gaccaccaca tatgctaata cctatctact gctgagttgt cagtatgtta tcactakaaa    120
acaaagaaaa atgattaata aatgacaatt cagagccatt tattctctgc atgctctaga    180
taaaaatgat tattatttac tgggtcagtt cttagatttc tttcttttga gtaaaatgaa    240
agtaagaaat gaaagaaaat agaatgtgaa gaggctgtgc tggccctcat agtgttaagc    300
acaaaaaggg agaaaggtaa gagggtagga aagctgtttt agctaaatgc cacctagagt    360
tattggaggt ctgaatttgg aaaaaaaaac tatgtccagg agcagctgta acvtgtaggg    420
aaat                                                                 424
```

<210> 76
<211> 424
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 320
<223> 10-85-320 : polymorphic base A or T

<220>
<221> misc_binding
<222> 300..319
<223> 10-85-320.mis1, potential

<220>
<221> misc_binding
<222> 321..340
<223> 10-85-320.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 405..424
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 308..332
<223> 10-85-320 potential probe

<400> 76
```
gtttcttggg tcacttccta aatatatctg ctattctcca tactctgtat cacttgtatt     60
gaccaccaca tatgctaata cctatctact gctgagttgt cagtatgtta tcactagaaa    120
acaaagaaaa atgattaata aatgacaatt cagagccatt tattctctgc atgctctaga    180
taaaaatgat tattatttac tgggtcagtt cttagatttc tttcttttga gtaaaatgaa    240
agtaagaaat gaaagaaaat agaatgtgaa gaggctgtgc tggccctcat agtgttaagc    300
```

acaaaaaggg agaaaggtaw gagggtagga aagctgtttt agctaaatgc cacctagagt 360
tattggaggt ctgaatttgg aaaaaaaaac tatgtccagg agcagctgta acvtgtaggg 420
aaat 424

<210> 77
<211> 352
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 121
<223> 10-86-121 : polymorphic base A or C

<220>
<221> misc_binding
<222> 102..120
<223> 10-86-121.mis1

<220>
<221> misc_binding
<222> 122..141
<223> 10-86-121.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 334..352
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 109..133
<223> 10-86-121 potential probe

<400> 77
aagggagaaa ggthagaggg taggaaagct gttttagcta aatgccacct agagttattg 60
gaggtctgaa tttggaaaaa aaaactatgt ccaggagcag ctgtaacctg tagggaaata 120
mtggaacaat catccataag agggatgaac attaagtgtt tgaattcatg ctctgctttt 180
gtgttactgt aaacacaaga tcaagatttg gataatcttt ttcctttgtg tttccaactt 240
agatcatgtc taaatatatg ctttcatatg gctaatcatg tgttaatgac tgttattttt 300
ctcttccaaa caagagcaaa atctccagaa atcctcacca ggctttattt tt 352

<210> 78
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-244-275 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-244-275.mis1, potential

<220>

<221> misc_binding
<222> 502..521
<223> 12-244-275.mis2, potential complement

<220>
<221> primer_bind
<222> 228..247
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 660..678
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-244-275 potential probe

<400> 78
```
atcacgttct gtccagtgtc tgcctattcc cttcttcttt ttttcttccc ttgatgccct     60
tttatcacat gcattgtctc agacccttcg aatatgtgct cataaatgca tggcatcatc    120
tccttcccac atcgattcac tttcaattaa aagccaaaac tctttcattt caactttgga    180
tttaacatgc ttttgaaaga agggttgaga aatatagaga aacagattgg gaaaccatgc    240
tctgctgttt cttttttttta aactttctat gtaagtgtgg aatttttcat tctgttttat   300
tattaacttt aagccaagac tttttaatag aaggatatat aaatacatct ttgtctatac    360
atttctgctg aatttgaaga aatgctgaat attcttaaac cattgtgttc cctggtgggc    420
tgatggactg tgattttata aggtggcctc agccaactgc agcagctgtt ccctgtcaga    480
ggggctagag gtttggcaag rgcggtggaa gaggtgcagt ggtgtgttcg ttcactagaa    540
gcatcaggga gaaggttttg cctgtttgta tttcatcttc tctcatcaag tcctcagaaa    600
ccacagtgct gtctgcaggg tgctgtggat ctggcatggc ccatacaggc aacatgactg    660
agtagaaagg acacacagct ctggatgtcc ttgggcccca cagcaactgc ccttgaaaca    720
tttagtcctt gtgagcattt gatgatttac ttgccttcaa ttttccatgg acctaatact    780
ctttataaag ggaaatattt taaacctatg aaacattgtg gagaatggca tgggaaatac    840
ccatgtatgc accacccagc ttaacaaatg ctctcctgtc atttctaacc acaatctctt    900
tgaagagctc ttttgtcttt caatctctct tccctgtttg gcccacatta cccttcatcg    960
tatgaagact tggatggctc ctgtgtcaga ctcttgctgt g                       1001
```

<210> 79
<211> 950
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 450
<223> 12-251-153 : polymorphic base A or C

<220>
<221> misc_binding
<222> 431..449
<223> 12-251-153.mis1

<220>
<221> misc_binding
<222> 451..470
<223> 12-251-153.mis2, potential complement

<220>
<221> primer_bind
<222> 298..318
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 806..826
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 438..462
<223> 12-251-153 potential probe

<220>
<221> misc_feature
<222> 52,54,100
<223> n=a, g, c or t

<400> 79
taggaagctg agagaaaagg atcttctccc ctgtgcacag gagccaggaa tnanttatct 60
gttacattgt ccccttggat attccaaaag aataatacan tgtgtagaaa gaaaaaataa 120
aaacctgatt gtactaaagt tttgagcata gacgttatgg agtggtggga ggggaaggtg 180
tttgatagct gttggctggc agtgactggg gcaggaaagt tacaatgagg aagttggaat 240
aacttcaatc ccttcattat tttgctgagg ataccaccaa aatatgaaat attaaacctt 300
cccaccactt ctaatttctt ttctccaatc ttaaatttta aaagactctg taaaggctat 360
aggtagggca atgctattgt ttgttgtctg aactggaatg taatttgaat tatgctggaa 420
caacatgtgt aagctgagcc tgtcctgggm agactgggga catgtggtca ctcagctatg 480
ggatgccccg atcaactttg gagtgatcta tttgtttaat caatatcact gttagttctt 540
acttttacaa aaataatctg ccctcagagc aacctcagat cccaggagtt ggggaaaagc 600
aggtgtttca ggaggcttat cagggagtgc agcggagaca tgacgttcac agcaagtctg 660
aacagggtgt ggctgttcta taaagtgctg aagagacatc agctctgggc gtagactgtg 720
gggtctggca atgtcaaatt tattgattgg ccgagaaaga gttaattatt ttattcttgt 780
cctgcagaag cacagtgttg acacaccttt taccatccac actcaacaca aactactgta 840
attgtctgat tattgggtct gtgtctccct atgactgagg tccttgagct cagaggtggg 900
tctaactcac cttagtgtct ccatcactcc cagcacaggg ccagctgcat 950

<210> 80
<211> 746
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 246
<223> 12-254-115 : polymorphic base A or T

<220>
<221> misc_binding
<222> 226..245
<223> 12-254-115.mis1, potential

<220>
<221> misc_binding
<222> 247..266
<223> 12-254-115.mis2, potential complement

<220>
<221> primer_bind
<222> 132..152
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 586..603
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 234..258
<223> 12-254-115 potential probe

<400> 80
ctgccacaat ctcctgagtc cagacaatct agagcagaag ggtagactga ggaaaatata 60
cacagtataa aaaagtaaca aaatcaaaac ctgaaacaaa gatcaacatc caataaatgc 120
ttctgaataa agggagagta gataagaact ggattttaat cccaacactg ccatttacca 180
gctggccaat actgagctag ttactctaaa gagttcagtt ttctcatttg tacaaatagg 240
atttgwcttt ccatctcact gagttgtgat gagagtcata tgcaacagca tatgaagagg 300
ctagcaaaag gtatttaaca agcgttcaac attctcatga tgacatgaat aacactgtac 360
atacaacata ccaacttgat aaatacacag cacagttaat agctgagggc agagttatgg 420
ttgggaagag agagagtgca acataggcag agtgaggggg gattcccaca attttctaag 480
acagaaaagt gggggaatca gtagttactg gaaagaatag gcaatgcctg actggataga 540
aaaagattct atgcctttgt caaatttcac aaaagtgact taagcctata ctgcgggatg 600
ttcacactac gtccctttag tgcagttacg gtacttcagg ctgcaagtaa ccaaatacaa 660
ctaaaattgt cttatacaat aagggcgtaa ttatctcata taacaagaag cttggcatga 720
aggaaatttc aacaatttca caacgg 746

<210> 81
<211> 811
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 311
<223> 12-254-180 : polymorphic base A or G

<220>
<221> misc_binding
<222> 292..310
<223> 12-254-180.mis1

<220>
<221> misc_binding
<222> 312..331
<223> 12-254-180.mis2, potential complement

<220>
<221> primer_bind
<222> 132..152
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 586..603
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 299..323
<223> 12-254-180 potential probe

<400> 81
ctgccacaat ctcctgagtc cagacaatct agagcagaag ggtagactga ggaaaatata 60
cacagtataa aaaagtaaca aaatcaaaac ctgaaacaaa gatcaacatc caataaatgc 120
ttctgaataa agggagagta gataagaact ggattttaat cccaacactg ccatttacca 180
gctggccaat actgagctag ttactctaaa gagttcagtt ttctcatttg tacaaatagg 240
atttgtcttt ccatctcact gagttgtgat gagagtcata tgcaacagca tatgaagagg 300
ctagcaaaag rtatttaaca agcgttcaac attctcatga tgacatgaat aacactgtac 360
atacaacata ccaacttgat aaatacacag cacagttaat agctgagggc agagttatgg 420

ttgggaagag agagagtgca acataggcag agtgaggggg gattcccaca attttctaag 480
acagaaaagt gggggaatca gtagttactg gaaagaatag gcaatgcctg actggataga 540
aaaagattct atgcctttgt caaatttcac aaaagtgact taagcctata ctgcgggatg 600
ttcacactac gtccctttag tgcagttacg gtacttcagg ctgcaagtaa ccaaatacaa 660
ctaaaattgt cttatacaat aagggcgtaa ttatctcata taacaagaag cttggcatga 720
aggaaatttc aacaatttca caacggcaac aaaaactctg tttcttctac ctttccacca 780
ttcctgtgtt ctcagttcca atatggctgc t 811

<210> 82
<211> 999
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 499
<223> 12-265-300 : polymorphic base T or C

<220>
<221> misc_binding
<222> 479..498
<223> 12-265-300.mis1, potential

<220>
<221> misc_binding
<222> 500..519
<223> 12-265-300.mis2, potential complement

<220>
<221> primer_bind
<222> 779..798
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 308..328
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 487..511
<223> 12-265-300 potential probe

<220>
<221> misc_feature
<222> 427,494,669..670,679,772,874,944
<223> n=a, g, c or t

<400> 82
taataatgtg ttttggggta agcctactca tattctcaac ctgtctgcag tagtcgttag 60
aatctgaact tcctgaagtt catgtgcaaa gttgagttaa ttgtttaata ttcaacaagg 120
attatgccag taagatggta ggaaaatatt agatatgtgt catcactgct ggtattattt 180
aaactgcaac atattttagc tggctgctga tctcagccac catgcctgca ttttatctct 240
gtctcgtggt ctgcaacctt ggaagctttg aacttagctc atagaatcct gggcatcaag 300
aacatgtggt tctaatggct agatagggaa tgagagtaaa aggattttgc ccacggtcac 360
gtgagtaaac aacagatttg gaggggtctg gactactgtg atgacttcat tctgacaata 420
tgttccnagt tgtcctttca tttcctccta atcacatgtc tggtctgatc tggctgtttc 480
ccaccttcca attncctgyc ttctccaatg ctcccttccg taggtcactc tgtggctcag 540
agaccctgct tagcaagcgc ccaacctttc aattatttgt tcagtaaaac ttgaactcat 600
gtctcccctt cttgataaaa agaaaatacg ttatgtaatg tcgggttact ctataactct 660
tgtcctgtnn ctctcggcna actactgaac taactgtttt catattgagc aaacgtttat 720
ggaaggactg ccaagagtca ggtactaggc ttggtaatat tccccgttct cntctagtca 780
aagccaacac cagccagact tgcagatcta ggtcccaagc ccactgcaga tcacaggcca 840

```
gggtctggtc tcctctgagc tcctttggga gggnaaagac agaattatta acacccattt    900
tgtagattag gcaactgagg ctgaggaagt ttaaataact cagnacaggg cctgcacgtc    960
agtcatattc caaggatccc tactcactgt cttctctct                           999

<210> 83
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-271-118 : polymorphic base T or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-271-118.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-271-118.mis2, potential complement

<220>
<221> primer_bind
<222> 598..618
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 122..141
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-271-118 potential probe

<220>
<221> misc_feature
<222> 205,525,542,571,657
<223> n=a, g, c or t

<400> 83
gactgagtcc gaaaaggagt ctgcaaaggg agataggggt gggtcagttt tataggactg     60
gggtaagcag tggaaagttg cagttaaagg aagttatcta ttgtcagcag aggagggggt    120
cacaaggtgc atggtaggga gatcataaga ctcattgtcc agaagaagaa tgtcacgagg    180
tcgatcaatc gatcagttgg ggcangggca gtaacaagtc ataatggaac gttgtaaggt    240
tggtcaatca gttaagacag gagctggctg tttcacctat ttgtagtttt tggttgcctc    300
aggccatctg gatgtaccca tgcaggcttg ggctaagagg cctgaaaccc accactttcc    360
catgtcaaat ctttagtaga tgtacccccca agatacacat tcctcggacc ttcttttcca   420
tagttaaaac ttcacccctg aaatgtagaa acaggaaggt tttttttta agtttcagtg    480
caaactcgga gcaagtgtca yaattttctg tctccgatgt gtagnaggtg acatttctc    540
angaactttc acgttaagct ggaaaactgg naaagcgagt ccactttgtc attctgtcac    600
tcactcattt tctcactcaa caaacatgcc tcacacttat ctaaatctgc tagactnaaa    660
agaggtccct ggtgtctgta actttctaat tctgctagaa ttctagagtg agctcatgaa    720
ataaatgaaa aggatgaaga acaaagagaa aaaagactgc acgttccctt ctggcgctca    780
ctcacattcc ctcagcctca gtttctccac atgcccctag aggtgatcat tcaaggattt    840
atgagatttt agagacaaca catgaaaaag caaagagaca tcagaaagac aaggagttac    900
ttagtattta tacacaagga taagacattc agtatcgaca acacttaaag aaaattcaag    960
agtgatttta aatttcccat ttcaaatacc tcctctattt t                       1001
```

<210> 84
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-272-112 : polymorphic base A or C

<220>
<221> misc_binding
<222> 482..500
<223> 12-272-112.mis1

<220>
<221> misc_binding
<222> 502..521
<223> 12-272-112.mis2, potential complement

<220>
<221> primer_bind
<222> 390..409
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 768..788
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-272-112 potential probe

<400> 84
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aagaggggcc caacttgtaa tcataggagc ttatgctatt ttaatgccat ccatcagact     60
acaatcaatt accactcatc tagctttttg tccatctctc attcttgtac atcctgagat    120
agtcaattct gagaactgta gcctagatct atcacctgat gcctctcaaa gatataatcc    180
gtgcttctca agctaggcta tgcacacaaa tcactgcatc ttgtgaaagt tcagattttg    240
aatcagtagt tcaagggtgg ggtttgagat tttgcatttc taatgagctc tcagatgctt    300
ctgacccatg gaccacactt tgaataccaa gaagtggtct gtagaccaat attggtccct    360
taagttccct caaacatatc ttcgggaaac gtcctttgat tttccctaca tttaaccatt    420
agtgttgcaa attctctcaa agtttgtcaa gatatattgt agctaaaata aattacattt    480
ttcttggggg agagtactac mtcatattaa cttacaataa agtactttta ggatcattca    540
aggaacacac ccataacact gagtatgtta tgcggaaatg ctctctctgg aaattacaca    600
gctgtgcagg tggcgggggt ggcatgagga ggagtggatg gcccacattc tcgaagacct    660
tggggaaaac tggattaaaa tgatttgcct tattctggtt ctgtaagata cacatcagaa    720
tgaaaccacc cccagtgtac ctctgaattg cttttctatt cttttccctt agggatttga    780
gggcttcact tagatttctc ttcatctaaa ctgtgatgcc ctacattgat ctgatttacc    840
taaaatgtct ttcctctcct ttcagctctg tccgatctgg agctcgtggc ccaatcaatt    900
atctttattt ttgctggcta tgaaaccacg agcagtgttc tctccttcat tatgtatgaa    960
ctggccactc accctgatgt ccagcagaaa ctgcaggagg a                       1001
```

<210> 85
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 10-216-182 : polymorphic base A or G

<220>
<221> misc_binding
<222> 483..502
<223> 10-216-182.mis1, potential

<220>
<221> misc_binding
<222> 504..522
<223> 10-216-182.mis2, complement

<220>
<221> primer_bind
<222> 323..339
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 800..819
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 10-216-182 potential probe

<220>
<221> misc_feature
<222> 76,80,96,319,399,556,578,667,676,731,752,759,914,933
<223> n=a, g, c or t

<400> 85
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tgctatcctt cccccctctc cccaccccac aacaggcccc agtgtgtgat gttccccttc     60
ctgtgtccat gtgttnctcn attgtatatt tttttnaaat ctaccacatc aaggcacctc    120
tttttcatgt tgcccatggt ttaggtgaac ataaagacag agctcgtctg aggcaacata    180
cagtccaaca aagccacctg cctctctgtc tccactctct ctctacactg cacgcgtgct    240
aggtgttgat cctgtctatt ccagtggaag aacaggttcc gtaccatgtg gagaatttgc    300
atgtaaaagg agactgggna tatacaggct ggagaccaca tcaggtggct gggcatgtgg    360
gataaatcct attgagcatc tgtcataggg cctgtcacnt tagtagacag tcactaaata    420
tttgttaaat acatgatgcc tgtttaacac attttctaca accatggaga cctccacaac    480
tgatgtagga caaaatcttt ctrctttgaa ctctagcctt tcgggccagt gggatttatg    540
aaaaatgcca tctctnatag ctgaggatga agaatggnaa gagaatacga tcattgctgt    600
ctccaacatt caccagcgga aaactcaagg aggtatgaaa ataacttggg ttttaattag    660
aaacttnaaa gaatgnaatc aggtggggac aggtagaaag taagatcaga gttcctttcc    720
gaggagtagt nctgctgaat ttgagcttcc tnaaaaatna gtctttttat gtacagaaaa    780
cacatcataa aattcattac acaatgtcac ttattgttcc atgccaggca aagtcatgtc    840
cttctgggac ttatgtctgc acatttaact atgggtggtg ttgtgttttg tgcttagatg    900
gtccctatca ttgncccagt atggagatgt gtntggtgag aaatctgagg cgggaagcag    960
agacaggcaa gcctgtcacc ttgaaacagt aagtaggagc a                       1001
```

<210> 86
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-217-91 : polymorphic base C or T

<220>
<221> misc_binding
<222> 482..500

<223> 10-217-91.mis1

<220>
<221> misc_binding
<222> 502..521
<223> 10-217-91.mis2, potential complement

<220>
<221> primer_bind
<222> 411..427
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 761..777
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-217-91 potential probe

<220>
<221> misc_feature
<222> 20,100,257,279,368,377,432,453,460,615,634,921,946,986
<223> n=a, g, c or t

<400> 86
catgtaaaag gagactgggn atatacaggc tggagaccac atcaggtggc tgggcatgtg 60
ggataaatcc tattgagcat ctgtcatagg gcctgtcacn ttagtagaca gtcactaaat 120
atttgttaaa tacatgatgc ctgtttaaca catttctac aaccatggag acctccacaa 180
ctgatgtagg acaaaatctt tctgctttga actctagcct ttcgggccag tgggatttat 240
gaaaaatgcc atctctnata gctgaggatg aagaatggna agagaatacg atcattgctg 300
tctccaacat tcaccagcgg aaaactcaag gaggtatgaa aataacttgg gttttaatta 360
gaaacttnaa agaatgnaat caggtgggga caggtagaaa gtaagatcag agttcctttc 420
cgaggagtag tnctgctgaa tttgagcttc ctnaaaaatn agtcttttta tgtacagaaa 480
acacatcata aaattcatta yacaatgtca cttattgttc catgccaggc aaagtcatgt 540
ccttctggga cttatgtctg cacatttaac tatgggtggt gttgtgtttt gtgcttagat 600
ggtccctatc attgncccag tatggagatg tgtntggtga gaaatctgag gcgggaagca 660
gagacaggca agcctgtcac cttgaaacag taagtaggag cacagccatg gggttctgag 720
ctgtcatgag cccctccagc tgcctgctat ggagctgata ctcccgctgt tgggttattc 780
cagtgaccag acaaaaggag ggctgtggta atgcaacttc aatgggtctc ccaagatggg 840
gcagctccga tgaggaggtg gggcagctgg aggaaaagga tcttctcccc tgtgcacaga 900
ggtcagggtt tacatatctg nttaaattgt caccttggat attctnggag gactaaatac 960
atcctttagg gggaaaagtg tgattngtat caaagtttta a 1001

<210> 87
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 10-213-292 : polymorphic base G or C

<220>
<221> misc_binding
<222> 484..502
<223> 10-213-292.mis1

<220>
<221> misc_binding

<222> 504..523
<223> 10-213-292.mis2, potential complement

<220>
<221> primer_bind
<222> 212..230
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 590..608
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 10-213-292 potential probe

<220>
<221> misc_feature
<222> 86,281,718,743,788,878,885,890,1000
<223> n=a, g, c or t

<400> 87
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attagtcatg tttgcttcca tgagaaagaa aaaccactac atggttatgc taaggatttc      60
agtcattggg gttagagcct tcccgnaatg tctcctgctt tcataactcc tccacacatc     120
ttagtgggcc attgagcaca tcaaagggca tgacagttat taaaatactt tatgaatgct     180
acaatccttt gccagtatga gttgttctct ggaacttcta acagttcaac agtactacat     240
ggactgagtt aaaagttaat tcaaaaatct caatttatcc naaatctgtt tctttctttt     300
caggcaccac ccacctatga tactgtgcta cagttggagt atcttgacat ggtggtgaat     360
gaaacactca gattattccc agttgctatg agacttgaga gggtctgcaa aaaagatgtt     420
gaaatcaatg ggatgtttat tcccaaaggg gtggtggtga tgattccaag ctatgttctt     480
catcatgacc caaagtactg gasagagcct gagaagttcc tccctgaaag gtaggaggcc     540
cctgggaagg gagccctccc tgaaccagcc tggttcaagc atattctgcc tctctacagg     600
acagtctggg cttgtacaat catttgcttg tctttttatg tttaaaaggt tttttcaaat     660
catgaaattg atcattgtca cactttacaa accacagact agataaaaga aaactatnag     720
ccagtcacag tcccagcaac ttnaagatga aggtcctcaa ttatgtcctt atgggtcata     780
agtgtccnaa aatgtaagga ctcttttaaa aacacatgat cacaatgcta ttattatgtc     840
ccacaaatga atattttttc ctgaatataa tcaaatcntt caggnaatcn aaatttgaat     900
aaaaaacatg cgtctaatct tcaaagaatt tataggttag tgcaacagat agacaaagaa     960
agcagtgatg acactgcttt ccatcaatac agtagcatcn a                        1001
```

<210> 88
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-214-279 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 10-214-279.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-214-279.mis2, potential complement

<220>

<221> primer_bind
<222> 154..174
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 746..763
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-214-279 potential probe

<400> 88
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ctcatccatt ttacttaaaa tttaaatcaa aaaagaacac aggtttccat gaatttgtct     60
caggcctggc acagaatagt actccataaa tattttgtta aatgatagat gatgaatgct    120
ctcactgtcc aatcttcaca catcttatag actaagtata aagaatccaa gatttatagt    180
gctgaaagta gtttttatat gtttacaaag cattattgtc attactgcat tttttttgcc    240
cattactcca tagagatcag aatatcactc tgttgtgtcc cctcaacact gaaggagtgt    300
ctcactcact ttgatgctat actttctact tttgtttatt taatgcttct caatatgctt    360
gtttaactgt tgcagatccc cctgaaatta agcttaggag gacttcttca accagaaaaa    420
cccgttgttc taaaggttga gtcaagggat ggcaccgtaa gtggagcctg aattttccta    480
aggacttctg ctttgctctt yaagaaatct gtgcctgaga acaccagaga cctcaaatta    540
ctttgtgaat agaactctga aatgaagatg ggcttcatcc aatggactgc ataaataacc    600
ggggattctg tacatgcatt gagctctctc attgtctgtg tagagtgtta tacttgggaa    660
tataaaggag gtgaccaaat cagtgtgagg aggtagattt ggctcctctg cttctcacgg    720
gactatttcc accaccccca gttagcacca ttaactcctc ctgagctctg ataagagaat    780
caacatttct caataatttc ctccacaaat tattaatgaa aataagaatt attttgatgg    840
ctctaacaat gacatttata tcacatgttt tctctggagt attctataag ttttatgtta    900
aatcaataaa gaccacttta caaaagtatt atcagatgct ttcctgcaca ttaaggagaa    960
atctatagaa ctgaatgaga accaacaagt aaatattttt g                       1001
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<210> 89
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-214-380 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 10-214-380.mis1, potential

<220>
<221> misc_binding
<222> 502..520
<223> 10-214-380.mis2, complement

<220>
<221> primer_bind
<222> 124..143
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 647..664
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-214-380 potential probe

<220>
<221> misc_feature
<222> 398,723,730,789
<223> n=a, g, c or t

<400> 89
gaacacgggt tcccatgaat ttgtctcagg tcaaacctca cacagaatag gtgctccatg 60
aatattttgt taaatgatag atgatgaatg ttctcactat ccaatcttca cacatcttat 120
agagtaagta taacgaatcc aagatttata gtgctgaaag tagtttttat atgtttacaa 180
agcattattg tcagtaattt ttttttactt tgatgctata ctttctactt ttgctttatt 240
taatgcttct caatatgctc gtttaactgt tgcagatccc cctgaaatta cgctttggag 300
gacttcttct aacagaaaaa cccattgttc taaaggctga gtcaagggat gagaccgtaa 360
gtggagcctg atttccctaa ggacttctgg tttgctcntt taagaaagct gtgccccaga 420
acaccagaga cctcaaatta ctttacaaat agaaccctga aatgaagacg ggcttcatcc 480
aatgtgctgc ataaataatc rgggattctg tacgtgcatt gtgctctctc atggtctgta 540
tagagtgtta tacttggtaa tatagaggag atgaccaaat cagtgctggg gaagtagatt 600
tggcttctct gcttctcata ggactatctc caccaccccc agttagcacc attaactcct 660
cctgagctct gataacataa ttaacatttc tcaataattt caaccacaat cattaataaa 720
aantaggaan ttattttgat ggctctaaca gtgacattta tatcatgtgt tatatctgta 780
gtattctant agtaagcttt atattaagca aatcaataaa aacctcttta caaaagtatt 840
attggatgtt tcctgcacat taaggagaaa tctatagaac tgaatgactg agaaccaaca 900
actaaatatt ttgatcattg taatcactgt tggtgtggga actggagtgc agtggtgcaa 960
tcttggctca ctgcgagctc tgcctcccag gttcacgcca t 1001

<210> 90
<211> 437
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 216
<223> 2-1-216 : polymorphic base A or G

<220>
<221> misc_binding
<222> 196..215
<223> 2-1-216.mis1, potential

<220>
<221> misc_binding
<222> 217..236
<223> 2-1-216.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 417..437
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 204..228
<223> 2-1-216 potential probe

<400> 90
gcccaaagaa gtgtgttgtg tttgcttatt tcttacagag taatgctgaa atctgtgttg 60
cttttcccca ccaggtcatt atcagtacca gaagtgcttc ctgggtcatg agtcgggtct 120
gggatgatgg ctatccttgg gatatgatgt atgttacccg ctttgcatcc tttctccgga 180
atgtccttcc ttcattcatc tctgactggt tatatrtcca gaagatgaac acgtggttta 240
agcatgagaa ctatggcctg atgcctttaa atgggtactt aaaaatggaa attttttta 300
ttcaaaaaag gggggcactc atttaatgaa tttattctct ctagaactta cttttgttgt 360
ctcattgagc ctagaaacat taaactcaag gtttcatagg tgacggaata tgcccagaga 420
ccacgtatgg cttggaa 437

<210> 91
<211> 437
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 397
<223> 2-1-397 : polymorphic base C or T

<220>
<221> misc_binding
<222> 377..396
<223> 2-1-397.mis1, potential

<220>
<221> misc_binding
<222> 398..417
<223> 2-1-397.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 417..437
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 385..409
<223> 2-1-397 potential probe

<400> 91
gcccaaagaa gtgtgttgtg tttgcttatt tcttacagag taatgctgaa atctgtgttg 60
cttttcccca ccaggtcatt atcagtacca gaagtgcttc ctgggtcatg agtcgggtct 120
gggatgatgg ctatccttgg gatatgatgt atgttacccg ctttgcatcc tttctccgga 180
atgtccttcc ttcattcatc tctgactggt tatatgtcca gaagatgaac acgtggttta 240
agcatgagaa ctatggcctg atgcctttaa atgggtactt aaaaatggaa attttttta 300
ttcaaaaaag gggggcactc atttaatgaa tttattctct ctagaactta cttttgttgt 360
ctcattgagc ctagaaacat taaactcaag gtttcayagg tgacggaata tgcccagaga 420
ccacgtatgg cttggaa 437

<210> 92
<211> 426
<212> DNA
<213> Homo Sapiens

<220>
<221> allele

<222> 232
<223> 2-3-232 : polymorphic base C or T

<220>
<221> misc_binding
<222> 212..231
<223> 2-3-232.mis1, potential

<220>
<221> misc_binding
<222> 233..252
<223> 2-3-232.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 406..426
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 220..244
<223> 2-3-232 potential probe

<220>
<221> misc_feature
<222> 419
<223> n=a, g, c or t

<400> 92
gagtvgcaga cttttcagtg cctttccatt catgacactt cttgaatctc tggcagaacc 60
agccagccgt gttcacagtg tcaaatgaag ggatgtcttt gattgcttcc aggtgttcct 120
cagcaccacc ggagggggat gggtgatcag ccgaatcttt gactcgggct acccatggga 180
catggtgttc atgacacgct ttcagaacat gttgagaaat tccctcccaa cyccaattgt 240
gacttggttg atggagcgaa agataaacaa ctggctcaat catgcaaatt acggcttaat 300
accagaagac aggtaaatat aatgtgactg ccaagggctt ttaggaagaa ggagcctctg 360
cctgtccagc agcctataca agccaggcag taccacagca acatggctga atgtgtggna 420
acactt 426

<210> 93
<211> 429
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 51
<223> 2-4-51 : polymorphic base A or C

<220>
<221> misc_binding
<222> 31..50
<223> 2-4-51.mis1, potential

<220>
<221> misc_binding
<222> 52..71
<223> 2-4-51.mis2, potential complement

<220>
<221> primer_bind
<222> 3..24
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 405..429
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 39..63
<223> 2-4-51 potential probe

<400> 93
gygctgttac tgtaaagaca ttgcattact actgttgacc tcagagcacg mgcctcttgc 60
ctaattctag gactcctaac taagtctttg gagtttcagc tggaagaatg ctggaggaat 120
acggaactcc tcccatttct cacagccacc tccaactctt aaaaacgctt ccaactgcct 180
cccagcacac aaccaaggga gaaaactatt ctgtcaaaga gacggtgcca aaaggcaaaa 240
acaaaggtaa ggatgatcgc tggggaaaga agctgaaaag gaaaagctca gaactctagc 300
tggaaatttg gctcacatcc ctagtatgtt actgcatagt ctggctttgt tcaatgggtc 360
gcttttaaat attaaagcta gatgtaagca aggtttgcaa caaagtccat aagaaactca 420
gcttttctc 429

<210> 94
<211> 429
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 126
<223> 2-4-126 : polymorphic base A or G

<220>
<221> misc_binding
<222> 106..125
<223> 2-4-126.mis1, potential

<220>
<221> misc_binding
<222> 127..146
<223> 2-4-126.mis2, potential complement

<220>
<221> primer_bind
<222> 3..24
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 405..429
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 114..138
<223> 2-4-126 potential probe

<400> 94
gygctgttac tgtaaagaca ttgcattact actgttgacc tcagagcacg agcctcttgc 60
ctaattctag gactcctaac taagtctttg gagtttcagc tggaagaatg ctggaggaat 120

```
acggarctcc tcccatttct cacagccacc tccaactctt aaaaacgctt ccaactgcct    180
cccagcacac aaccaaggga gaaaactatt ctgtcaaaga gacggtgcca aaaggcaaaa    240
acaaaggtaa ggatgatcgc tggggaaaga agctgaaaag gaaaagctca gaactctagc    300
tggaaatttg gctcacatcc ctagtatgtt actgcatagt ctggctttgt tcaatgggtc    360
gcttttaaat attaaagcta gatgtaagca aggtttgcaa caaagtccat aagaaactca    420
gcttttctc                                                            429
```

<210> 95
<211> 420
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 202
<223> 2-5-202 : polymorphic base A or G

<220>
<221> misc_binding
<222> 182..201
<223> 2-5-202.mis1, potential

<220>
<221> misc_binding
<222> 203..222
<223> 2-5-202.mis2, potential complement

<220>
<221> primer_bind
<222> 1..25
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 400..420
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 190..214
<223> 2-5-202 potential probe

<400> 95

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tgtttaaagc caatthcctg agcacatcat aaggattctc ttaccggttg tcccagttaa     60
gtaatgttga ttgatcaact ccttgacagg agctgatggc aaagaaggta gctgtgattg    120
gagctggggt cagtggccta atttctctga agtgctgtgt ggatgaggga cttgagccca    180
cttgctttga gagaactgaa grtattggag gagtgtggag gttcaaagta agtgagattt    240
tcttgggtct tgaacaggtt gtgttgttat ttcagggtga atcacagtta ctgatgggtc    300
atattgagaa atttattaaa caactctgat cagattttat ttctacttat tgatgtggcc    360
ataatggaac tgaagtcata ggctggcatc tctcccccag tcaatactaa cccaacccag    420
```

<210> 96
<211> 420
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 275
<223> 2-5-275 : polymorphic base A or G

<220>
<221> misc_binding

<222> 255..274
<223> 2-5-275.mis1, potential

<220>
<221> misc_binding
<222> 276..295
<223> 2-5-275.mis2, potential complement

<220>
<221> primer_bind
<222> 1..25
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 400..420
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 263..287
<223> 2-5-275 potential probe

<400> 96
tgtttaaagc caatthcctg agcacatcat aaggattctc ttaccggttg tcccagttaa 60
gtaatgttga ttgatcaact ccttgacagg agctgatggc aaagaaggta gctgtgattg 120
gagctggggt cagtggccta atttctctga agtgctgtgt ggatgaggga cttgagccca 180
cttgctttga gagaactgaa gatattggag gagtgtggag gttcaaagta agtgagattt 240
tcttgggtct tgaacaggtt gtgttgttat ttcarggtga atcacagtta ctgatgggtc 300
atattgagaa atttattaaa caactctgat cagattttat ttctacttat tgatgtggcc 360
ataatggaac tgaagtcata ggctggcatc tctcccccag tcaatactaa cccaacccag 420

<210> 97
<211> 420
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 346
<223> 2-5-346 : polymorphic base C or T

<220>
<221> misc_binding
<222> 326..345
<223> 2-5-346.mis1, potential

<220>
<221> misc_binding
<222> 347..366
<223> 2-5-346.mis2, potential complement

<220>
<221> primer_bind
<222> 1..25
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 400..420
<223> downstream amplification primer, complement

<220>

<221> misc_binding
<222> 334..358
<223> 2-5-346 potential probe

<400> 97
tgtttaaagc caatthcctg agcacatcat aaggattctc ttaccggttg tcccagttaa 60
gtaatgttga ttgatcaact ccttgacagg agctgatggc aaagaaggta gctgtgattg 120
gagctggggt cagtggccta atttctctga agtgctgtgt ggatgaggga cttgagccca 180
cttgctttga gagaactgaa gatattggag gagtgtggag gttcaaagta agtgagattt 240
tcttgggtct tgaacaggtt gtgttgttat ttcagggtga atcacagtta ctgatgggtc 300
atattgagaa atttattaaa caactctgat cagattttat ttctayttat tgatgtggcc 360
ataatggaac tgaagtcata ggctggcatc tctcccccag tcaatactaa cccaacccag 420

<210> 98
<211> 430
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 171
<223> 2-8-171 : polymorphic base A or G

<220>
<221> misc_binding
<222> 151..170
<223> 2-8-171.mis1, potential

<220>
<221> misc_binding
<222> 172..191
<223> 2-8-171.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 405..427
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 159..183
<223> 2-8-171 potential probe

<400> 98
ggttcaagat ycctcagcaa atgatccttc agaatgtttt tcttctgtat gtctcagata 60
cattatgaag gaacctgtac taaatgatga tgtcccaagt cgtctactct gtggagccat 120
caaggtgaaa tctacagtga aagagctcac agaaacttct gccatctttg rggatggaac 180
agtggaggag aacattgatg tcatcatttt tgcaacagga tatagtttct cttttccctt 240
ccttgaagat tcactcgtta aagtagagaa taatatggtc tcactgtata aatacatatt 300
ccccgctcac ctggacaagt caaccctcgc gtgcattggt ctcatccagc ccctaggttc 360
cattttccca actgctgaac ttcaagctcg ttgggtgaca agagtttcaa aggtaagtgt 420
gtaggcaggt 430

<210> 99
<211> 428
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 188
<223> 2-9-188 : polymorphic base A or G

<220>
<221> misc_binding
<222> 168..187
<223> 2-9-188.mis1, potential

<220>
<221> misc_binding
<222> 189..208
<223> 2-9-188.mis2, potential complement

<220>
<221> primer_bind
<222> 1..21
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 396..420
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 176..200
<223> 2-9-188 potential probe

<400> 99
```
tcacatwgag tgctatgggg gtggcacccc ctgaagttca acagcacgga agccctgact      60
ggtatgacat ggttcaatgt ccagagttta attttaagaa tcaacaacta gacaaagtaa     120
tgatattgac tcaaacttac tattcaaacc aaccttttat tccttaggct tgtgtagcct     180
gccctcarag agaactatga tgatggacat tatcaaaagg aatgaaaaaa gaattgacct     240
gtaagaattt tttttaattc tttacatgaa gcagtgtttc tcaaagtaca gtgatctaac     300
tacttacaag aaccacctag ctgcctgata aaatgcaaat ttctgggcta tagcccagat     360
gattgaatca gaaactccgt gtgtgaggct aaaaagttgc atttttatct tcttcctaag     420
ggtcatag                                                              428
```

<210> 100
<211> 428
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 223
<223> 2-9-223 : polymorphic base G or T

<220>
<221> misc_binding
<222> 203..222
<223> 2-9-223.mis1, potential

<220>
<221> misc_binding
<222> 224..243
<223> 2-9-223.mis2, potential complement

<220>
<221> primer_bind
<222> 1..21

<223> upstream amplification primer

<220>
<221> primer_bind
<222> 396..420
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 211..235
<223> 2-9-223 potential probe

<400> 100
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tcacatwgag tgctatgggg gtggcacccc ctgaagttca acagcacgga agccctgact     60
ggtatgacat ggttcaatgt ccagagttta attttaagaa tcaacaacta gacaaagtaa    120
tgatattgac tcaaacttac tattcaaacc aaccttttat tccttaggct tgtgtagcct    180
gccctcagag agaactatga tgatggacat tatcaaaagg aakgaaaaaa gaattgacct    240
gtaagaattt tttttaattc tttacatgaa gcagtgtttc tcaaagtaca gtgatctaac    300
tacttacaag aaccacctag ctgcctgata aaatgcaaat ttctgggcta tagcccagat    360
gattgaatca gaaactccgt gtgtgaggct aaaaagttgc atttttatct tcttcctaag    420
ggtcatag                                                             428
```

<210> 101
<211> 450
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 107
<223> 2-10-107 : polymorphic base C or T

<220>
<221> misc_binding
<222> 87..106
<223> 2-10-107.mis1, potential

<220>
<221> misc_binding
<222> 108..127
<223> 2-10-107.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 423..443
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 95..119
<223> 2-10-107 potential probe

<400> 101
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caaactgagc aaatcgccta atcttccaaa ttctttttcc tggcttgtta gagcagccaa     60
gggtggggtg gagcttgtga ataaaaagcc tgcttcatct tcctcaygca ggagaacatg    120
gccaagcgag ttgccattgt gggagctggg gtcagcggcc tggcctccat caagtgctgt    180
ctggaagaag gactggagcc cacctgcttt gagaggagcg atgaccttgg ggggctgtgg    240
agattcaccg taagtggggt ttcaacaact ttatctgtct atggagaatg gcttggcagc    300
```

tgggaaatta tatctgtgct tctttcacaa gggttggtgg ccttgaggaa ggttagaaat 360
gtctgctgaa caggggacca tgaggagcca ctgaaattgt aaaagaaaca ggacatgggt 420
gagctagggt ggaagtcaga acaggtcata 450

<210> 102
<211> 450
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 377
<223> 2-10-378 : polymorphic base A or G

<220>
<221> misc_binding
<222> 357..376
<223> 2-10-378.mis1, potential

<220>
<221> misc_binding
<222> 378..397
<223> 2-10-378.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 423..443
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 365..389
<223> 2-10-378 potential probe

<400> 102
caaactgagc aaatcgccta atcttccaaa ttctttttcc tggcttgtta gagcagccaa 60
gggtggggtg gagcttgtga ataaaaagcc tgcttcatct tcctcatgca ggagaacatg 120
gccaagcgag ttgccattgt gggagctggg gtcagcggcc tggcctccat caagtgctgt 180
ctggaagaag gactggagcc cacctgcttt gagaggagcg atgaccttgg ggggctgtgg 240
agattcaccg taagtggggt ttcaacaact ttatctgtct atggagaatg gcttggcagc 300
tgggaaatta tatctgtgct tctttcacaa gggttggtgg ccttgaggaa ggttagaaat 360
gtctgctgaa caggggrcca tgaggagcca ctgaaattgt aaaagaaaca ggacatgggt 420
gagctagggt ggaagtcaga acaggtcata 450

<210> 103
<211> 446
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 284
<223> 2-11-284 : polymorphic base A or G

<220>
<221> misc_binding
<222> 264..283
<223> 2-11-284.mis1, potential

<220>
<221> misc_binding
<222> 285..304
<223> 2-11-284.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 429..446
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 272..296
<223> 2-11-284 potential probe

<400> 103
tcagctagtc agactcacat ttattcggta agattaatta acagaagctt gagtcaacac 60
cgttagaggg taattgatat tatggacttc ccaagtaaaa agcacttaag cacctgccgt 120
acatcaaagg ttagttttaa gatcacatga gtaaacaaac taggtaggta aactactctg 180
ccttcctttg ttactacttt aatttgttta actaaaggta aagatcaggt tgccttcaac 240
catatctatt actgaagtta tgcaaacttc tcggccttcc aagragattt gtgtctatct 300
ccataactat ctttaatatt tttcccacca gcctgattga accccagcat agatatttaa 360
taaaaatttg gccattccgt tgttggaagt tttaagataa atttattatt attattttaa 420
tgagaaaagc ctcagtaaag ctgact 446

<210> 104
<211> 446
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 156
<223> 2-11-156 : polymorphic base A or C

<220>
<221> misc_binding
<222> 136..155
<223> 2-11-156.mis1, potential

<220>
<221> misc_binding
<222> 157..176
<223> 2-11-156.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 429..446
<223> downstream amplification primer, complement

<220>
<221> misc_binding

<222> 144..168
<223> 2-11-156 potential probe

<400> 104
tcagctagtc agactcacat ttattcggta agattaatta acagaagctt gagtcaacac 60
cgttagaggg taattgatat tatggacttc ccaagtaaaa agcacttaag cacctgccgt 120
acatcaaagg ttagttttaa gatcacatga gtaaamaaac taggtaggta aactactctg 180
ccttcctttg ttactacttt aatttgttta actaaaggta aagatcaggt tgccttcaac 240
catatctatt actgaagtta tgcaaacttc tcggccttcc aagaagattt gtgtctatct 300
ccataactat ctttaatatt tttcccacca gcctgattga accccagcat agatatttaa 360
taaaaatttg gccattccgt tgttggaagt tttaagataa atttattatt attattttaa 420
tgagaaaagc ctcagtaaag ctgact 446

<210> 105
<211> 446
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 379
<223> 2-11-379 : polymorphic base A or G

<220>
<221> misc_binding
<222> 359..378
<223> 2-11-379.mis1, potential

<220>
<221> misc_binding
<222> 380..399
<223> 2-11-379.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 429..446
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 367..391
<223> 2-11-379 potential probe

<400> 105
tcagctagtc agactcacat ttattcggta agattaatta acagaagctt gagtcaacac 60
cgttagaggg taattgatat tatggacttc ccaagtaaaa agcacttaag cacctgccgt 120
acatcaaagg ttagttttaa gatcacatga gtaaacaaac taggtaggta aactactctg 180
ccttcctttg ttactacttt aatttgttta actaaaggta aagatcaggt tgccttcaac 240
catatctatt actgaagtta tgcaaacttc tcggccttcc aagaagattt gtgtctatct 300
ccataactat ctttaatatt tttcccacca gcctgattga accccagcat agatatttaa 360
taaaaatttg gccattccrt tgttggaagt tttaagataa atttattatt attattttaa 420
tgagaaaagc ctcagtaaag ctgact 446

<210> 106
<211> 423
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 223
<223> 2-12-223 : polymorphic base A or T

<220>
<221> misc_binding
<222> 203..222
<223> 2-12-223.mis1, potential

<220>
<221> misc_binding
<222> 224..243
<223> 2-12-223.mis2, potential complement

<220>
<221> primer_bind
<222> 1..25
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 399..420
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 211..235
<223> 2-12-223 potential probe

<400> 106
```
ctgttgcagg tatttcttgg aaatgagcta tttacagcaa gggtgtttgc ctctcattgc    60
tgtagttccc tgagaaaaga gcctgtgttc aatgatgagc tcccatcccg catcctgtgt   120
ggcactctgt ccatcaagcc cagtgtgaag gagttcacgg aaacctcagc tgtgtttgag   180
gatgggacca tgtttgaggc tatcgactct gtcatctttg cawcaggcta tgattattcc   240
taccccttcc ttgatgagac catcatgaaa agcagaaaca atgaggttac cttgtttaaa   300
ggcatcttcc ccccactaat ggagaagcca accttggctg tgattggctt ggttcagtcc   360
cttggagctg ccatccccac agcagacctg caagcctggt gggctgctaa agtatttgca   420
ggt                                                                  423
```

<210> 107
<211> 418
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 239
<223> 2-14-239 : polymorphic base C or T

<220>
<221> misc_binding
<222> 219..238
<223> 2-14-239.mis1, potential

<220>
<221> misc_binding
<222> 240..259
<223> 2-14-239.mis2, potential complement

<220>
<221> primer_bind
<222> 1..23

<223> upstream amplification primer

<220>
<221> primer_bind
<222> 398..418
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 227..251
<223> 2-14-239 potential probe

<400> 107
gttcactgaa rggvacacaa ttcttggctt tctctttaag ctttcttatt ctccctagga 60
ccacacagaa gaaggcagag ccagcattta ccagtctgta ttcacaaact cttccaaaga 120
aatgatgtgc tttccagact tcccttatcc ggatgattac ccaaactata tacaccacag 180
caagctccag gaatatataa agacatatgc tcaaaagaag gatcttttaa gatacataya 240
gtttgaggta ggggtctcat aacttgtact gttgaaatta agatatgtgt gggttagaga 300
aaaaggaggc agcaaactat tataaaaatt agagccaaat gtttgggcac ctcagtaatc 360
aaatgttggc tctgattata aagcattcat gcattgattt tttctcctag acttacta 418

<210> 108
<211> 418
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 370
<223> 2-14-370 : polymorphic base G or C

<220>
<221> misc_binding
<222> 350..369
<223> 2-14-370.mis1, potential

<220>
<221> misc_binding
<222> 371..390
<223> 2-14-370.mis2, potential complement

<220>
<221> primer_bind
<222> 1..23
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 398..418
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 358..382
<223> 2-14-370 potential probe

<400> 108
gttcactgaa rggvacacaa ttcttggctt tctctttaag ctttcttatt ctccctagga 60
ccacacagaa gaaggcagag ccagcattta ccagtctgta ttcacaaact cttccaaaga 120
aatgatgtgc tttccagact tcccttatcc ggatgattac ccaaactata tacaccacag 180
caagctccag gaatatataa agacatatgc tcaaaagaag gatcttttaa gatacataya 240
gtttgaggta ggggtctcat aacttgtact gttgaaatta agatatgtgt gggttagaga 300
aaaaggaggc agcaaactat tataaaaatt agagccaaat gtttgggcac ctcagtaatc 360

aaatgttggs tctgattata aagcattcat gcattgattt tttctcctag acttacta 418

<210> 109
<211> 445
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 104
<223> 2-17-104 : polymorphic base A or G

<220>
<221> misc_binding
<222> 84..103
<223> 2-17-104.mis1, potential

<220>
<221> misc_binding
<222> 105..124
<223> 2-17-104.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 427..445
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 92..116
<223> 2-17-104 potential probe

<400> 109
cgttgatgga aaattcccct ctgctctctg aagatttgct aaaaatctac tgacaaaagg 60
catattgata gaagaaaatg tacacaaatt tattaacttc cacrggagtt ggggtaaaaa 120
tcacatgatt atcccagcat gcaatggggt acggatgctt atatatccct tccttaggtg 180
acagggagat gagaaagtgt ggattgattt tagggtgact atgaaatgat ctctagggga 240
cccaacgggc ttgaagaaca tacaatggcc tggaataaag tatgttgggc ccgcagcgca 300
aacaatggct tatgacaagt ctgtctaggt gtgttgacag aattctttct tcctgcagta 360
tgagttcagt taatgaaaac tcagggaagg taccaaaggt aattgatttc ttctttggca 420
agtctagact ttaggcaaat aaggg 445

<210> 110
<211> 445
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 395
<223> 2-17-396 : polymorphic base A or C

<220>
<221> misc_binding
<222> 375..394
<223> 2-17-396.mis1, potential

<220>

<221> misc_binding
<222> 396..415
<223> 2-17-396.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 427..445
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 383..407
<223> 2-17-396 potential probe

<400> 110
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cgttgatgga aaattcccct ctgctctctg aagatttgct aaaaatctac tgacaaaagg     60
catattgata gaagaaaatg tacacaaatt tattaacttc cacaggagtt ggggtaaaaa    120
tcacatgatt atcccagcat gcaatggggt acggatgctt atatatccct tccttaggtg    180
acagggagat gagaaagtgt ggattgattt tagggtgact atgaaatgat ctctagggga    240
cccaacgggc ttgaagaaca tacaatggcc tggaataaag tatgttgggc ccgcagcgca    300
aacaatggct tatgacaagt ctgtctaggt gtgttgacag aattctttct tcctgcagta    360
tgagttcagt taatgaaaac tcagggaagg taccmaaggt aattgatttc ttctttggca    420
agtctagact ttaggcaaat aaggg                                          445
```

<210> 111
<211> 436
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 43
<223> 2-22-43 : polymorphic base A or G

<220>
<221> misc_binding
<222> 23..42
<223> 2-22-43.mis1, potential

<220>
<221> misc_binding
<222> 44..63
<223> 2-22-43.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 416..436
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 31..55
<223> 2-22-43 potential probe

<400> 111
aaggagttca cggaaacctc agctgtgttt gaggatggga ccrtgtttga ggctatcgac 60
tctgtcatct ttgcaacagg ctatgattat tcctacccct tccttgatga gaccatcatg 120
aaaagcagaa acaatgaggt taccttgttt aaaggcatct tccccccact aatggagaag 180
ccaaccttgg ctgtgattgg cttggttcag tcccttggag ctgccatccc cacagcagac 240
ctgcaagcct ggtgggctgc taaagtattt gcaagtaggt gggccattct gtctttcatt 300
cattttatca atgaacattt actgaacacc tgctatatgc aaagcactgt gctagggata 360
caatgagaac aagacaaaca tgttccttga cctctcaagg cttaaaatgg ggtgtggggg 420
atgcataata ggggaa 436

<210> 112
<211> 436
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 138
<223> 2-22-138 : polymorphic base A or G

<220>
<221> misc_binding
<222> 118..137
<223> 2-22-138.mis1, potential

<220>
<221> misc_binding
<222> 139..158
<223> 2-22-138.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 416..436
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 126..150
<223> 2-22-138 potential probe

<400> 112
aaggagttca cggaaacctc agctgtgttt gaggatggga ccatgtttga ggctatcgac 60
tctgtcatct ttgcaacagg ctatgattat tcctacccct tccttgatga gaccatcatg 120
aaaagcagaa acaatgargt taccttgttt aaaggcatct tccccccact aatggagaag 180
ccaaccttgg ctgtgattgg cttggttcag tcccttggag ctgccatccc cacagcagac 240
ctgcaagcct ggtgggctgc taaagtattt gcaagtaggt gggccattct gtctttcatt 300
cattttatca atgaacattt actgaacacc tgctatatgc aaagcactgt gctagggata 360
caatgagaac aagacaaaca tgttccttga cctctcaagg cttaaaatgg ggtgtggggg 420
atgcataata ggggaa 436

<210> 113
<211> 420
<212> DNA
<213> Homo Sapiens

<220>
<221> allele

<222> 82
<223> 2-23-82 : polymorphic base A or G

<220>
<221> misc_binding
<222> 62..81
<223> 2-23-82.mis1, potential

<220>
<221> misc_binding
<222> 83..102
<223> 2-23-82.mis2, potential complement

<220>
<221> primer_bind
<222> 1..25
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 396..420
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 70..94
<223> 2-23-82 potential probe

<400> 113
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caattatttc ctccacagaa acaaggcaag aaggaaaaaa actttcacat gtagaattat     60
aaatggaaaa ataaattttc trgttttctt aaagaccctg gtttccggta taaagaaatg    120
tcccagcttc ttagtcacgg gccaatgggt tgttgttact gaaaaggatg ggaaacagga    180
atctactatt tttgatgctg taatgatttg ttcaggacat cacgtatacc ccaatctgcc    240
aacggattcc tttcctggta agtttggaaa atatataata atctagggac ttatatgcaa    300
acatcaagag ttagaaacat atctttctat aggtattaca taatgattat tcttagattt    360
caaaagaaaa aaattaagtt taatgatagg atatagtaat aaatagccyc ataagtcctt    420
```

<210> 114
<211> 420
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 166
<223> 2-23-166 : polymorphic base A or G

<220>
<221> misc_binding
<222> 146..165
<223> 2-23-166.mis1, potential

<220>
<221> misc_binding
<222> 167..186
<223> 2-23-166.mis2, potential complement

<220>
<221> primer_bind
<222> 1..25
<223> upstream amplification primer

<220>

<221> primer_bind
<222> 396..420
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 154..178
<223> 2-23-166 potential probe

<400> 114
caattatttc ctccacagaa acaaggcaag aaggaaaaaa actttcacat gtagaattat 60
aaatggaaaa ataaattttc tagttttctt aaagaccctg gtttccggta taaagaaatg 120
tcccagcttc ttagtcacgg gccaatgggt tgttgttact gaaaargatg ggaaacagga 180
atctactatt tttgatgctg taatgatttg ttcaggacat cacgtatacc ccaatctgcc 240
aacggattcc tttcctggta agtttggaaa atatataata atctagggac ttatatgcaa 300
acatcaagag ttagaaacat atctttctat aggtattaca taatgattat tcttagattt 360
caaaagaaaa aaattaagtt taatgatagg atatagtaat aaatagccyc ataagtcctt 420

<210> 115
<211> 420
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 244
<223> 2-23-244 : polymorphic base G or T

<220>
<221> misc_binding
<222> 224..243
<223> 2-23-244.mis1, potential

<220>
<221> misc_binding
<222> 245..264
<223> 2-23-244.mis2, potential complement

<220>
<221> primer_bind
<222> 1..25
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 396..420
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 232..256
<223> 2-23-244 potential probe

<400> 115
caattatttc ctccacagaa acaaggcaag aaggaaaaaa actttcacat gtagaattat 60
aaatggaaaa ataaattttc tagttttctt aaagaccctg gtttccggta taaagaaatg 120
tcccagcttc ttagtcacgg gccaatgggt tgttgttact gaaaaggatg ggaaacagga 180
atctactatt tttgatgctg taatgatttg ttcaggacat cacgtatacc ccaatctgcc 240
aackgattcc tttcctggta agtttggaaa atatataata atctagggac ttatatgcaa 300
acatcaagag ttagaaacat atctttctat aggtattaca taatgattat tcttagattt 360
caaaagaaaa aaattaagtt taatgatagg atatagtaat aaatagccyc ataagtcctt 420

<210> 116

<211> 434
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 115
<223> 2-24-115 : polymorphic base C or T

<220>
<221> misc_binding
<222> 95..114
<223> 2-24-115.mis1, potential

<220>
<221> misc_binding
<222> 116..135
<223> 2-24-115.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 416..434
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 103..127
<223> 2-24-115 potential probe

<400> 116
aatgcacttc aactagggaa ttttttaatt acaactgata ataggtttaa aaagacacaa 60
agaaaacatc ttcataattt ctgaaaatca gttcaaacaa cttgccatgt tccayttagg 120
cctggaccag tttcgaggca actacctcca tagccgggat tataagaatc cagaagcctt 180
caaggggaag agggtcctcg tgattggtct ggggaattcg ggatctgaca ttgctgttga 240
gctcagccgt ctggctacac aggtacatga cgtaaaggtt ttgggaaata aacctaaggt 300
agggctgtgc tactaaatca gtagccaagg cacagaggat ggtacttcta tgtcacacca 360
caagagatcc acctcttcta tgtggccctt caaatcaagg aggacttgag acatcctcca 420
tgtgaagcca ggta 434

<210> 117
<211> 420
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 36
<223> 2-25-36 : polymorphic base G or C

<220>
<221> misc_binding
<222> 16..35
<223> 2-25-36.mis1, potential

<220>
<221> misc_binding
<222> 37..56
<223> 2-25-36.mis2, potential complement

<220>
<221> primer_bind
<222> 1..21
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 396..420
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 24..48
<223> 2-25-36 potential probe

<400> 117
aggaaaatgc acggaagtgc ccaaagaagt gtgttstgtt tgcttatttc ttacagagta 60
atgctgaaat ctgtgttgct tttccccacc aggtcattat cagtaccaga agtgcttcct 120
gggtcatgag tcgggtctgg gatgatggct atccttggga tatgatgtat gttacccgct 180
ttgcatcctt tctccggaat gtccttcctt cattcatctc tgactggtta tatgtccaga 240
agatgaacac gtggtttaag catgagaact atggcctgat gcctttaaat gggtacttaa 300
aaatggaaat tttttttatt caaaaaaggg gggcactcat ttaatgaatt tattctctct 360
agaacttact tttgttgtct cattgagcct agaaacatta aactcaaggt ttcacaggtg 420

<210> 118
<211> 429
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 185
<223> 2-27-185 : polymorphic base A or G

<220>
<221> misc_binding
<222> 165..184
<223> 2-27-185.mis1, potential

<220>
<221> misc_binding
<222> 186..205
<223> 2-27-185.mis2, potential complement

<220>
<221> primer_bind
<222> 1..19
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 405..429
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 173..197
<223> 2-27-185 potential probe

<400> 118
cttattccag tatgttctct tctttcttca tgtttggcca gagccagact ttgcagacag 60
attacatcac atatgtggat gagctgggct ctttcatagg ggccaagcct aacataccat 120

```
ggctcttcct gacagatccc cgcctggccc tggaggtgta ctttggccct tgcagcccat    180
accartttcg actgatggga ccagggaagt gggatggggc cagaaatgcc atcctgaccc    240
agtggaaccg gacagtgaag ccaaccagga caagagttgt cagtgaagtt cagcgacccc    300
atccctttta caatttgctt aaaatgcttt cattcccatt actccttctg gctgttacac    360
ttacatttta ttaatgagaa agtctttgag gtctcaaaat tcagcataga agtgtaatca    420
cacaataca                                                            429
```

<210> 119
<211> 429
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 378
<223> 2-27-378 : polymorphic base G or C

<220>
<221> misc_binding
<222> 358..377
<223> 2-27-378.mis1, potential

<220>
<221> misc_binding
<222> 379..398
<223> 2-27-378.mis2, potential complement

<220>
<221> primer_bind
<222> 1..19
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 405..429
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 366..390
<223> 2-27-378 potential probe

<400> 119

```
cttattccag tatgttctct tctttcttca tgtttggcca gagccagact ttgcagacag     60
attacatcac atatgtggat gagctgggct ctttcatagg ggccaagcct aacataccat    120
ggctcttcct gacagatccc cgcctggccc tggaggtgta ctttggccct tgcagcccat    180
accagtttcg actgatggga ccagggaagt gggatggggc cagaaatgcc atcctgaccc    240
agtggaaccg gacagtgaag ccaaccagga caagagttgt cagtgaagtt cagcgacccc    300
atccctttta caatttgctt aaaatgcttt cattcccatt actccttctg gctgttacac    360
ttacatttta ttaatgasaa agtctttgag gtctcaaaat tcagcataga agtgtaatca    420
cacaataca                                                            429
```

<210> 120
<211> 440
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 142
<223> 2-29-142 : polymorphic base A or G

<220>

<221> misc_binding
<222> 122..141
<223> 2-29-142.mis1, potential

<220>
<221> misc_binding
<222> 143..162
<223> 2-29-142.mis2, potential complement

<220>
<221> primer_bind
<222> 1..21
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 422..439
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 130..154
<223> 2-29-142 potential probe

<220>
<221> misc_feature
<222> 9,433
<223> n=a, g, c or t

<400> 120
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caattawtna ctccagaaag gaaaagctgg caatgcagtt ttattgaaat tagcttgaca     60
tagttgctct ggagctcaca gacttctctc ttcttccccc tgaaggtatg gagaggttca    120
aaggccaata tttccatagc crccaataca agcatccaga tggatttggg gaaaacgcat    180
cctggtgatt ggaatgggaa acttgggctc agatattgct gttgagctga gtaagaatgc    240
tgctcaggtg tgatgctctc tgcttaccat gtacctggag gggaggaagt ggggatgcca    300
tactggagaa ccycagccat ataatcgcgg ctccaatcct cattaactag ttggttggta    360
gcgcattgtg gcatcataga aaatctggaa gtcaagaaac cactttacct cctagctctg    420
tcactaacca gcnatgaatg                                                440
```

<210> 121
<211> 440
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 166
<223> 2-29-166 : polymorphic base C or T

<220>
<221> misc_binding
<222> 146..165
<223> 2-29-166.mis1, potential

<220>
<221> misc_binding
<222> 167..186
<223> 2-29-166.mis2, potential complement

<220>
<221> primer_bind
<222> 1..21
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 422..439
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 154..178
<223> 2-29-166 potential probe

<220>
<221> misc_feature
<222> 9,433
<223> n=a, g, c or t

<400> 121
caattawtna ctccagaaag gaaaagctgg caatgcagtt ttattgaaat tagcttgaca 60
tagttgctct ggagctcaca gacttctctc ttcttccccc tgaaggtatg gagaggttca 120
aaggccaata tttccatagc cgccaataca agcatccaga tggatytggg gaaaacgcat 180
cctggtgatt ggaatgggaa acttgggctc agatattgct gttgagctga gtaagaatgc 240
tgctcaggtg tgatgctctc tgcttaccat gtacctggag gggaggaagt ggggatgcca 300
tactggagaa ccycagccat ataatcgcgg ctccaatcct cattaactag ttggttggta 360
gcgcattgtg gcatcataga aaatctggaa gtcaagaaac cactttacct cctagctctg 420
tcactaacca gcnatgaatg 440

<210> 122
<211> 440
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 204
<223> 2-29-205 : polymorphic base C or T

<220>
<221> misc_binding
<222> 184..203
<223> 2-29-205.mis1, potential

<220>
<221> misc_binding
<222> 205..224
<223> 2-29-205.mis2, potential complement

<220>
<221> primer_bind
<222> 1..21
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 422..439
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 192..216
<223> 2-29-205 potential probe

<220>
<221> misc_feature

<222> 9,433
<223> n=a, g, c or t

<400> 122
caattawtna ctccagaaag gaaaagctgg caatgcagtt ttattgaaat tagcttgaca 60
tagttgctct ggagctcaca gacttctctc ttcttccccc tgaaggtatg gagaggttca 120
aaggccaata tttccatagc cgccaataca agcatccaga tggatttggg gaaaacgcat 180
cctggtgatt ggaatgggaa actygggctc agatattgct gttgagctga gtaagaatgc 240
tgctcaggtg tgatgctctc tgcttaccat gtacctggag gggaggaagt ggggatgcca 300
tactggagaa ccycagccat ataatcgcgg ctccaatcct cattaactag ttggttggta 360
gcgcattgtg gcatcataga aaatctggaa gtcaagaaac cactttacct cctagctctg 420
tcactaacca gcnatgaatg 440

<210> 123
<211> 440
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 205
<223> 2-29-206 : polymorphic base A or G

<220>
<221> misc_binding
<222> 185..204
<223> 2-29-206.mis1, potential

<220>
<221> misc_binding
<222> 206..225
<223> 2-29-206.mis2, potential complement

<220>
<221> primer_bind
<222> 1..21
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 422..439
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 193..217
<223> 2-29-206 potential probe

<220>
<221> misc_feature
<222> 9,433
<223> n=a, g, c or t

<400> 123
caattawtna ctccagaaag gaaaagctgg caatgcagtt ttattgaaat tagcttgaca 60
tagttgctct ggagctcaca gacttctctc ttcttccccc tgaaggtatg gagaggttca 120
aaggccaata tttccatagc cgccaataca agcatccaga tggatttggg gaaaacgcat 180
cctggtgatt ggaatgggaa acttrggctc agatattgct gttgagctga gtaagaatgc 240
tgctcaggtg tgatgctctc tgcttaccat gtacctggag gggaggaagt ggggatgcca 300
tactggagaa ccycagccat ataatcgcgg ctccaatcct cattaactag ttggttggta 360
gcgcattgtg gcatcataga aaatctggaa gtcaagaaac cactttacct cctagctctg 420
tcactaacca gcnatgaatg 440

<210> 124
<211> 440
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 313
<223> 2-29-314 : polymorphic base C or T

<220>
<221> misc_binding
<222> 293..312
<223> 2-29-314.mis1, potential

<220>
<221> misc_binding
<222> 314..333
<223> 2-29-314.mis2, potential complement

<220>
<221> primer_bind
<222> 1..21
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 422..439
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 301..325
<223> 2-29-314 potential probe

<220>
<221> misc_feature
<222> 9,433
<223> n=a, g, c or t

<400> 124
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caattawtna ctccagaaag gaaaagctgg caatgcagtt ttattgaaat tagcttgaca     60
tagttgctct ggagctcaca gacttctctc ttcttccccc tgaaggtatg gagaggttca    120
aaggccaata tttccatagc cgccaataca agcatccaga tggatttggg gaaaacgcat    180
cctggtgatt ggaatgggaa acttgggctc agatattgct gttgagctga gtaagaatgc    240
tgctcaggtg tgatgctctc tgcttaccat gtacctggag gggaggaagt ggggatgcca    300
tactggagaa ccycagccat ataatcgcgg ctccaatcct cattaactag ttggttggta    360
gcgcattgtg gcatcataga aaatctggaa gtcaagaaac cactttacct cctagctctg    420
tcactaacca gcnatgaatg                                                440
```

<210> 125
<211> 432
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 68
<223> 2-32-68 : polymorphic base A or G

<220>
<221> misc_binding
<222> 48..67

<223> 2-32-68.mis1, potential

<220>
<221> misc_binding
<222> 69..88
<223> 2-32-68.mis2, potential complement

<220>
<221> primer_bind
<222> 1..21
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 413..432
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 56..80
<223> 2-32-68 potential probe

<400> 125
cctatgagta tcgcctggtt gggcctgggc aatgggaagg agccagaaat gccatcttca 60
cccagaarca aagaatactg aagccactca agactcgggc cctgaaggat tcatctaatt 120
tctcagtttc ttttctgttg aaaatcctgg gccttcttgc tgttgttgtg gccttttttt 180
gccaacttca atggtcctag tcagcataat gctttgggct ttattatctt gtcagtcact 240
acctcctaaa gaaaaaaaaa aaggctagaa gaaaaaacat tacattcatg ttctaattat 300
agattttaga gttaggtagt acagghaagg gggaaattgt aaagaattag cagaattagg 360
catatgtaca aaaccaaaat tttgtcatga aattttgcct ttccacgctt ccctcagttc 420
accaaagtta cc 432

<210> 126
<211> 424
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 357
<223> 2-35-357 : polymorphic base C or T

<220>
<221> misc_binding
<222> 337..356
<223> 2-35-357.mis1, potential

<220>
<221> misc_binding
<222> 358..377
<223> 2-35-357.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 404..423
<223> downstream amplification primer, complement

<220>

<221> misc_binding
<222> 345..369
<223> 2-35-357 potential probe

<400> 126
gaagagccta ttgacatcat tgtctttgcc actggataca catttgcttt ccccttcctt 60
gatgagtctg tagtgaaagt tgaagatggc caggcctcac tgtacaagta tatcttcccct 120
gcacatctgc aaaagccaac cctggccatt attggcctca tcaaaccctt gggctccatg 180
atacctacag gagaaacaca agctcggtgg gctgttcgag tcctgaaagg taagtataag 240
aaatagcagg gcatgtgttt ttggtgtgcc atgtgattct ggatactgga aatgttgaga 300
ctattattcc tcctgcttct atttaaaata acagaatctt taaaagcagg atgcatycta 360
ttgtttgctg aattatactg tcataatgat ttgttccatt actgcataaa tggtatatca 420
gggg 424

<210> 127
<211> 435
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 256
<223> 2-36-256 : polymorphic base G or C

<220>
<221> misc_binding
<222> 236..255
<223> 2-36-256.mis1, potential

<220>
<221> misc_binding
<222> 257..276
<223> 2-36-256.mis2, potential complement

<220>
<221> primer_bind
<222> 1..21
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 411..435
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 244..268
<223> 2-36-256 potential probe

<400> 127
atatcaatgg tacatcaact ggcaagtgct taatggaaca ttgacaactg ctaatcatat 60
ctgtgattct tttttcagac caaagtctgc agtgtaacaa aatgctcaga ttctgctgtc 120
tctggccaat gggaggtggt cactatgcat gaagagaagc aagagtcagc catctttgat 180
gctgtcatgg tctgcactgg ctttcttact aatccttatt tgccactgga ttcctttcca 240
ggtacagcat tttctstaac taactttaag ttttctcgtg ggagccattc tgatgcttga 300
ttggtctggg aatgaattcc tatggctgtt ccattaaata gttaaagttg ggaggtagga 360
ggaggctttt tttgttttgt tttgtttttt tctagccagc attttctggc cagtttttgg 420
ctttcatttg ttcca 435

<210> 128
<211> 435
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 353
<223> 2-36-354 : polymorphic base A or C

<220>
<221> misc_binding
<222> 333..352
<223> 2-36-354.mis1, potential

<220>
<221> misc_binding
<222> 354..373
<223> 2-36-354.mis2, potential complement

<220>
<221> primer_bind
<222> 1..21
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 411..435
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 341..365
<223> 2-36-354 potential probe

<400> 128
atatcaatgg tacatcaact ggcaagtgct taatggaaca ttgacaactg ctaatcatat 60
ctgtgattct tttttcagac caaagtctgc agtgtaacaa aatgctcaga ttctgctgtc 120
tctggccaat gggaggtggt cactatgcat gaagagaagc aagagtcagc catctttgat 180
gctgtcatgg tctgcactgg ctttcttact aatccttatt tgccactgga ttcctttcca 240
ggtacagcat tttctgtaac taactttaag ttttctcgtg ggagccattc tgatgcttga 300
ttggtctggg aatgaattcc tatggctgtt ccattaaata gttaaagttg ggmggtagga 360
ggaggctttt tttgttttgt tttgtttttt tctagccagc attttctggc cagtttttgg 420
ctttcatttg ttcca 435

<210> 129
<211> 449
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 236
<223> 2-42-236 : polymorphic base C or T

<220>
<221> misc_binding
<222> 216..235
<223> 2-42-236.mis1, potential

<220>
<221> misc_binding
<222> 237..256
<223> 2-42-236.mis2, potential complement

<220>
<221> primer_bind

<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 428..449
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 224..248
<223> 2-42-236 potential probe

<400> 129
agtgggtttg cgtgtttgga ggcagatttt ttccccact cacactttgg gcactsacag 60
tttttcagct gtctcatgga gtttgcagcg gcaagccact tctttcaaag gtcctgtgaa 120
ttcttttggt tttcctggta tgttcatgca gtacttcttg gaggaaaatt tcactgtgtg 180
agtctccaca tgctgttctg tctgtctgcg tggaaactgc aagttagtcc tgcctyctat 240
ccaccatttt ccaacaatct gtcgttaacc atttcaaagt atagaattca gtggcattta 300
gtacattcat aatgctgtgt aaccacaacc tctatccagt ttcaaaacac tttcatcaca 360
cccaaaagaa aactccatac tcattagcaa tccttcccca ttcccttctt tccccagccc 420
ctggcagcca ctcgatcatg cctatttta 449

<210> 130
<211> 429
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 139
<223> 2-43-139 : polymorphic base A or G

<220>
<221> misc_binding
<222> 119..138
<223> 2-43-139.mis1, potential

<220>
<221> misc_binding
<222> 140..159
<223> 2-43-139.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 395..419
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 127..151
<223> 2-43-139 potential probe

<400> 130
cattakcaat ccttccccat tcccttcttt ccccagcccc tggcagccac tcgatcatgc 60
ctattttaaa ttgaggaaac taaagctgag aaaagttata caatttttcc aacatgactc 120
tgataatagc tggtgaacrc aatactcgaa cccaggactt gtgattccca agatcagact 180
cctcccatat acctgtcttt tatttcccaa gtgcttgggc aatcagctgc acttaaaaag 240

cctttacaaa ttgagtttac taatgtgagt aatatatgat tttttaaaaa taataattgt 300
ccctaaaggt gaaatggatc aaagccctta aaagtgaatc tgtggtgtag taactgttaa 360
cataattgtc ttattttatt ctcatcccct taaagaataa aattgatgaa caagtgaggg 420
gtcatagct 429

<210> 131
<211> 425
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 213
<223> 2-44-215 : polymorphic base C or T

<220>
<221> misc_binding
<222> 193..212
<223> 2-44-215.mis1, potential

<220>
<221> misc_binding
<222> 214..233
<223> 2-44-215.mis2, potential complement

<220>
<221> primer_bind
<222> 3..23
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 398..420
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 201..225
<223> 2-44-215 potential probe

<400> 131
rhcctgcttt tatttcccaa gtgcttgggc aatcagctgc acttaaaaag cctttacaaa 60
ttgagtttac taatgtgagt aatatatgat tttttaaaaa taataattgt ccctaaaggt 120
gaaatggatc aaagccctta aaagtgaatc tgtggtgtag taactgttaa cataattgtc 180
ttattttatt ctcatcccct taaagaataa aaytgatgaa caagtgagga tgctggtgta 240
actccctaac ttagtttata gtctgtaagc agaagagtga gtctaaagta catatcacca 300
gacagtgttt ctcctagcat ttcgctgttg cattaatcaa caagttaaaa tataaacaac 360
ggctaacctt gggtttcaaa tttaacattc cttatctctt agaccaggtt tatccactgt 420
ggtca 425

<210> 132
<211> 442
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 38
<223> 2-45-38 : polymorphic base C or T

<220>
<221> misc_binding
<222> 18..37

<223> 2-45-38.mis1, potential

<220>
<221> misc_binding
<222> 39..58
<223> 2-45-38.mis2, potential complement

<220>
<221> primer_bind
<222> 1..21
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 418..442
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 26..50
<223> 2-45-38 potential probe

<400> 132
gatgtaggaa gagtaaaaaa caaaaaattt ttgaatgygt aattatcact aattatttta 60
tttgatcctt caggagaatg tggaagatgg ccgagcaagt atctatcaat ctgtcgttac 120
caacaccagc aaagaaatgt cctgtttcag tgactttcca atgcctgaag attttccaaa 180
cttcctgcat aattctaaac ttctggaata tttcaggatt tttgctaaaa aatttgatct 240
gctaaaatat attcagttcc aggtattgta tttttgggga aatgggtttc tctgcattag 300
ttcagctcat atttagatag aaaagttact ctgataatga aagcaattat gaatgaagta 360
tcccattcta agtatttgtt gaaatataac agcctcatat aaaacccaaa aagtagtgtc 420
attacccttg gtattataga tt 442

<210> 133
<211> 442
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 183
<223> 2-45-183 : polymorphic base C or T

<220>
<221> misc_binding
<222> 163..182
<223> 2-45-183.mis1, potential

<220>
<221> misc_binding
<222> 184..203
<223> 2-45-183.mis2, potential complement

<220>
<221> primer_bind
<222> 1..21
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 418..442
<223> downstream amplification primer, complement

<220>

<221> misc_binding
<222> 171..195
<223> 2-45-183 potential probe

<400> 133
gatgtaggaa gagtaaaaaa caaaaaattt ttgaatgcgt aattatcact aattatttta 60
tttgatcctt caggagaatg tggaagatgg ccgagcaagt atctatcaat ctgtcgttac 120
caacaccagc aaagaaatgt cctgtttcag tgactttcca atgcctgaag attttccaaa 180
ctycctgcat aattctaaac ttctggaata tttcaggatt tttgctaaaa aatttgatct 240
gctaaaatat attcagttcc aggtattgta tttttgggga aatgggtttc tctgcattag 300
ttcagctcat atttagatag aaaagttact ctgataatga aagcaattat gaatgaagta 360
tcccattcta agtatttgtt gaaatataac agcctcatat aaaacccaaa aagtagtgtc 420
attacccttg gtattataga tt 442

<210> 134
<211> 442
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 335
<223> 2-45-335 : polymorphic base A or T

<220>
<221> misc_binding
<222> 315..334
<223> 2-45-335.mis1, potential

<220>
<221> misc_binding
<222> 336..355
<223> 2-45-335.mis2, potential complement

<220>
<221> primer_bind
<222> 1..21
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 418..442
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 323..347
<223> 2-45-335 potential probe

<400> 134
gatgtaggaa gagtaaaaaa caaaaaattt ttgaatgcgt aattatcact aattatttta 60
tttgatcctt caggagaatg tggaagatgg ccgagcaagt atctatcaat ctgtcgttac 120
caacaccagc aaagaaatgt cctgtttcag tgactttcca atgcctgaag attttccaaa 180
cttcctgcat aattctaaac ttctggaata tttcaggatt tttgctaaaa aatttgatct 240
gctaaaatat attcagttcc aggtattgta tttttgggga aatgggtttc tctgcattag 300
ttcagctcat atttagatag aaaagttact ctgawaatga aagcaattat gaatgaagta 360
tcccattcta agtatttgtt gaaatataac agcctcatat aaaacccaaa aagtagtgtc 420
attacccttg gtattataga tt 442

<210> 135
<211> 442
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 394
<223> 2-45-394 : polymorphic base C or T

<220>
<221> misc_binding
<222> 374..393
<223> 2-45-394.mis1, potential

<220>
<221> misc_binding
<222> 395..414
<223> 2-45-394.mis2, potential complement

<220>
<221> primer_bind
<222> 1..21
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 418..442
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 382..406
<223> 2-45-394 potential probe

<400> 135
gatgtaggaa gagtaaaaaa caaaaaattt ttgaatgcgt aattatcact aattatttta 60
tttgatcctt caggagaatg tggaagatgg ccgagcaagt atctatcaat ctgtcgttac 120
caacaccagc aaagaaatgt cctgtttcag tgactttcca atgcctgaag attttccaaa 180
cttcctgcat aattctaaac ttctggaata tttcaggatt tttgctaaaa aatttgatct 240
gctaaaatat attcagttcc aggtattgta tttttgggga aatgggtttc tctgcattag 300
ttcagctcat atttagatag aaaagttact ctgataatga aagcaattat gaatgaagta 360
tcccattcta agtatttgtt gaaatataac agcytcatat aaaacccaaa aagtagtgtc 420
attacccttg gtattataga tt 442

<210> 136
<211> 426
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 39
<223> 2-48-39 : polymorphic base A or G

<220>
<221> misc_binding
<222> 19..38
<223> 2-48-39.mis1, potential

<220>
<221> misc_binding
<222> 40..59
<223> 2-48-39.mis2, potential complement

<220>
<221> primer_bind

<222> 1..24
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 404..426
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 27..51
<223> 2-48-39 potential probe

<400> 136
gttttatttt attgatgggc tgtctggctc cctcaactrc aaagtaaact ccacaaaggc 60
agagagtttt gcctctttta ttcattgctg tacctgcatc acttagaaag tttctggcac 120
ctaggaagtg ttcagtaaat atttattgaa taagtttatg taaaacgtct cagactcctt 180
agagaaactg gtcttttggg gttggagaat aaagttcttt acctcatcag ttagactcta 240
tctaaggtac acgagggctt gctagtctcc taagttagtc tgctaataaa tgttaacccт 300
aataactgaa attattagca gaggtaatta tccagttcta tatcaaggca aaaagacagc 360
agtggataga aagatcttag aagtcccact aggttcatcc aagccaccat acacataggc 420
agaaaa 426

<210> 137
<211> 426
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 72
<223> 2-48-72 : polymorphic base C or T

<220>
<221> misc_binding
<222> 52..71
<223> 2-48-72.mis1, potential

<220>
<221> misc_binding
<222> 73..92
<223> 2-48-72.mis2, potential complement

<220>
<221> primer_bind
<222> 1..24
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 404..426
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 60..84
<223> 2-48-72 potential probe

<400> 137
gttttatttt attgatgggc tgtctggctc cctcaactac aaagtaaact ccacaaaggc 60
agagagtttt gyctctttta ttcattgctg tacctgcatc acttagaaag tttctggcac 120
ctaggaagtg ttcagtaaat atttattgaa taagtttatg taaaacgtct cagactcctt 180
agagaaactg gtcttttggg gttggagaat aaagttcttt acctcatcag ttagactcta 240

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tctaaggtac acgagggctt gctagtctcc taagttagtc tgctaataaa tgttaaccct    300
aataactgaa attattagca gaggtaatta tccagttcta tatcaaggca aaaagacagc    360
agtggataga aagatcttag aagtcccact aggttcatcc aagccaccat acacataggc    420
agaaaa                                                               426

<210> 138
<211> 426
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 156
<223> 2-48-156 : polymorphic base G or T

<220>
<221> misc_binding
<222> 136..155
<223> 2-48-156.mis1, potential

<220>
<221> misc_binding
<222> 157..176
<223> 2-48-156.mis2, potential complement

<220>
<221> primer_bind
<222> 1..24
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 404..426
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 144..168
<223> 2-48-156 potential probe

<400> 138
gttttatttt attgatgggc tgtctggctc cctcaactac aaagtaaact ccacaaaggc     60
agagagtttt gcctctttta ttcattgctg tacctgcatc acttagaaag tttctggcac    120
ctaggaagtg ttcagtaaat atttattgaa taagtktatg taaaacgtct cagactcctt    180
agagaaactg gtcttttggg gttggagaat aaagttcttt acctcatcag ttagactcta    240
tctaaggtac acgagggctt gctagtctcc taagttagtc tgctaataaa tgttaaccct    300
aataactgaa attattagca gaggtaatta tccagttcta tatcaaggca aaaagacagc    360
agtggataga aagatcttag aagtcccact aggttcatcc aagccaccat acacataggc    420
agaaaa                                                               426

<210> 139
<211> 426
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 285
<223> 2-48-285 : polymorphic base A or G

<220>
<221> misc_binding
<222> 265..284
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<223> 2-48-285.mis1, potential

<220>
<221> misc_binding
<222> 286..305
<223> 2-48-285.mis2, potential complement

<220>
<221> primer_bind
<222> 1..24
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 404..426
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 273..297
<223> 2-48-285 potential probe

<400> 139
gtttatttt attgatgggc tgtctggctc cctcaactac aaagtaaact ccacaaaggc 60
agagagtttt gcctctttta ttcattgctg tacctgcatc acttagaaag tttctggcac 120
ctaggaagtg ttcagtaaat atttattgaa taagtttatg taaaacgtct cagactcctt 180
agagaaactg gtcttttggg gttggagaat aaagttcttt acctcatcag ttagactcta 240
tctaaggtac acgagggctt gctagtctcc taagttagtc tgctrataaa tgttaacccct 300
aataactgaa attattagca gaggtaatta tccagttcta tatcaaggca aaaagacagc 360
agtggataga aagatcttag aagtcccact aggttcatcc aagccaccat acacataggc 420
agaaaa 426

<210> 140
<211> 420
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 167
<223> 2-49-167 : polymorphic base A or G

<220>
<221> misc_binding
<222> 147..166
<223> 2-49-167.mis1, potential

<220>
<221> misc_binding
<222> 168..187
<223> 2-49-167.mis2, potential complement

<220>
<221> primer_bind
<222> 1..20
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 396..420
<223> downstream amplification primer, complement

<220>

<221> misc_binding
<222> 155..179
<223> 2-49-167 potential probe

<400> 140
aagtcccact aggttcatcc aagccaccat acacataggc agaaaaatca aaataagata 60
tgagcctgga cagggtgagc aatctgggaa aagatgaaca cagtatgcta ggacccagaa 120
atcatcaagt ctatgaaaac taagccagaa cacaaatgtg aattccrtaa gatcaggaac 180
ataatctgtc ttgttcatcc aggcatggta atctgccaga aatagtgctt aactgcaaga 240
actgaatatt tgttagataa ttaaaccatc aactaaatga gattcatgca accatgaaaa 300
atgctgctat aggtacacaa tattgatata ctagaaagtt aaaaaatcaa gttggaaatt 360
agactattcc atttctgttt gtgtgtatgt atctacaaat aggtggaakg atataccaaa 420

<210> 141
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-436-43 : polymorphic base G or C

<220>
<221> misc_binding
<222> 482..500
<223> 10-436-43.mis1

<220>
<221> misc_binding
<222> 502..521
<223> 10-436-43.mis2, potential complement

<220>
<221> primer_bind
<222> 459..476
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 859..878
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-436-43 potential probe

<220>
<221> misc_feature
<222> 297,539,629,650,976..1001
<223> n=a, g, c or t

<400> 141
tatatttaat acatatattt aataaaaaca ttaaatacat atatttaata aaaatataat 60
ttatatataa tatacatata tttatatata aatatattta tatataatat gcatatgttt 120
attttacata tataaatata tttatatata aatatacgta tatttatttt atatatatat 180
gtgtgtgtgt atatatatat atacacacac acacgtatat acccagggag aggcactaat 240
tgtgcagttt tgaaaagttt cctagtgatg ctgccgtggc ctactttcaa agcactntgc 300
ttaggtttac cacttaaaat gttattacat ttttccagaa gtacacttta aaatactttg 360
tttttaaagt gaggcattac aatggtgtca tgagctgaca ttcccagcca ctgactggaa 420
gatttgggtc aacccaggga acaggcttgg tttaagggag ttcaagtgtt ggtggccttt 480
gggtaaaagt ttatgtctat stttgtatgt gggattcagt agggattttc tttaatgtnt 540

```
aaaaattcta gtttcctctg tatttgcttt ccttcttccc ctgtcctccc tgagcctcca    600
cacatgtgta acacatttta tttgccaant aggtcaagga ggttaaaaan gactttgtcg    660
ggcttggaag tcagcatggt tactgcagtt cccggtaggc taccagtcat gaccatgatt    720
ccagatgttg actgcctgct ctgggccatt gggcgggtcc cgaataccaa ggacctgagt    780
ttaaacaaac tggtaagctg gcttggtctg cccgaaacat ttgtgaatct actgggagtc    840
ttatggtttt attttccccc cagacaccca aaacttgggt ggattccatt ggattctttt    900
ctctttttcc catgtattca gtttgtgatc aaatttcatt gcttcttcct ttgaaattaa    960
aaaaaaaagt tttctnnnnn nnnnnnnnnn nnnnnnnnnn n                       1001
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<210> 142
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-436-376 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 10-436-376.mis1, potential

<220>
<221> misc_binding
<222> 502..520
<223> 10-436-376.mis2, complement

<220>
<221> primer_bind
<222> 126..143
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 526..545
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-436-376 potential probe

<220>
<221> misc_feature
<222> 206,296,317,643..685,853
<223> n=a, g, c or t

<400> 142

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tccagaagta cactttaaaa tactttgttt ttaaagtgag gcattacaat ggtgtcatga     60
gctgacattc ccagccactg actggaagat ttgggtcaac ccagggaaca ggcttggttt    120
aagggagttc aagtgttggt ggcctttggg taaaagttta tgtctatgtt tgtatgtggg    180
attcagtagg gattttcttt aatgtntaaa aattctagtt tcctctgtat ttgctttcct    240
tcttcccctg tcctccctga gcctccacac atgtgtaaca cattttattt gccaantagg    300
tcaaggaggt taaaaangac tttgtcgggc ttggaagtca gcatggttac tgcagttccc    360
ggtaggctac cagtcatgac catgattcca gatgttgact gcctgctctg ggccattggg    420
cgggtcccga ataccaagga cctgagttta aacaaactgg taagctggct tggtctgccc    480
gaaacatttg tgaatctact rggagtctta tggttttatt ttccccccag acacccaaaa    540
cttgggtgga ttccattgga ttcttttctc tttttcccat gtattcagtt tgtgatcaaa    600
tttcattgct tcttcctttg aaattaaaaa aaaaagtttt ctnnnnnnnn nnnnnnnnnn    660
nnnnnnnnnn nnnnnnnnnn nnnnntcttt ttgtttttga gaaaggtctt gctctgtcac    720
ccaggctgga gttcagtggt gtgatcatag ctcaccgcag tcttaacctc ctaggctcaa    780
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gtgatccacc cacctcagct tctggagtag atggaactat gtgtgtgcca caatgcccag 840
ctaatttttt tantttatt ttttttagag atgaggtttc accatgttgc ccaggctggt 900
ctcctcggct caagcgattc gcccatctca gcctcccaga gtgctgggac tataggcatg 960
tcccagcatg tcccagaaaa aggccgccac gtctggcctt t 1001

<210> 143
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-431-51 : polymorphic base A or C

<220>
<221> misc_binding
<222> 482..500
<223> 10-431-51.mis1

<220>
<221> misc_binding
<222> 502..521
<223> 10-431-51.mis2, potential complement

<220>
<221> primer_bind
<222> 451..468
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 853..872
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-431-51 potential probe

<400> 143
agcatcccctt atctgaaatg cttgggacca gaagtgtttt cagtttcaga ttttggaata 60
tttgcatata tataatgaga tattttgcag atgcgaccca agtcgaaaca cggaattcat 120
ttgttttaca tacaccttat acacatagtt ggaaggtaac tttatacgat attttaaatg 180
tgtgcatgag gcatactttt gtctgcgttt ttgactgcaa cccttcacat gaggtcaggt 240
gtggaatttt ctgcttgtgg catcatggtg ctccaacatt ttggattttg gattttgaat 300
ttctggatta gggatgctca acctgtaata gaatgtatag gattctcata agccaatcat 360
tttgagttgt tcgctgaggc atgacatatc ttcgctgtat taaactatct agatagtgta 420
atgaacaatg gtgtgaaact gtcagaacta gggcattaag gtagatggat aaatggctag 480
tggaacaatt tagctatgtt maaacagaca gtaagataaa cactgatttt aaaatatctc 540
catagttgca atagctgctg gccgaaaact tgcccatcga ctttttgaat ataaggaaga 600
ttccaaatta gattataaca acatcccaac tgtggtcttc agccaccccc ctattgggac 660
agtgggactc acggaaggta ggtatttaaa aactgaaggt catttgtggt ttccttcctc 720
tttcccctgc ccccaacttt aaattaggtc tctgtcagct gatgaaacct atctcagccc 780
cagattacat tgcttttttgg ttactctctt gtcacagttc cagttttctc ccctgctact 840
actttgagtg tacagtatct ttccttcaca ccaccctatc tctttgatct ttttttttta 900
gctttttat ttgaactaat tttaaattta aagaaaagct ctaaaaataa tacaaaggac 960
tcctctctaa ccttaatatt tttgcttttt tattttttca c 1001

<210> 144
<211> 980
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 477
<223> 10-432-93 : polymorphic base A or G

<220>
<221> misc_binding
<222> 457..476
<223> 10-432-93.mis1, potential

<220>
<221> misc_binding
<222> 481..499
<223> 10-432-93.mis2, complement

<220>
<221> primer_bind
<222> 388..407
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 758..775
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 465..489
<223> 10-432-93 potential probe

<220>
<221> misc_feature
<222> 297,477,629
<223> n=a, g, c or t

<400> 144
acacacacac atgtctatct ttcctaagaa ctggccctta cataaaccga gtatcatttt 60
cttttttttt ttctttttga gacaagctct cccactgtca cccaggctgg agtgcagtgg 120
cacgatctct gctcactgca acctccgcct ctgggttcaa gcaattcttc tgcctcagcc 180
tcccgaatag ctgggactac caggcctgca ccaccaccat gcctggctaa ttttttgtag 240
agatggggtt tcactgtgtt gcccaggctg gtctcaatct cctgggctca agcgatncca 300
cctgcctctg cctctcaaag tgcagggatt acaggcatga gccactgtgc ctggcctttc 360
ttttcatcta gaggcagaat tcctcagccc ttcttttgtc ttatatgaca ctgacattta 420
ttttgtagaa tacttctcat tttggcgtgg tttgatattt cctcgtggtt tgattgragg 480
ttatgtattt ctggtcatct ccctctttga tagttcagtg taattgttta gttttctgat 540
agatgctttt tttaatgtgc attgtagatg aagccattca taaatatgga atagaaaatg 600
tgaagaccta ttcaacgagc tttaccccng atgtatcacg cagttaccaa aaggaaaaca 660
aaatgtgtga tgaaaatggt ctgtgctaac aaggaagaaa aggtaaggaa aaatccagca 720
aactaaatag tgccttgcaa aatggacagg gatggcagta ttttgcaggg gtggaaagga 780
gggagaccaa gcagttgagc cttctgattc aactggacag gcccactttg atctgtctta 840
cctgcatttt ggggttcttc ataatatttc atctagaagg aggttccact ccttttaaaa 900
aataaagacg atgccaggcg tggtggctca cacctgtaat cccagcacgc tgggaggccg 960
aggcaggcat atcacctgag 980

<210> 145
<211> 933
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 433

<223> 12-631-208 : polymorphic base A or G

<220>
<221> misc_binding
<222> 414..432
<223> 12-631-208.mis1

<220>
<221> misc_binding
<222> 434..453
<223> 12-631-208.mis2, potential complement

<220>
<221> primer_bind
<222> 226..245
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 705..725
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 421..445
<223> 12-631-208 potential probe

<220>
<221> misc_feature
<222> 30
<223> n=a, g, c or t

<400> 145
gcaggcctgt aatcccagca ctttgagagn ccgaggcagg aggatctctt gaacccagga 60
gttcgagacc agcctgggca acatagtgag accctgtctc taaaaacaaa acaaaaaact 120
tctcagccta aattctcaca agaccttcat cttatcaacc tgtttatttc cttttcagtg 180
ttcgccagga tgcgaaagca ctgtctatga ttgcccctgt gctctttgcc tctaccctct 240
tacacgtaaa accatcacac ctggagggaa aaggttcctc gaagtgaagt cagctccgga 300
agtggggggg caggggcgat gcagtctggg agttgtagtc aaagctgctc cgaagccacg 360
cagccgaaga ggcggtcgtt ctatgcaaca ttcctgtgaa aattacccag ctgtgactgt 420
cgaagggaaa aartcacact tacctatatc cgggatccca cgccggagct ccagacacac 480
aagggggaca gcagagagga agaaaatgcc aacaacccca cgtgaagcca tggtggcgga 540
agcgcctggt gcaggcggaa agcccgcccc ttccggccgc gttttccggg aaggaagtgg 600
aactcttctt gccgcgggcc ggctggagag ggtcaataac gtggtaaata ctgacggccg 660
tgtcgttatt gagggggagc taagccccgt gttttaaagt tatagtctgt agccgtgttt 720
cagaagaaag gcaagtcgtc ccccaagtca catgatgtcc agaggagcct gggctctaga 780
gcggtggctc cctggagggt agcagggcag gggctgcccc ttcggtcttt gcagcgtctg 840
tgagaaagcg ctttccagag ggaaatgaag ccgaagaaaa agctgatgct gtgaggaggc 900
agcctgggcc ccccggcctt gtggccgtat agg 933

<210> 146
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-260-282 : polymorphic base G or T

<220>
<221> misc_binding
<222> 481..500

<223> 10-260-282.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-260-282.mis2, potential complement

<220>
<221> primer_bind
<222> 220..238
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 636..655
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-260-282 potential probe

<400> 146
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tatcttcctc acagggctga atgatgaatc tatgtaaagt atttaaaata gtaccttgca     60
catagtaagt gctcaataac ttgtgggttt ctttttgtta tttgcatttt gctttttttgc   120
ttctctctct tcaatacgta gagataaact atcacagaat ctggaagctc tctgggttcc    180
actctccccc ttccactctc ccaaggtaac cactaatcta cagttggtgt gtcctcagta    240
aatataggcc agactttcca tgggattcca tttgcaggaa gacaacccgt tcacaggtgc    300
cctacccctg tcccattctc tcttcttgat cacaggtggt gagctatgcc ccattcacgc    360
tcttcccctc actggtcccc agtgccctgc tggagcaagc ctatgctgtg cagatggact    420
tcaacctgct agtggatgct gtcagccaga acgctgcctt cctggagcaa actctttcca    480
ggtaggggac agtgaagcat kgggggccca ggagctgcca gagccaagga actggaagat    540
tgcagagccg tgaggtgtta ctgtgtcagc tgacttggtg ggatagagga aaggtacctc    600
caaagaacaa aaagtcatag gagtcaggaa agctggcttc taatcctggc tcgaccagtt    660
atttatatgg cctcaagcca ctccctttcc ttctctgggc ctaaggtttc ttcatctgaa    720
aaatgaagag actggcttaa atccaagatc ccttttattg ttgacattct gtaatccgtg    780
acaccctact ttgaagactg atatttccat ttggaattag gggaagtcag cctggttttg    840
gaggaaaaca gaggtaggga aggttattgg gttaaagtca gattttctac ttctcctaag    900
cagcgacact ttcttgtcac ctcaggcctc tcatctttgg atgggatggg gtacagactg    960
ggccacactc agggcatgag gaagcaacct ctgaaatggt t                       1001
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<210> 147
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 10-263-26 : polymorphic base A or C

<220>
<221> misc_binding
<222> 483..502
<223> 10-263-26.mis1, potential

<220>
<221> misc_binding
<222> 504..523
<223> 10-263-26.mis2, potential complement

<220>
<221> primer_bind

<222> 478..496
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 820..837
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 10-263-26 potential probe

<400> 147
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cagctatgat tgtgctttcc tgggccccgg gtcacatgtt gcccctggcc accccgacag 120
cagtttccac ttgtaatgag atccttggta tgtcagggag aaaaaggacc tcatagctca 180
tctagtcctg tccctccatt gtacaggcag agggaacaat atcttgagag ccccagagag 240
aggaatgcag ggacttctgt ctgggggctg ggcctggtag catccatttc tagccagcag 300
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aggcccagag taaggggctc cagctcactg ggacactagg gtaggttggg gtggggacag 420
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attccaacct gaagtggatc ttmcaggaat gtgatgggag gatgcttttt agtgctcagc 540
tgattctcag agtcatgttg ctgtatatat gaggtcatgg gcagaggggt cttccaggtc 600
catccaatta ctgaacagcc atctctcttc caacagacat gttctcagtg tcctgagtaa 660
gaccaaagaa gctggcaaga tcctctctaa taatcccagc aagggactgg ccctgggaat 720
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atcctgcttt agtttcagca ttcatgggtt tagcaacttc ttttcttgcc agccatcatt 840
agagaataag gggatttttc taggaataga aacttatacc tttacatgcc aaaattattt 900
taaggtttcc ttcttaaata acagatgctg actatgattt aactttttct tattgagtgg 960
aggtcatcat tatgactgtc aacaattgca gcttgctgta a 1001

<210> 148
<211> 981
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-258-408 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 10-258-408.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-258-408.mis2, potential complement

<220>
<221> primer_bind
<222> 95..112
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 504..521
<223> downstream amplification primer, complement

<220>

<221> misc_binding
<222> 489..513
<223> 10-258-408 potential probe

<400> 148
tcctgagggg tatcctccta aagacctcca aagtttttat ggaagggtaa atactggtac 60
cttcccccag ctttccatct gaggaccaga aaagttgtgt ctcccttaga tgagatctag 120
acgcccccaa atccttgaga tgtgggtata gctcagggta agctgctctg aggtaaaggt 180
ccatgaaccc tgccccactc ctgtcagccc ctcatcagcc ttttcagcag gttccagtgc 240
ctgacttggg ataggactga gtggtaggag gagggggagt ggagggggcat agcctttccc 300
taattctgcc ttaaataaaa ctgcattgct gattcagtga tgattcctta cttcgtgcat 360
agaggggagg cgggagctgt aatctacgtt agcccactta agatgtatta gagcagggaa 420
gtgactggtc tgtaatcagg gtccccctag accagtctct acaggtggaa ccctgaagtt 480
tcaatcctta gccacccact ratgctctta ctggatcaca gggaggaatg agagtccctg 540
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tcagtcactt tcctgcttag ctcaggggct tgtcaaaggc cctgtcagtg aagcctcctt 660
cgctctgccc aaaccaaaag ttctagaagg aagatattgg ggatagtcct aggaaatacc 720
cctcccttcc catctgccac acaaatcaga gccactaatg aatatacagc ctcagggcac 780
agatacctaa gaaaacaagt caccacttct tgagatcaca ggctttattc ctacaaccac 840
agggcttgag cctgactggg gcaagaaaac agagtttcat ctgagaatgt ctcttatggg 900
ctgggttctg ttcaggggag ggtgggaaca gaggacaagg aagacaagct cctctggccc 960
taggaacaaa acacatttac t 981

<210> 149
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-317-259 : polymorphic base G or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-317-259.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-317-259.mis2, potential complement

<220>
<221> primer_bind
<222> 742..759
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 297..317
<223> downstream amplification primer.

<220>
<221> misc_binding
<222> 489..513
<223> 12-317-259 potential probe

<220>
<221> misc_feature
<222> 426,432,443,459,841,849..850,898,914
<223> n=a, g, c or t

<400> 149
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gcatagagat ggaaaatagt ttcatggttg cctagagcta aggagtttgg tgggaaatag 120
gaagtgactg gtagtgagta caaggctgct tttgggggt gatgaagata ttctaaaatt 180
gattgtggta atggctgcac aactctatga atgtcctaaa aatcacgata ccatggttaa 240
ctaaatgggt gaattgcatg gtatgtgaat tgtacctcaa agctgttaaa aaaaaaaaaa 300
agtgagtgtg catgtccgca gaaaacagtg cagtgcagac agagagtggt gaccgctcca 360
atcggtgtgg tagagctgaa gagactcagg ggagcacagg cctcgtgagc tggttttccc 420
atcctncatc cnttgggact ganccttgtt gctaagctnc tggccattgc tttggagact 480
gtttcttgaa aatatttatc rcagaaagtc ttgtcaggcc tgcgcaagcc aggcaccaaa 540
agttggtggt gacttggaga ggggtcaggc tgccctgtct ctttcttcgc agacgttcat 600
ttctcagtag gacttgtgtg ccccacactg tgcccactgc ttgcataaac atccttccct 660
gcaggactcc ctagagcacc atgggctggg tgccgaggat gccaagcacg caaggtctca 720
cagcagtgca cgacagaggc aggattctgc gtgatagttc ttcaggttca cttcacagat 780
tagctgacac ttaactgttc tggaagctgg gccaaggagt gctaacatgg aaattgagta 840
nactatagnn ttttttgccc aaggtacagg agaataaata tgagtagata gaatctcntt 900
aaattaaaaa tttnctccag taaatttttc ctaagtcttt gcctcctgcc tgtttagttc 960
ccattaaaag cttggagatg aaaaagaata caaagtaaca a 1001

<210> 150
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-323-385 : polymorphic base T or C

<220>
<221> misc_binding
<222> 502..520
<223> 12-323-385.mis1, complement

<220>
<221> misc_binding
<222> 481..500
<223> 12-323-385.mis2, potential

<220>
<221> primer_bind
<222> 868..886
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 416..435
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-323-385 potential probe

<220>
<221> misc_feature
<222> 303,710
<223> n=a, g, c or t

<400> 150
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cgaggtgggc agatcacttg aggtcaggag accagcctgg ccaacagggt gaaaccctgt 120
ctctactaaa aatataaaaa ttagcccagc atggtggtgc atgcctgtag tcccagctac 180

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ttgggaggct gggacagaaa aattgcttga acccaggagg cagaggttgc agtgagcaga    240
gattgtgcca ttgcgctctg gcctgggcat cacagtgaga ctccgcctta aaaaaaaaaa    300
tcnttaaaat ttaagacaaa acaaaaaacc ataagaagtg ggctgggggt ggtgggacct    360
gttttgggaa ccatatactg agttagacag ggctagagga actggtgagc tacaagttac    420
agttgccaat aatagtagta gcttacattt gttttgtact agggaaaagg aaaagtggaa    480
gcagttgttc cccaatgccc yctgcacagc aaattcctgt cctccattac tagaaataga    540
ggcgagtatg ggattcatga gagcttctag gaatcatgca ctcgttttgg gcacattcac    600
tgataccctt gctaccaggt cctgtgcatt gagtctcagg agaaagggta ggatatatgc    660
cttcatcaaa gtatggtcag attatttggg aaatagatgc aggaacagan ttattaaaag    720
ttcatgtgat ctgtgcagtg aaagagaaac acccaatcca gtggaagtaa attagtggga    780
tgaaggatag caggtgttat ctgagtagca cggggatggt tcaaaatgag aaaagttgat    840
gtagtacatg ccatttacag attttaagga gtaatgagtg agaatagaac caaatagcac    900
aaggcattcc ataaaattat cattcttaat aaaagctagc aatagaagga aaacttataa    960
actatatata gggtatttat taaaatttaa cttataggat a                       1001
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<210> 151
<211> 857
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 357
<223> 12-324-219 : polymorphic base C or T

<220>
<221> misc_binding
<222> 337..356
<223> 12-324-219.mis1, potential

<220>
<221> misc_binding
<222> 358..377
<223> 12-324-219.mis2, potential complement

<220>
<221> primer_bind
<222> 139..157
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 579..599
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 345..369
<223> 12-324-219 potential probe

<220>
<221> misc_feature
<222> 442
<223> n=a, g, c or t

<400> 151

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gccacgtggg catctggtgc agctccctca gtcattcttg tctccctgct ggagacaggg    120
tgtctgatgc cagcattctt accctgcatg acttgccttg acagcctgcc tttcatgtac    180
ctttcatatc cacctggttt tcaaatcggt ccagggacag agtgacacag cgcaccagca    240
tgttggagtc caccagggag ctgttgatct gcttcaggaa tacctggaac tatacagaaa    300
ccaagctcac agcaggcagt gggctgctgg ccaggtatgg ccatggcccg gggggayagt    360
cactacaagg ggcatcagcg acctctacca gccccactgc ttcagatagg aagacagagg    420
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ctcagataag ctgagggacc tncccctcac cacccaggta ctaagaggca ctccccggaa 480
ttcagcacag atccgacact ctctccagtg gttttacgct caagggtgct ggattccttt 540
aatttttact tttaatttta cttcagctag cctgagctgg gtttctgtca cacacactcg 600
gtgagcctaa cacaccaggc ccagtccctc cctacagcgg ctcccaccgt ggcacccacc 660
atgctgcgtc acggcaggcg cacaagccac ccattcccac cctcactccc tacccacaag 720
cagccccggt tttcatccct gcattcccag ggtctagcac aaagccagac agagcaggtt 780
ccaatgaatg tttgccaaag actgcccaga ctccccgtc gtctctaacg taaaacctgt 840
gcctaaagcc tggcaga 857

<210> 152
<211> 973
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 473
<223> 12-324-335 : polymorphic base G or C

<220>
<221> misc_binding
<222> 454..472
<223> 12-324-335.mis1

<220>
<221> misc_binding
<222> 474..493
<223> 12-324-335.mis2, potential complement

<220>
<221> primer_bind
<222> 139..157
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 579..599
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 461..485
<223> 12-324-335 potential probe

<220>
<221> misc_feature
<222> 442
<223> n=a, g, c or t

<400> 152
attaaagtgt tgaacaaggc agcaaagcca attgccctgg aagccgccac cttgaggccg 60
gccacgtggg catctggtgc agctccctca gtcattcttg tctccctgct ggagacaggg 120
tgtctgatgc cagcattctt accctgcatg acttgccttg acagcctgcc tttcatgtac 180
ctttcatatc cacctggttt tcaaatcggt ccagggacag agtgacacag cgcaccagca 240
tgttggagtc caccagggag ctgttgatct gcttcaggaa tacctggaac tatacagaaa 300
ccaagctcac agcaggcagt gggctgctgg ccaggtatgg ccatggcccg gggggatagt 360
cactacaagg ggcatcagcg acctctacca gccccactgc ttcagatagg aagacagagg 420
ctcagataag ctgagggacc tncccctcac cacccaggta ctaagaggca ctsccggaa 480
ttcagcacag atccgacact ctctccagtg gttttacgct caagggtgct ggattccttt 540
aatttttact tttaatttta cttcagctag cctgagctgg gtttctgtca cacacactcg 600
gtgagcctaa cacaccaggc ccagtccctc cctacagcgg ctcccaccgt ggcacccacc 660
atgctgcgtc acggcaggcg cacaagccac ccattcccac cctcactccc tacccacaag 720
cagccccggt tttcatccct gcattcccag ggtctagcac aaagccagac agagcaggtt 780

ccaatgaatg tttgccaaag actgcccaga ctccccgtc gtctctaacg taaaacctgt 840
gcctaaagcc tggcagacca ggactccagg tgaacttctg gacaacccag cacactccac 900
agagccctgg gttaacttta cctttgcatc ggtgttgata tatttattga atctcttgaa 960
tgcatcaacg ttg 973

<210> 153
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-324-380 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-324-380.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-324-380.mis2, potential complement

<220>
<221> primer_bind
<222> 122..140
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 562..582
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-324-380 potential probe

<220>
<221> misc_feature
<222> 425
<223> n=a, g, c or t

<400> 153
ggcagcaaag ccaattgccc tggaagccgc caccttgagg ccggccacgt gggcatctgg 60
tgcagctccc tcagtcattc ttgtctccct gctggagaca gggtgtctga tgccagcatt 120
cttaccctgc atgacttgcc ttgacagcct gcctttcatg tacctttcat atccacctgg 180
ttttcaaatc ggtccaggga cagagtgaca cagcgcacca gcatgttgga gtccaccagg 240
gagctgttga tctgcttcag gaatacctgg aactatacag aaaccaagct cacagcaggc 300
agtgggctgc tggccaggta tggccatggc ccggggggat agtcactaca aggggcatca 360
gcgacctcta ccagccccac tgcttcagat aggaagacag aggctcagat aagctgaggg 420
acctnccccct caccacccag gtactaagag gcactccccg gaattcagca cagatccgac 480
actctctcca gtggttttac rctcaagggt gctggattcc tttaattttt acttttaatt 540
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ggcccagtcc ctccctacag cggctcccac cgtggcaccc accatgctgc gtcacggcag 660
gcgcacaagc cacccattcc caccctcact ccctacccac aagcagcccc ggttttcatc 720
cctgcattcc cagggtctag cacaaagcca gacagagcag gttccaatga atgtttgcca 780
aagactgccc agactccccc gtcgtctcta acgtaaaacc tgtgcctaaa gcctggcaga 840
ccaggactcc aggtgaactt ctggacaacc cagcacactc cacagagccc tgggttaact 900
ttacctttgc atcggtgttg atatatttat tgaatctctt gaatgcatca acgttgaact 960
tcatcagctc ccccaggagg tcaaagtaac tctggagcac a 1001

<210> 154
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-325-30 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-325-30.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-325-30.mis2, potential complement

<220>
<221> primer_bind
<222> 472..491
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 926..945
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-325-30 potential probe

<400> 154
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ctttgggagg tggaggcgtg tggatcacaa ggtcagaaga tcaagatcat cctggctaac     60
acggtgaaac cccgtctcta ctaaaataca aaaaattagc caggcgtggt ggtgtgtgcc    120
tgtaatccca gctactcagg gaggctgagg cgggagaatt acttgaaccc aggaggcgga    180
ggttgcagtg agccaagatc gagccactga actccagcct aggcgactga gtgagactcc    240
atatcaaaaa aaaaaaaata caaagcctca acccctcctt cccatcaggc ctcttgcatc    300
agagtctctg ggatggggcc caggaatctg tattctttcc cagctcccca gaatgttcag    360
ccaggtttgg aaactgatct atccgattct tcttgtttca cagttaggga atctgtagct    420
ctgggaaggg aaggaacttg ccccagtcac atctgatatt agtgcttctt tctccaatga    480
agagccttta ggctgggagt ycagagacat gggttcaagt ccaggctata ccagtcatca    540
cctcgggcaa gtcatttcac ctctccaagc ctctgcttcc ttactgtgag aataatgcca    600
ttgtgttggg aatcaaaaga gagagtggca atggaaatgc tttgtcaagc tttctatttt    660
gtgcacatgg aagttgttaa gagctagaac cagccagtgt tcactcctgt ataccacgct    720
gttcccttcc aacagaggtc agggtcctgc tgtgttgggg gtggccgcca gccagtttcg    780
gtggttgctg ggcttcaggc catctgttac caactctctt ctctccatct tttgcaggtg    840
ttgggatggc caccaactgg gggagcctct tgcaggataa acagcagcta gaggagctgg    900
cacggcaggc cgtggaccgg gccctggctg agggagtatt gctgaggacc tcacaggagc    960
ccacttcctc ggaggtaagc ccctagctcc tccccacagc a                       1001
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<210> 155
<211> 999
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 479

<223> 12-327-31 : polymorphic base G or T

<220>
<221> misc_binding
<222> 459..478
<223> 12-327-31.mis1, potential

<220>
<221> misc_binding
<222> 480..498
<223> 12-327-31.mis2, complement

<220>
<221> primer_bind
<222> 449..468
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 982..999
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 467..491
<223> 12-327-31 potential probe

<220>
<221> misc_feature
<222> 758
<223> n=a, g, c or t

<400> 155
tgtcttaaaa gctagttttt caatgttaac aggctggaaa tattgttaat acaaaaacct 60
atcactgtgt accttatggt acaccaaata aacaaggtaa aattatacaa atgtatcatt 120
aaaaagcagc agtagaaaac catgaccatg cagaggtagc cctaatcatg ctctgaaaac 180
agttctttgt ttctaaagtc cagttgtgtg cattccccag gctggctctg cagagttatc 240
aagtgcttca gagcagcctc ctctcctgag gctgaatatg aacctgccat tcactctgtt 300
attgtctagt tttagttagg aacatgaggt gatcataact atactttgta ggttattagg 360
gaatataatt ttacatgttg tagtcatatg taaaggtaga agtttgtgga ctccaacccc 420
agtttattct ctctctagat ttgcttttcc tcctgtgtca ctagatacaa ggtcttcckt 480
ggtctgtgta cggttttctt cccactcctt tatgatttg ggggagttct cattttagga 540
aatttacatt tttaaaaaat atgtgacttt ccaacatggc acatatatac atatgtaaca 600
aacctgcacg ttgtgcacat gtaccctaga acttaaagta taattttaaa aaaagtgact 660
ttcattataa ctaaattata cctcagagct ggtgtacaca cctccatata cattgacaaa 720
aggtagtatt tgctaagctc ctggtatgtg gcaaacgnct gggtaactgc tttacctaga 780
agtgatttta tttaatcctt caagtgccct gtggaataga gattagtatc cccattgcac 840
atgtgaggaa actgagggct agaaaggttc tgtattggat gcctgtgtat gccgaggcac 900
taagtaactt tcatctttta gtttcccatt taaggaatct attctggcag atgattttga 960
tcctgttagt attgattgct tgcttcagat gcctatttg 999

<210> 156
<211> 1000
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 500
<223> 12-327-415 : polymorphic base A or G

<220>
<221> misc_binding

<222> 480..499
<223> 12-327-415.mis1, potential

<220>
<221> misc_binding
<222> 501..520
<223> 12-327-415.mis2, potential complement

<220>
<221> primer_bind
<222> 86..105
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 615..633
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 488..512
<223> 12-327-415 potential probe

<220>
<221> misc_feature
<222> 395,958,975
<223> n=a, g, c or t

<400> 156
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ctgtgtacgg ttttcttccc actcctttat gattttgggg gagttctcat tttaggaaat 180
ttacattttt aaaaaatatg tgactttcca acatggcaca tatatacata tgtaacaaac 240
ctgcacgttg tgcacatgta ccctagaact taaagtataa ttttaaaaaa agtgactttc 300
attataacta aattatacct cagagctggt gtacacacct ccatatacat tgacaaaagg 360
tagtatttgc taagctcctg gtatgtggca aacgnctggg taactgcttt acctagaagt 420
gattttattt aatccttcaa gtgccctgtg gaatagagat tagtatcccc attgcacatg 480
tgaggaaact gagggctagr aaggttctgt attggatgcc tgtgtatgcc gaggcactaa 540
gtaactttca tcttttagtt tcccatttaa ggaatctatt ctggcagatg attttgatcc 600
tgttagtatt gattgctttc agatgcctat ttgtaaactg acttaagtaa aaccagcatt 660
acccattatt cttgaggaat gaactgttct ggtcagctgg gctttttga ttaactgaga 720
acggaaagcc cagtttttgt ttttgttttt ttatttggga gttttttctt aaagtctcta 780
taaaataatc tagattcact ttcatatctg tgtgactagc ctagtagaca gtctatgtgt 840
gattctgctt gtagcttttg ggataaagcc taaaagttgt agttccacac atgaggttgt 900
gcaggatctg acccttccca accctgacca taattcctac tccattccct tacccgcnac 960
gattttctcc attcnaaatg ccctgggaag gccaagctgg 1000

<210> 157
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-331-270 : polymorphic base G or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-331-270.mis1, potential

<220>

<221> misc_binding
<222> 502..521
<223> 12-331-270.mis2, potential complement

<220>
<221> primer_bind
<222> 751..770
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 285..305
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-331-270 potential probe

<400> 157
aactacggct tgggaggtgt actaagccaa gggccagaac acaaaatcag gtcctaacac 60
taagtgccat cctcttttgt ttctaccaga ttgctttctt tattcaccat tcttcctggc 120
tcagtggtca acctagtaga gtcctgctca atatatgggc ggggcttctg gttctcattt 180
tgttttctaa caaggaaaat gaagaaatag gcataatgga gttaaaatga gtcttaaagg 240
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taaggccaaa ggagtttact acctgctgca gcagtcctgg ctcttaacaa ctgctacaaa 360
attctgcctc cccgtaattt ctaccagtta gtcctgattt tcaggcacac ataaaataag 420
cccgattccc ccactgtctg aaagcagctc ttatgtctgc cattctactc gaatattccc 480
atcttaaaca ttgcagacct rgtaggggag ataaacagag ccccagtggc aggggtactt 540
acacagacac aggtattata caggatactc aagcagtcct tggacatttc atcacttact 600
gaaagtgaaa gggtaatgac tggttatttt tctcaatgaa aagatagtac aacagttacc 660
acattttttt cagcataaga actgttataa tcccctccaa gatgattatt tttcctttaa 720
tatacttctt ccagcccctg tctaccaaag gttttcatag tgcccatcag aacctacaag 780
cccatttgca tattgctttt ggtttgatac agcagctgtt ttcttattat gctccacagt 840
cttcataatt tcaacctgtt gttgtgccat catttaataa agccattttc ccttaatgtc 900
ttgcttagga tatatctagg atttgttttt tttgtttttt gtgtttttttg gctatttaag 960
tagaccacaa atgaacaact taatatatat gtgtatcctt t 1001

<210> 158
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-331-275 : polymorphic base T or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-331-275.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-331-275.mis2, potential complement

<220>
<221> primer_bind
<222> 756..775
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 290..310
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-331-275 potential probe

<400> 158
taagaaacta cggcttggga ggtgtactaa gccaagggcc agaacacaaa atcaggtcct 60
aacactaagt gccatcctct tttgtttcta ccagattgct ttctttattc accattcttc 120
ctggctcagt ggtcaaccta gtagagtcct gctcaatata tgggcggggc ttctggttct 180
cattttgttt tctaacaagg aaaatgaaga aataggcata atggagttaa aatgagtctt 240
aaaggtcaca gtctgccaac acttgtcacc ttttgacaag tgtccagttt ctacttggac 300
agctctaagg ccaaaggagt ttactacctg ctgcagcagt cctggctctt aacaactgct 360
acaaaattct gcctccccgt aatttctacc agttagtcct gattttcagg cacacataaa 420
ataagcccga ttcccccact gtctgaaagc agctcttatg tctgccattc tactcgaata 480
ttcccatctt aaacattgca kacctggtag gggagataaa cagagcccca gtggcagggg 540
tacttacaca gacacaggta ttatacagga tactcaagca gtccttggac atttcatcac 600
ttactgaaag tgaaagggta atgactggtt atttttctca atgaaaagat agtacaacag 660
ttaccacatt tttttcagca taagaactgt tataatcccc tccaagatga ttatttttcc 720
tttaatatac ttcttccagc ccctgtctac caaaggtttt catagtgccc atcagaacct 780
acaagcccat ttgcatattg cttttggttt gatacagcag ctgtttttctt attatgctcc 840
acagtcttca taatttcaac ctgttgttgt gccatcattt aataaagcca ttttccctta 900
atgtcttgct taggatatat ctaggatttg ttttttttgt tttttgtgtt ttttggctat 960
ttaagtagac cacaaatgaa caacttaata tatatgtgta t 1001

<210> 159
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 12-334-320 : polymorphic base A or G

<220>
<221> misc_binding
<222> 483..502
<223> 12-334-320.mis1, potential

<220>
<221> misc_binding
<222> 504..523
<223> 12-334-320.mis2, potential complement

<220>
<221> primer_bind
<222> 184..202
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 616..634
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 12-334-320 potential probe

<400> 159
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ccagcctggg caacagagtg agactccatc tcaaaaaaaa gaaaaggata acgtgataga      60
cttatagggt ggggcagcct ccagggatga aacatctgaa tgaccaaagg agccagtcat     120
gccaggattt tggaggaaag cacccaggca gagagtgcag aaagggcaaa cgctccctgg     180
aaagattctt agtcaagagt ccttcactcc cagtcctacc acaaactggg tcaccttgaa     240
caagtcacgt aacttctgag gctcagctgc cacatctaca aaatgggaat aaagacatct     300
tacctgccac attgtgagag gtttcaacca aagggctgtt aaggtctggg atcctcccca     360
aatctcacca tagacacctg atactcatca cttggcaccc gtcttggaag aggggaacct     420
gcacagagaa ccctgggtca tgcttttgat tttaatttc atgctgcact agaaatagct     480
tcttttgttc ctggttgacc cargagcctc ttcctgccac ctggggccta ttctagttaa     540
cagctgctta tcccctcagg tacaaaagcc aacaaggaaa ggacatcagg aaacattgtt     600
ctgggaataa ccagacacct atctgccacc atctcccccc atcccgtgac cacacacggg     660
agactggagg actcagcctg tcctgtagtc agataatgta catggtttat ttaaagagtc     720
aaaaggggcc gggcgcagtg gctaacgcct gtaatcctag cactctggga ggctggggtg     780
ggtggatcac ctgagctcaa gagtttcaga ccaatctggc caacatggtg aaaccctgtc     840
tctaccaaaa atacaaaaat tagccgggtg tggtggtgga cgcctgtaat cccagctact     900
tgggaggctg aggcaggaga attgcttgaa cctgggaagt ggaggttgca gtgagctgag     960
atcgtgccac tgcactccag cctgggcaac aacaacgaaa a                        1001
```

<210> 160
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 12-334-391 : polymorphic base A or G

<220>
<221> misc_binding
<222> 483..502
<223> 12-334-391.mis1, potential

<220>
<221> misc_binding
<222> 504..523
<223> 12-334-391.mis2, potential complement

<220>
<221> primer_bind
<222> 113..131
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 545..563
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 12-334-391 potential probe

<400> 160
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gggcagcctc cagggatgaa acatctgaat gaccaaagga gccagtcatg ccaggatttt      60
ggaggaaagc acccaggcag agagtgcaga aagggcaaac gctccctgga aagattctta     120
gtcaagagtc cttcactccc agtcctacca caaactgggt caccttgaac aagtcacgta     180
acttctgagg ctcagctgcc acatctacaa aatgggaata aagacatctt acctgccaca     240
ttgtgagagg tttcaaccaa agggctgtta aggtctggga tcctccccaa atctcaccat     300
agacacctga tactcatcac ttggcacccg tcttggaaga ggggaacctg cacagagaac     360
cctgggtcat gcttttgatt tttaatttca tgctgcacta gaaatagctt cttttgttcc     420
```

```
tggttgaccc aagagcctct tcctgccacc tggggcctat tctagttaac agctgcttat    480
cccctcaggt acaaaagcca acraggaaag gacatcagga aacattgttc tgggaataac    540
cagacaccta tctgccacca tctcccccca tcccgtgacc acacacggga gactggagga    600
ctcagcctgt cctgtagtca gataatgtac atggtttatt taaagagtca aaaggggccg    660
ggcgcagtgg ctaacgcctg taatcctagc actctgggag gctggggtgg gtggatcacc    720
tgagctcaag agtttcagac caatctggcc aacatggtga aaccctgtct ctaccaaaaa    780
tacaaaaatt agccgggtgt ggtggtggac gcctgtaatc ccagctactt gggaggctga    840
ggcaggagaa ttgcttgaac ctgggaagtg gaggttgcag tgagctgaga tcgtgccact    900
gcactccagc ctgggcaaca acaacgaaaa ctccgtctca aaaaaaaaaa aaaaaaaaaa    960
aagagtcaaa aggatcttgg tccctgggtt gggccactga t                       1001
```

<210> 161
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-335-417 : polymorphic base G or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-335-417.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-335-417.mis2, potential complement

<220>
<221> primer_bind
<222> 85..102
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 534..552
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-335-417 potential probe

<400> 161

```
agcctttgct gcttttgttc ctgcaatttg gaacactgtc cccatcccag cctctcacct     60
ctacccctac ctccttcact acctatacct tcctatccat ccttcaagac cccaaaaacc    120
atccctgatt ccttcagaaa ggcagtttat tgcctatctt atcagactga aagcagtggc    180
tgtgtcttat ttatggttaa ttccctagaa gctggactga tacattccat ttaactaaaa    240
ttcgtatcag gtgcttcgga ctgcagacaa gcctatcaca acccagaagg aagaaacagg    300
gaaggcacct gggggctgcc aagcaatgag gtggggggta ggaatcatga atccgcatat    360
ttttaaaaac tgccccagat cctgatgtaa acggtacaag agagtctgag aaacacaggg    420
ctcccctcaa acagtcctga cttcagcatt cctggaaaaa tgaaaatcct ttcctttgc     480
ctctaatgct ttccctgctg statcccagg ttaaaaaaaa atagataaaa tcagggggat    540
ttttctggga cttggctggg ctgggaaaca agcctgggtt ctaatacagg ctcagcccct    600
gacgtactat gggcccctgc ccctccttgg ggcctccatt accacggcca cccccaccct    660
tatcaattgt gtgcccctga ggtagtgact gtcccgctct gagcattagt ttccccatct    720
tccactagtc gtcgtcagct ctgacgctct atgagctatg catacccgta gctccccgcc    780
gaccccgatg gtcccctccc ctccttccca aggtccatcc gccagggtgc agccgacgca    840
ctcctaatgc taaggccgcc ctctcatcga ccgccccttc ctggcctcga ctcagcgcca    900
aaggtatggg tctctgcccc gcctgctctt taagcctagc cggggcggtc agcgcaagcg    960
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cactgggtcg catcgaggcc ccgccccctg agcctgggta g 1001

<210> 162
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-337-189 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-337-189.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-337-189.mis2, potential complement

<220>
<221> primer_bind
<222> 313..331
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 792..812
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-337-189 potential probe

<400> 162
gggcaactag tgtctagtga gggggttggg ctggcgcgca ctgatcccag actttccgga 60
tcttctgcct ttagatcggg ccggtgtcgg ggcatgtagg ccagtgagac tggagccagt 120
tagagctaca acggggagcg attagggcca aactttgtcc agggtggaag cgagcgggcc 180
cgtgaagtgg ggccagcctg ggcagccgac cgtgtcgttg cctcggggcc tttccaggca 240
ctggcctaag tcctggcgat aaagtgcgac cgatttcctt gtgggcgttt tgaggctttc 300
ggtgatctga cccgtctgtc attcattctt cattcattca tgtgatgaat gaatacagta 360
ctaagcgcgg ctaattacta ggtagagaag tgatcaagac aaacactgtt cctacggtac 420
agggaaaagt gatgggctgt agaatgtaga agcccggggc ggagaacagg gacagcttcc 480
ggaacgaaat cgcgagccca ratcaggagt ggtggcgaga gttccaaaga gaagacagca 540
cgtgccaagt cctggaaggg ggacagaggc caacatatcc tggtcactga agacacctga 600
ctctgaatct gtttcacgcc cagggaagag atgacagtgg ccggggctag gctacaaact 660
ctggaaatgg agataaataa aggaattcaa agtactatat acttaggcag caaaatccat 720
aggatttggg gagagtgaga tgtaggaaac aagtactcaa ggcttgggta cctgggtggg 780
gttcatcaga ggagaagcag atttgtggga gacaacaaca aattctattc tggttgtatg 840
gagactcgca ggaaaaaatt ggatattcta gtttgaaggt aggaaagtat tgctgtgaag 900
atgtagattt gaatgtcatc agcaaaacat aaataaagcc aagggagggt tgaggctgta 960
gaatgagaaa aacaaagggc ccacttagca ccttcatctg a 1001

<210> 163
<211> 881
<212> DNA
<213> Homo Sapiens

<220>
<221> allele

<222> 381
<223> 12-340-130 : polymorphic base A or G

<220>
<221> misc_binding
<222> 361..380
<223> 12-340-130.mis1, potential

<220>
<221> misc_binding
<222> 382..401
<223> 12-340-130.mis2, potential complement

<220>
<221> primer_bind
<222> 252..272
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 681..701
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 369..393
<223> 12-340-130 potential probe

<220>
<221> misc_feature
<222> 205,247,340,499,507
<223> n=a, g, c or t

<400> 163
aaaaattagc cacgtgtgat ggcatgaacc tgtagtccca gctactcggg agactgaggc 60
aggaggatca ctagagccca ggggttcaag gctgcagtga gctaggatcg taccactgca 120
ctccagcctg tgacacagtg caactctatc tctaaaatca tcccaacaat ttttaaaagc 180
tgtaattaaa aaaaattctg ttaanacaaa ttctaggtta atataaacag aaaaaaataa 240
atgttangaa aggaatactc ccgaatctta acagtggttg aattttggtg acaagtccca 300
agacagtttt tcacattttc cttgacaaac accttttccn ttttaaaatg agaaaaatta 360
ggacctttgt tttccaaaaa rgtccaattt tcacttaaag catttaaaaa ttatctatat 420
gctgagaata tgactaagcc catatgttta aagacattcc ctatatacgt atgtattttt 480
tattattgtt taaatcaang ctaggangct accccagaac aaaaagaaaa attcttcctt 540
agccccttct agctataggc caatacttag gcagcatgtc caagacacct caagccaaat 600
gaagaaggaa gattccatag catttttaa attaaaaagc cagcaggcaa atctttgaga 660
ctagacagtt cagcttgagg gtctgagaaa gcctctgctc atctcaaacc agcaacaaat 720
ctttagaaag taattcacat gccatgagat tgctcgtggc atgaatgtga cactataatt 780
caacatcctg aattaagaga gatgtgttat tttagcttaa agcagcagat taaaaataaa 840
aatcctaaac tactacacca cagattgtca attctagaga a 881

<210> 164
<211> 961
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 461
<223> 12-340-210 : polymorphic base C or T

<220>
<221> misc_binding
<222> 442..460

<223> 12-340-210.mis1

<220>
<221> misc_binding
<222> 462..481
<223> 12-340-210.mis2, potential complement

<220>
<221> primer_bind
<222> 252..272
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 681..701
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 449..473
<223> 12-340-210 potential probe

<220>
<221> misc_feature
<222> 205,247,340,499,507
<223> n=a, g, c or t

<400> 164
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aaaaattagc cacgtgtgat ggcatgaacc tgtagtccca gctactcggg agactgaggc     60
aggaggatca ctagagccca ggggttcaag gctgcagtga gctaggatcg taccactgca    120
ctccagcctg tgacacagtg caactctatc tctaaaatca tcccaacaat ttttaaaagc    180
tgtaattaaa aaaaattctg ttaanacaaa ttctaggtta atataaacag aaaaaaataa    240
atgttangaa aggaatactc ccgaatctta acagtggttg aattttggtg acaagtccca    300
agacagtttt tcacattttc cttgacaaac accttttccn ttttaaaatg agaaaaatta    360
ggacctttgt tttccaaaaa agtccaattt tcacttaaag catttaaaaa ttatctatat    420
gctgagaata tgactaagcc catatgttta aagacattcc ytatatacgt atgtattttt    480
tattattgtt taaatcaang ctaggangct accccagaac aaaaagaaaa attcttcctt    540
agccccttct agctataggc caatacttag gcagcatgtc caagacacct caagccaaat    600
gaagaaggaa gattccatag catttttaa attaaaaagc cagcaggcaa atctttgaga    660
ctagacagtt cagcttgagg gtctgagaaa gcctctgctc atctcaaacc agcaacaaat    720
ctttagaaag taattcacat gccatgagat tgctcgtggc atgaatgtga cactataatt    780
caacatcctg aattaagaga gatgtgttat tttagcttaa agcagcagat taaaaataaa    840
aatcctaaac tactacacca cagattgtca attctagaga agcactgggc tcagctttct    900
gcacatctgt atttattgtt aactgcactt gcaggaggga aaagaaagaa gtctcatgac    960
t                                                                   961
```

<210> 165
<211> 973
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 473
<223> 12-340-222 : polymorphic base G or T

<220>
<221> misc_binding
<222> 453..472
<223> 12-340-222.mis1, potential

<220>
<221> misc_binding

<222> 474..493
<223> 12-340-222.mis2, potential complement

<220>
<221> primer_bind
<222> 252..272
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 681..701
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 461..485
<223> 12-340-222 potential probe

<220>
<221> misc_feature
<222> 205,247,340,499,507
<223> n=a, g, c or t

<400> 165
aaaaattagc cacgtgtgat ggcatgaacc tgtagtccca gctactcggg agactgaggc 60
aggaggatca ctagagccca ggggttcaag gctgcagtga gctaggatcg taccactgca 120
ctccagcctg tgacacagtg caactctatc tctaaaatca tcccaacaat ttttaaaagc 180
tgtaattaaa aaaaattctg ttaanacaaa ttctaggtta atataaacag aaaaaaataa 240
atgttangaa aggaatactc ccgaatctta acagtggttg aattttggtg acaagtccca 300
agacagtttt tcacattttc cttgacaaac accttttccn ttttaaaatg agaaaaatta 360
ggacctttgt tttccaaaaa agtccaattt tcacttaaag catttaaaaa ttatctatat 420
gctgagaata tgactaagcc catatgttta aagacattcc ctatatacgt atktattttt 480
tattattgtt taaatcaang ctaggangct accccagaac aaaaagaaaa attcttcctt 540
agccccttct agctataggc caatacttag gcagcatgtc caagacacct caagccaaat 600
gaagaaggaa gattccatag catttttttaa attaaaaagc cagcaggcaa atctttgaga 660
ctagacagtt cagcttgagg gtctgagaaa gcctctgctc atctcaaacc agcaacaaat 720
ctttagaaag taattcacat gccatgagat tgctcgtggc atgaatgtga cactataatt 780
caacatcctg aattaagaga gatgtgttat tttagcttaa agcagcagat taaaaataaa 840
aatcctaaac tactacacca cagattgtca attctagaga agcactgggc tcagctttct 900
gcacatctgt atttattgtt aactgcactt gcaggaggga aaagaaagaa gtctcatgac 960
ttgaggcaac aat 973

<210> 166
<211> 975
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 491
<223> 12-340-240 : polymorphic base C or T

<220>
<221> misc_binding
<222> 471..490
<223> 12-340-240.mis1, potential

<220>
<221> misc_binding
<222> 492..511
<223> 12-340-240.mis2, potential complement

<220>

<221> primer_bind
<222> 252..272
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 681..701
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 479..503
<223> 12-340-240 potential probe

<220>
<221> misc_feature
<222> 205,247,340,499,507
<223> n=a, g, c or t

<400> 166
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aggaggatca ctagagccca ggggttcaag gctgcagtga gctaggatcg taccactgca   120
ctccagcctg tgacacagtg caactctatc tctaaaatca tcccaacaat ttttaaaagc   180
tgtaattaaa aaaaattctg ttaanacaaa ttctaggtta atataaacag aaaaaaataa   240
atgttangaa aggaatactc ccgaatctta acagtggttg aattttggtg acaagtccca   300
agacagtttt tcacattttc cttgacaaac accttttccn ttttaaaatg agaaaaatta   360
ggacctttgt tttccaaaaa agtccaattt tcacttaaag catttaaaaa ttatctatat   420
gctgagaata tgactaagcc catatgttta aagacattcc ctatatacgt atgtattttt   480
tattattgtt yaaatcaang ctaggangct accccagaac aaaaagaaaa attcttcctt   540
agccccttct agctataggc caatacttag gcagcatgtc caagacacct caagccaaat   600
gaagaaggaa gattccatag catttttaa attaaaaagc cagcaggcaa atctttgaga   660
ctagacagtt cagcttgagg gtctgagaaa gcctctgctc atctcaaacc agcaacaaat   720
ctttagaaag taattcacat gccatgagat tgctcgtggc atgaatgtga cactataatt   780
caacatcctg aattaagaga gatgtgttat tttagcttaa agcagcagat taaaaataaa   840
aatcctaaac tactacacca cagattgtca attctagaga agcactgggc tcagctttct   900
gcacatctgt atttattgtt aactgcactt gcaggaggga aaagaaagaa gtctcatgac   960
ttgaggcaac aatga                                                    975
```

<210> 167
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-341-99 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-341-99.mis1, potential

<220>
<221> misc_binding
<222> 502..520
<223> 12-341-99.mis2, complement

<220>
<221> primer_bind
<222> 403..422
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 927..947
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-341-99 potential probe

<220>
<221> misc_feature
<222> 133,141,738,898
<223> n=a, g, c or t

<400> 167
ttgttttcca aaaaagtcca attttcactt aaagcattta aaaattatct atatgctgag 60
aatatgacta agcccatatg tttaaagaca ttccctatat acgtatgtat tttttattat 120
tgtttaaatc aangctagga ngctacccca gaacaaaaag aaaaattctt ccttagcccc 180
ttctagctat aggccaatac ttaggcagca tgtccaagac acctcaagcc aaatgaagaa 240
ggaagattcc atagcatttt ttaaattaaa aagccagcag gcaaatcttt gagactagac 300
agttcagctt gagggtctga gaaagcctct gctcatctca aaccagcaac aaatctttag 360
aaagtaattc acatgccatg agattgctcg tggcatgaat gtgacactat aattcaacat 420
cctgaattaa gagagatgtg ttattttagc ttaaagcagc agattaaaaa taaaaatcct 480
aaactactac accacagatt rtcaattcta gagaagcact gggctcagct ttctgcacat 540
ctgtatttat tgttaactgc acttgcagga gggaaaagaa agaagtctca tgacttgagg 600
caacaatgaa aactgccctg aacatatgcc tgctttgctt tgtataatag agacctaagg 660
tcatcctcta gaaaaggtga agtaattatt atacagtata taaccatttt atagcctgtt 720
ttcatcatga attttccnca tattactata actttaacat tatattaaca acttcataaa 780
attcaacaaa atagatagaa taaccattat cttctcctgg tagatagtca ttacaaataa 840
tgttacacct aacggtcttg gtatacacaa gctttatctc attttgactt acgtcttnca 900
tcagagtcac agaaatggaa acaacagggc aaaatgagta gtaatgttta aagctctgaa 960
gtatactaca ccaattcttc tcaaaagaga tcacattcat c 1001

<210> 168
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-342-32 : polymorphic base T or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-342-32.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-342-32.mis2, potential complement

<220>
<221> primer_bind
<222> 513..532
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 81..101
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-342-32 potential probe

<400> 168
tgtacttcaa atgggtgaaa tgtatggtat atgaaccata tcttaataaa gctgattaaa 60
aaaaactatg gaaaaatatc acttttctca taactgctta gtaaatactt aaaatacact 120
gtttgtggaa gggggcttct gggtactggt aatgttctat ttcctaattt gggtggtagt 180
gcaaaagtga atgtattttg tggtaattat tggtgtactt ttctgtatga aggttatact 240
tcagtaacaa agtctataaa aatacacaca taaacacagt atgttggtga tggtatgggt 300
aaacagacgc tcatactttg ttcctgggga tataaactga caaaacttct taggtaggta 360
aacttcagat ttataaacaa taaaaaacat acgttcttgt tccaaaggta tatactcaca 420
tgtatacaaa aatatgtaaa agatctttac tgcaaccttg tctgtaagag aaatggtgtg 480
gaaaaattat aaatgccagt yaactggggc ctgggtaaat aaattatggc acaatcacac 540
caggaaacac taaccattta attttttttt gagagctcat cacccaggct agagtgcagt 600
ggtatgatct tggctcacgg caacctctgc ctcccggctt caagcaattc tcctgcctca 660
gcctcctgag tagctgggat tacaagtgcc tgccaccgtg cccatctaat tttggtattt 720
ttagtagaga cagggtttca ccatcttgga caggttggtc tcgaactcct gacctcacga 780
tccacctgcc ttggcctccc aaagtgctgg gattacaggc gtgagccact gcgcccggcc 840
taaaattgtt ttaattaaaa aaaaaaaaag aagaagaaag aaggtacaga atagtgtagc 900
cgtgtatatg gtatatcact ctatgtgcgg agaaaataaa ctaaggtgga ggtggtgggg 960
aatatttaca cacacacaca cacacacaca caaaaaaaac a 1001

<210> 169
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-344-349 : polymorphic base G or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-344-349.mis1, potential

<220>
<221> misc_binding
<222> 502..520
<223> 12-344-349.mis2, complement

<220>
<221> primer_bind
<222> 154..173
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 685..705
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-344-349 potential probe

<400> 169
cttaggatat atctaggatt tgtttttttt gttttttgtg ttttttggct atttaagtag 60
accacaaatg aacaacttaa tatatatgtg tatccttttc atgtttgtat taaactagtt 120

```
cctcaagata cattttcaaa agtagaacta ctagaatcta aagtataggc atcttttttt    180
tgttcatttg ttttggtttt ttaaatgagg tcttactctg tcactcaggg gcacaatcac    240
agctcactgt agtctcgaac tcctaggctc aagcaatttt ccctcctcac cctcccgagt    300
ggctaggact gcatgcgcgt gtaccacgcc tggctaaaag ttaaaagtat aagcatctca    360
attgctcttg ttataaattt ccattgaaag ttctactgca gcaaacaaaa ataccatttt    420
tatcagactc attaactgag catttctttt tttgttgctg ttatctgtgt tgggcaaatg    480
gctcttaatg tctgatctat kactaattct tataaagaaa ctactacttc cctgtgagca    540
ggaacaggaa agtagcataa aaacgaaact taattttcat gagcccaaaa ccaaaagatg    600
atgaaactga gtatgaacca tggacaaagt gctttatttg gcacttgctt ctattttta     660
aaattgtttc cattcactcc taagctgcta ggaatgctaa aatgctaggt ctccttctca    720
gatcccaatg ggcagccctg ccaagctagc ttgactagat gggttgtctc ataatcctga    780
gacaacgcag acgctctgca tcccttatca ccacctttca acctactggg gctctgtgat    840
tgatttattt aacgacttca gagcagggtg aaacactgct ctgcatgtct cactatatat    900
ctcactattt ctagatcctc catttttaaa aggaattggg attcactcat tcatcaagta    960
ttgttcagca tctactctag agcagataca gtggtgaggg a                       1001
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<210> 170
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-345-453 : polymorphic base G or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-345-453.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-345-453.mis2, potential complement

<220>
<221> primer_bind
<222> 53..70
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 558..578
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-345-453 potential probe

<400> 170

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cagatcccaa tgggcagccc tgccaagcta gcttgactag atgggttgtc tcataatcct     60
gagacaacgc agacgctctg catcccttat caccaccttt caacctactg gggctctgtg    120
attgatttat ttaacgactt cagagcaggg tgaaacactg ctctgcatgt ctcactatat    180
atctcactat ttctagatcc tccattttta aaaggaattg ggattcactc attcatcaag    240
tattgttcag catctactct agagcagata cagtggtgag ggaaaaaaag tctcagcctt    300
catggaacct ataaatctag tgggaagaag agagactaaa caagtgcacc aacaaataat    360
tacaatatgc tacttgctat gagggtacat agagaacatg aaagaccaag ttagaataca    420
cagctgagac attaaaaatg aatataaatc ctcttaataa ccactactgc atgcacaaat    480
gaggccttat acagtatgtc stattggggt aaaaaaaaaa tcttttaaat taaaaaaacg    540
caaagttggt aggagggcat tcaccaaaca ttaactgaag tcatctctgg cttttaacac    600
cagagtaaag tgcattcact tttttatttt aaattaaata ccgaagctgg gtgcggtggc    660
```

```
tcatgcctgt aatcccagca cttgggaggc tgaggtgggc agatcacttg aggtcaggag     720
ttcgagacca gcctggtcaa catggtgaaa ccccatctct actaaaaaaa aaaatacaaa     780
aattagccgg gtatggtggt gggcgcctgt aatcccagct acttgagagg gtgaggcagg     840
aaaatcactt gagctcagga ggcggaggtt gcagtgagcc aagatcatgc cactgcactc     900
cagcctgggc aacagagcga gagactgtct caaaaaaaaa aaaattgaat acctaaaaag     960
aattatttgt aacgtgtaag ttataaaaaa taataataga a                        1001
```

<210> 171
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-346-204 : polymorphic base G or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-346-204.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-346-204.mis2, potential complement

<220>
<221> primer_bind
<222> 684..704
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 248..267
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-346-204 potential probe

<220>
<221> misc_feature
<222> 664,706
<223> n=a, g, c or t

<400> 171

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aaagcaggct gctagctcat gcagtgggca gccccctccc tgcctggagt gaaatgagat      60
ccccatcaca gagattacaa ggggaagtgg ctagagggcc tcaggcagaa tttttttttt     120
tttttttttt tgagacacag tctcactctg ttgcccaggc tggagtgcag tggcgtgatc     180
tcagctcact gcaacctctg cctcctgggt tcaagcaatt ctggtggccg ctccacagac     240
attacaaaac acgaggcaac actccaccct gaggtctgaa gacccaaaca caagcattag     300
tgccccatga gcaatcgaaa gagaccttaa gaaagtattt taaaaatgat taaaaacaga     360
atatgcagca gaaaaaagat attaacatca tggctaagca gtttccgaat tgagccagac     420
agaacatcta gaaatgcaaa atatatttgc ttgaaattaa aaactcaaat gataaagcag     480
aagacaggtc gctgagggaa rtccccagag tgcagtgaag agaagagggc cccatggcac     540
caggccgatg gctgggtggc acttttaggt cccagagcac tttccttctc atgctggtag     600
gcagggtgcc gactagccgg ggggccaata ggggaaagag tattatcctt cttttgcaag     660
aaanacagag gctcagagat tcagtgattc attcaagctc ttccancaag ccttccaatg     720
tcctgttcag agctctctca aggggactgt gagagacaca agctaaagga gagtgcttgg     780
gctcaaaaaa ccaaagccac cttttttttgt atgagacagt gtctttgctc tgtcacccag     840
gccggatgtg cagtggcttg atcttagttc actgcaacct ctacctcccg ggttcaagtg     900
```

attctcccac ctcagcctcc tgagtagcag ggattacagg tgccccacca acatgcctgg 960
ctaatttttg tatttttagt agagacgggg tttcaccatg t 1001

<210> 172
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-364-55 : polymorphic base G or T

<220>
<221> misc_binding
<222> 481..500
<223> 10-364-55.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-364-55.mis2, potential complement

<220>
<221> primer_bind
<222> 447..464
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 849..867
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-364-55 potential probe

<220>
<221> misc_feature
<222> 180
<223> n=a, g, c or t

<400> 172
tactcacaag taattttaca tttttttttgt acggagtctt caaaatctgg tgtatatttt 60
actctcacag catgtgcatg ttttcattag gacaagccat atttcaagta ctcagtggcc 120
actgtgtgcc tggtagcttc tggactaaac aagcatgagt ctggaggata attattaatn 180
cctgcagaga tgagggaggg aggagcaagg tattggggct ccagagatgc ctgggcaaag 240
tgggtactaa agtttgacca aagtctttgg agttaatttg ggacatgttg caaacagtga 300
aagcagacca tggcagactt tgaacacctg aattgatttg gtaagttaca gggagccttg 360
ggagcagggg ttgagcagga gacagaactg cattctcgag caggagccaa agaattgata 420
ctaatgcaaa atctttaatc acaaagttcc cttgtagtgt cttgacacca cagatacatt 480
ttctgttgag ttgtcttaga kaactaattt gaggtatgat ttcattccac ttacttgtat 540
gtaatcaaat tcttctttta cacgatgact cttaggtgac caatttatga cgtttggttg 600
tctgttttag taccttaaca agaaatatcc gacataggag aggagaaaag gttgtcatca 660
atgtaccaag taagtctact gagaggtggt ggggtgggag agagacatgt tgtattgttg 720
tttaatcctg gattctaaac catttttatt tttgtatttt tataatacag tatttaagga 780
caagaataca ccatctccat ttatagaaac atttactgag gatgatgaag cttcaagggc 840
ttctaagccg gatcatattt acatggatgc catgggattt ggaatgggca attgctgtct 900
ccaggtatag tttcaaatat acagagaggc aaagtgttcc atccatttct gtttttttaac 960
ttctttatat atgcatgttt cctgttccaa aaatcacatt t 1001

<210> 173

<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-364-108 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 10-364-108.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-364-108.mis2, potential complement

<220>
<221> primer_bind
<222> 394..411
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 796..814
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-364-108 potential probe

<220>
<221> misc_feature
<222> 127
<223> n=a, g, c or t

<400> 173
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atattttact ctcacagcat gtgcatgttt tcattaggac aagccatatt tcaagtactc      60
agtggccact gtgtgcctgg tagcttctgg actaaacaag catgagtctg gaggataatt     120
attaatncct gcagagatga gggagggagg agcaaggtat tggggctcca gagatgcctg     180
ggcaaagtgg gtactaaagt ttgaccaaag tctttggagt taatttggga catgttgcaa     240
acagtgaaag cagaccatgg cagactttga acacctgaat tgatttggta agttacaggg     300
agccttggga gcaggggttg agcaggagac agaactgcat tctcgagcag gagccaaaga     360
attgatacta atgcaaaatc tttaatcaca aagttccctt gtagtgtctt gacaccacag     420
atacattttc tgttgagttg tcttagagaa ctaatttgag gtatgatttc attccactta     480
cttgtatgta atcaaattct ycttttacac gatgactctt aggtgaccaa tttatgacgt     540
ttggttgtct gttttagtac cttaacaaga aatatccgac ataggagagg agaaaaggtt     600
gtcatcaatg taccaagtaa gtctactgag aggtggtggg gtgggagaga gacatgttgt     660
attgttgttt aatcctggat tctaaaccat ttttattttt gtatttttat aatacagtat     720
ttaaggacaa gaatacacca tctccattta tagaaacatt tactgaggat gatgaagctt     780
caagggcttc taagccggat catatttaca tggatgccat gggatttgga atgggcaatt     840
gctgtctcca ggtatagttt caaatataca gagaggcaaa gtgttccatc catttctgtt     900
ttttaacttc tttatatatg catgtttcct gttccaaaaa tcacatttta atgaggttga     960
aatggtagct ggtatgcctt tctgaaaaac aatgaagtta t                        1001
```

<210> 174
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-364-267 : polymorphic base A or T

<220>
<221> misc_binding
<222> 481..500
<223> 10-364-267.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-364-267.mis2, potential complement

<220>
<221> primer_bind
<222> 235..252
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 637..655
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-364-267 potential probe

<400> 174
ttggggctcc agagatgcct gggcaaagtg ggtactaaag tttgaccaaa gtctttggag 60
ttaatttggg acatgttgca aacagtgaaa gcagaccatg gcagactttg aacacctgaa 120
ttgatttggt aagttacagg gagccttggg agcaggggtt gagcaggaga cagaactgca 180
ttctcgagca ggagccaaag aattgatact aatgcaaaat ctttaatcac aaagttccct 240
tgtagtgtct tgacaccaca gatacatttt ctgttgagtt gtcttagaga actaatttga 300
ggtatgattt cattccactt acttgtatgt aatcaaattc ttcttttaca cgatgactct 360
taggtgacca atttatgacg tttggttgtc tgttttagta ccttaacaag aaatatccga 420
cataggagag gagaaaaggt tgtcatcaat gtaccaagta agtctactga gaggtggtgg 480
ggtgggagag agacatgttg wattgttgtt taatcctgga ttctaaacca tttttatttt 540
tgtattttta taatacagta tttaaggaca agaatacacc atctccattt atagaaacat 600
ttactgagga tgatgaagct tcaagggctt ctaagccgga tcatatttac atggatgcca 660
tgggatttgg aatgggcaat tgctgtctcc aggtatagtt tcaaatatac agagaggcaa 720
agtgttccat ccatttctgt tttttaactt ctttatatat gcatgtttcc tgttccaaaa 780
atcacatttt aatgaggttg aaatggtagc tggtatgcct ttctgaaaaa caatgaagtt 840
atattagtaa attcattgga agctgtctat gactaatagt tctacagact ctgttgttca 900
ccacaaaggt atatacggta tatatacctt tataactgta atttcagtta acttaaaatg 960
caatatattc tgtcattgtt tcccttctct ttttatatgc c 1001

<210> 175
<211> 997
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 497
<223> 10-367-20 : polymorphic base G or T

<220>
<221> misc_binding
<222> 477..496
<223> 10-367-20.mis1, potential

<220>
<221> misc_binding
<222> 498..517
<223> 10-367-20.mis2, potential complement

<220>
<221> primer_bind
<222> 478..495
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 889..908
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 485..509
<223> 10-367-20 potential probe

<400> 175
agcgttgtta acttgcccct ctctgcccag caccttcctt ctctgacttc actgcttggg 60
gagcatgcta atgattcctt ggtgttaata actttgcaat tcttaaacag gtgacattcc 120
aagcctgcag tatatctgag gccagatacc tttatgatca gttggctact atctgtccaa 180
ttgttgtaag tagaaattac ctcttatttt aaatactact tcgtatgaaa taagatagca 240
tgtgcagaat ttactgacag tgtgctattt aagtccagtt aagacctcag tcagagatgg 300
actaatataa atagtatgta ggtttaggta taatgaactg agagtctaca ctgtagaagt 360
ttactcttgc tagtacaaca ttgatttgtt aaatgtgaag tttgaatgtg gccattttcc 420
ctcccccata cttcatgtcc tcacattaga gagaggatga tttaagtgaa tcaaacccaa 480
ggaactggat tcttcckggt atatttcact gtaagatagg cacaggtaca tgtgctctgt 540
atgggttgca taaacatgct ttttgatcag aaatataact gcatggagct ttttttagca 600
tgtaagtgac actttgaatt tgcaggagct gacttttgtt tgtttttaga tggctttgag 660
tgctgcatct cccttttacc gaggctatgt gtcagacatt gattgtcgct ggggagtgat 720
ttctgcatct gtagatgata gaactcggga ggagcgagga ctggaggtgg gaattgtttt 780
tccttaatag cccttttaag tcaagcaggt aaaatggatc ttttgtaact acttgcaatt 840
tcaggatgtc tccctgcaat ttttatctga aatggggaaa aagatttggt ctaggtgggg 900
agttaatttt tatcgtatgt tgatgtctgt atttgtttta gcttcattta aaattagtag 960
tccgattttt ctatattttg gaagtgctga tggctgt 997

<210> 176
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-351-389 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 10-351-389.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-351-389.mis2, potential complement

<220>
<221> primer_bind
<222> 113..132

<223> upstream amplification primer

<220>
<221> primer_bind
<222> 518..537
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-351-389 potential probe

<400> 176
gtgatctgct tttaaaagat aaaagtatat ttaaatcata ccagaaaaaa agggtattta 60
aattgccttc agattttaaa aaacataatt ttccttaata atacttttta gggctcacta 120
actttttttc tgtatcttat gttgaggttt ttatataatt atcatatata aaaatatatt 180
ccactcattt tatatagcat attcatttat atatattttt aatctttagc cattgaagaa 240
caataactat aggatcagta aatcccgata tgactcaata gacagctatt tatctaagtg 300
tggtgagaaa tataatgaca tcgacttgac gatagataaa gagatctacg aacagctgtt 360
gcaggaaggt gggtttctac tccatctttc tgggtttgaa tgtacgcctt tagttcttca 420
aagctctttt acactttttt gctgactcct ggtctggttt ctatttttag tgcaaagtct 480
ttaacttctc tcatgaggct rcttgttcct aaagtttcag gttccaaata cttgtgagat 540
tttcttgatt tttagcaaaa ggagcttact ttggaggtct gtgtctaggt ccacaccagt 600
gccccagcag gcattgtgta agtagtgaat aaaacgctga cactcccgca gtgtccgcag 660
gataaaatac tgggtgaggt gaggatacta atcaaaccag ctatttcaag cttctagaca 720
ccctttcttc aaacttcctg agctatcctg tcgtctttct ggactaagag gaagtggtat 780
ctctcgcttt gcagtgagtt cccatgtgat ctctttttgc aggcattgat catctcctgg 840
cccagcatgt tgctcatctc tttattagag acccactgac actgtttgaa gagaaaatac 900
acctggatga tgctaatgag tctgaccatt ttgaggtatc ttctcagttt tatttttatt 960
tatttatgta ttgacttctg agagtctgga atcctctgtt t 1001

<210> 177
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-353-102 : polymorphic base A or T

<220>
<221> misc_binding
<222> 481..500
<223> 10-353-102.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-353-102.mis2, potential complement

<220>
<221> primer_bind
<222> 400..417
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 800..819
<223> downstream amplification primer, complement

<220>
<221> misc_binding

<222> 489..513
<223> 10-353-102 potential probe

<400> 177
ctttcccccca ccaaactcac aaaaggagat ataaatcctt ccagtcttgc catcgggtcc 60
caagatggtc aggacggaga aagaactctc tctcagtgta ttgagaaaca gctacccttc 120
ttaggctctt gggtcatcga agcagcagca ttcccaggag aggaggaaga aaggaaacaa 180
ctgtcatgtg acagggttct cagatgaaag tgtccagtgt cacctggaaa ggcaggctgg 240
ctcctaaaat tctcagggat gaaggtgggg gccccgtggc tcttcagatg ctgctctgta 300
gctgggagat agggagtagg agctgggtga gattaagctt gcagtgatag ggcctcatag 360
cttttgttaa acacttggct gttttgtttt cctaaaagag cacactcgaa gaaaatcttc 420
aattgtacct ttttgtcttt gtcaattgaa atttggtatg gacagtgagc agtcttcttc 480
cttaattaaa taccagatca wcttaatatt ttcctggatg tgtgaaaagt tggtttttctt 540
ctctgctttt gtatcacaga atattcagtc cacaaattgg cagacaatga gatttaagcc 600
ccctcctcca aactcagaca ttggatggag agtagaattt cgacccatgg aggtaagaca 660
catgcatcag caagaactga ctcaaaagta ctctttcgcc agctgttcat caccccttctg 720
atgctgctat gagaaggctc ttatatataa aataaaaatt aagtatgtgc atggtagcaa 780
gtcagtccaa gttaaggagg gttgatttct gagaatagat gtgggcaaag ggcttccaga 840
cccagatggg gaattaggag atggcttggg aatgacatga tctgaggaag ggcctgggtc 900
agggaagagc atgtttgtgt agttggttca taacttctct gggcttctgc ttgtctaggt 960
gcaattaaca gactttgaga actctgccta tgtggtgttt g 1001

<210> 178
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-354-72 : polymorphic base A or G

<220>
<221> misc_binding
<222> 482..500
<223> 10-354-72.mis1

<220>
<221> misc_binding
<222> 502..521
<223> 10-354-72.mis2, potential complement

<220>
<221> primer_bind
<222> 430..447
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 830..849
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-354-72 potential probe

<400> 178
tagcttttgt taaacacttg gctgttttgt tttcctaaaa gagcacactc gaagaaaatc 60
ttcaattgta cctttttgtc tttgtcaatt gaaatttggt atggacagtg agcagtcttc 120
ttccttaatt aaataccaga tcatcttaat attttcctgg atgtgtgaaa agttggtttt 180
cttctctgct tttgtatcac agaatattca gtccacaaat tggcagacaa tgagatttaa 240
gccccctcct ccaaactcag acattggatg gagagtagaa tttcgaccca tggaggtaag 300

acacatgcat cagcaagaac tgactcaaaa gtactctttc gccagctgtt catcaccctt 360
ctgatgctgc tatgagaagg ctcttatata taaaataaaa attaagtatg tgcatggtag 420
caagtcagtc caagttaagg agggttgatt tctgagaata gatgtgggca aagggcttcc 480
agacccagat ggggaattag ragatggctt gggaatgaca tgatctgagg aagggcctgg 540
gtcagggaag agcatgtttg tgtagttggt tcataacttc tctgggcttc tgcttgtcta 600
ggtgcaatta acagactttg agaactctgc ctatgtggtg tttgtggtac tgctcaccag 660
agtgatcctt tcctacaaat tggattttct cattccactg tcaaaggtaa ggatatgttt 720
ctttatggtg atgggtatag atctatctgt agatatattt atttatatat gctatttatt 780
tcccacctaa tttcatttga aattgtttac cctttgcaat aaaatgtttc tccatcagcc 840
ctattcttta ttttctttta aacctaagct taatttctag acgctttcca ttcaagatga 900
ttgatggcta gaagtagtcc tacacattga tttcatccac cacaaaatcc caggttgatt 960
acaatgttaa attaggatgg ggagggaaag tgtaactgct g 1001

<210> 179
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-354-320 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 10-354-320.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-354-320.mis2, potential complement

<220>
<221> primer_bind
<222> 182..199
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 582..601
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-354-320 potential probe

<400> 179
ctccaaactc agacattgga tggagagtag aatttcgacc catggaggta agacacatgc 60
atcagcaaga actgactcaa aagtactctt tcgccagctg ttcatcaccc ttctgatgct 120
gctatgagaa ggctcttata tataaaataa aaattaagta tgtgcatggt agcaagtcag 180
tccaagttaa ggagggttga tttctgagaa tagatgtggg caaagggctt ccagacccag 240
atggggaatt aggagatggc ttgggaatga catgatctga ggaagggcct gggtcaggga 300
agagcatgtt tgtgtagttg gttcataact tctctgggct tctgcttgtc taggtgcaat 360
taacagactt tgagaactct gcctatgtgg tgtttgtggt actgctcacc agagtgatcc 420
tttcctacaa attggatttt ctcattccac tgtcaaaggt aaggatatgt ttctttatgg 480
tgatgggtat agatctatct rtagatatat ttatttatat atgctattta tttcccacct 540
aatttcattt gaaattgttt accctttgca ataaaatgtt tctccatcag ccctattctt 600
tattttcttt taaacctaag cttaatttct agacgctttc cattcaagat gattgatggc 660
tagaagtagt cctacacatt gatttcatcc accacaaaat cccaggttga ttacaatgtt 720
aaattaggat ggggagggaa agtgtaactg ctggaatgcc ggtaaaagtc tcctcagtag 780
aactgaactt gagatatttc tgaagaattc ggatgggatt gaactctcag aaaaacaaat 840

tggagttaat ctgcccccca aaagaccaaa aaacaagctt tctgggagga gtttgccagc 900
aaaacaactc caggtgatga gggagcagag ctgtgggttg tggagcagta gctgaggagg 960
tgaacgcctt tggtttctgg gccagggttc ctcttggcag a 1001

<210> 180
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-354-360 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 10-354-360.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-354-360.mis2, potential complement

<220>
<221> primer_bind
<222> 142..159
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 542..561
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-354-360 potential probe

<400> 180
catggaggta agacacatgc atcagcaaga actgactcaa aagtactctt tcgccagctg 60
ttcatcaccc ttctgatgct gctatgagaa ggctcttata tataaaataa aaattaagta 120
tgtgcatggt agcaagtcag tccaagttaa ggagggttga tttctgagaa tagatgtggg 180
caaagggctt ccagacccag atggggaatt aggagatggc ttgggaatga catgatctga 240
ggaagggcct gggtcaggga agagcatgtt tgtgtagttg gttcataact tctctgggct 300
tctgcttgtc taggtgcaat taacagactt tgagaactct gcctatgtgg tgtttgtggt 360
actgctcacc agagtgatcc tttcctacaa attggatttt ctcattccac tgtcaaaggt 420
aaggatatgt ttctttatgg tgatgggtat agatctatct gtagatatat ttatttatat 480
atgctattta tttcccacct ratttcattt gaaattgttt accctttgca ataaaatgtt 540
tctccatcag ccctattctt tattttcttt taaacctaag cttaatttct agacgctttc 600
cattcaagat gattgatggc tagaagtagt cctacacatt gatttcatcc accacaaaat 660
cccaggttga ttacaatgtt aaattaggat ggggagggaa agtgtaactg ctggaatgcc 720
ggtaaaagtc tcctcagtag aactgaactt gagatatttc tgaagaattc ggatgggatt 780
gaactctcag aaaaacaaat tggagttaat ctgcccccca aaagaccaaa aaacaagctt 840
tctgggagga gtttgccagc aaaacaactc caggtgatga gggagcagag ctgtgggttg 900
tggagcagta gctgaggagg tgaacgcctt tggtttctgg gccagggttc ctcttggcag 960
agagtggctg ggaaaaactg ctaaatagag agggccctgc c 1001

<210> 181
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-355-87 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 10-355-87.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-355-87.mis2, potential complement

<220>
<221> primer_bind
<222> 415..434
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 821..840
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-355-87 potential probe

<400> 181
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agtgtggtgg tgcaggcctg taatcccagc tgcttgggag gctgaggcac aaagaattgc      60
ttgaacccag gagacagagg ttggggtgag atgagattgc accactgcac tccaacctgg     120
gcaacagagc gagactccat ctcaaaaaaa cagaagaaga actgggttct agtcctgcct     180
tctgccttcg ttaccctggg actcctggtg agacactgct atataaaggg aaccagccac     240
ctgccctccc aacactgtat atctgttgca aggctcagtc acagaggtgc tttgaaatgc     300
agacgttcca catgaatata agttttgggt tttaagtttc tcttaaaatt ccctgattgg     360
ttgaaaaatc acataccaat ccatgattga gtgatacagt cctcacataa ataaaaagcc     420
tgttcctccc actgggaagc atttgagcag aaagtagaat ccctaaggga atgagtccta     480
attgcaaagg tgaggaaggt rctgcaactt gtatgtctga tcaagaatat tttgacttag     540
tcgtgattct ttttttccct taggttgatg agaacatgaa ggtagcacag aaaagagatg     600
ctgtcttgca gggaatgttt tatttcagga aagatatttg caaaggtatt acattatctt     660
agatttctaa tgtcagctta tgctgcaaca agctgctaaa gctcccctga ccctcttctc     720
cggcaggtgg caatgcagtg gtggatggtt gtggcaaggc ccagaacagc acggagctcg     780
ctgcagagga gtacaccctc atgagcatag acaccatcat caatgggaag gtaggagggt     840
ggccctgtac agtacgcctc actgtgcaca tccccggca gggagttcat aaagtgtcct     900
gcttcttgta ggaaggtgtg tttcctggac tgatcccaat tctgaactct taccttgaaa     960
acatggaagt ggatgtggac accagatgta gtattctgaa c                       1001
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<210> 182
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-358-60 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 10-358-60.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-358-60.mis2, potential complement

<220>
<221> primer_bind
<222> 442..460
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 870..889
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-358-60 potential probe

<400> 182
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tttctggagt cacaaaggat agccgtagaa ccctacctca cccctcaaat ggtatactgc     60
caatttccca cttcattcac tctacttact gttctttatt ctctccacct ctttgatcaa    120
agatcgctca aggaccctac agtcctctga ggcagtctca tgacactggc atttgtagtc    180
ctagccctct ggccaaatgg gagggcacat gttcttgtac acatgtgctg gctcctgttc    240
cttaagagct ggcagtgtca gcatatgggt ggcatctaac aggtaccata gaaactggat    300
gtatgtgttc tcattgcctg cctgcaacct agaattcctg cccaggagga gttcttcaaa    360
cgctatgaaa gatgttccca ccccctgcca tgcagctaca ctaaaaggac atattgattt    420
ctctccagaa ttgtgtttat gctgaccact aaatatcaac ttattaaaaa aaaaacttac    480
gtggttttaa tttttttttc rctccccccct cgcccacagg agaactaatg acagttgcca    540
gatggatgag ggagtttatc gcaaaccatc ctgactacaa gcaagacagt gtcataactg    600
atgaaatgaa ttatagcctt attttgaagt gtaaccaaat tgcaaatgaa ttatgtgaat    660
gcccagagtt acttggatca gcatttagga aagtaaaata tagtggaagt aaaactgact    720
catccaacta gacattctac agaaagaaaa atgcattatt gacgaactgg ctacagtacc    780
atgcctctca gccagcccgt gtgtataata tgaagaccaa atgatagaac tgtactgttt    840
tctgggccag tgagccagaa attgattaag gctttctttg gtaggtaaat ctagagttta    900
tacagtgtac atgtacatag taaagtattt ttgattaaca atgtatttta ataacatatc    960
taaagtcatc atgaactggc ttgtacattt ttaaattctt a                       1001
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<210> 183
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-468-63 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-468-63.mis1, potential

<220>
<221> misc_binding
<222> 502..520
<223> 12-468-63.mis2, complement

<220>
<221> primer_bind
<222> 439..458

<223> upstream amplification primer

<220>
<221> primer_bind
<222> 946..966
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-468-63 potential probe

<220>
<221> misc_feature
<222> 376,386,618
<223> n=a, g, c or t

<400> 183
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cagtgcaaag acccagaacc cagccttcct tcacctgaaa cagctgcagc gtgcacacac     60
acttcttgtg catatatctc tggtctattt attttcaaaa ctaagtataa tccaaattga    120
atgctggaat cagatttttc cattctgaat gtgtttaaat aacatggcca aggataattt    180
ctttctgttt tcttgacatt tataggtagt ataaaatatg tgacttccaa ataaacataa    240
accatcacac ttcacgaaaa aagagatctt tcgactttta actgcctgtt tcctatctta    300
attacaagta tttctaaaga aaaccattaa gttctagagc ttacagtaca tggttttaaa    360
attgtataag tgctgnttaa gagtanttga ttgccttttc ttggtttaat attaaaccag    420
ggtgttctgc caaagaccgc atagtttctc tgatatggtt ccaaagggat attctttcca    480
ctgaaacact gtatgtatac yagtaaatgc ttcctaatgg tagatgataa atatttttgt    540
tgcttgtaga tagaattttt ccatctagtg taagcttagg attgttttct ttttcccagt    600
gacatgtaca gtttcacnta ctccacttaa aaaaaatcgt tagctcagat aaagtgtgtg    660
gcacatgaaa tgaattttgc caattcacca ccgaaatccc tgctttatat ctcttcagtg    720
gaacactaaa ccaacttctt tcccaagtac actgatttga tctttacaaa ttatatgaat    780
gtattaaatt atcacatgtg ccctgaaact gtgtacatct attatgtatc attagagaga    840
tggaaaaaaa aaaaagaaac tgcttagtaa agtagaaaaa atagttttaa agtaattttg    900
taaggctaat ggaagactta ctgtataaaa caaaaaggat tttaaccaca ttcaaattat    960
tgactgtttt ggggcttttc aggaatcact taaaaagcac c                      1001
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<210> 184
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-468-388 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-468-388.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-468-388.mis2, potential complement

<220>
<221> primer_bind
<222> 113..132
<223> upstream amplification primer

<220>
<221> primer_bind

<222> 620..640
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-468-388 potential probe

<220>
<221> misc_feature
<222> 50,60,292,676
<223> n=a, g, c or t

<400> 184
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ttaagttcta gagcttacag tacatggttt taaaattgta taagtgctgn ttaagagtan     60
ttgattgcct tttcttggtt taatattaaa ccagggtgtt ctgccaaaga ccgcatagtt    120
tctctgatat ggttccaaag ggatattctt tccactgaaa cactgtatgt ataccagtaa    180
atgcttccta atggtagatg ataaatattt ttgttgcttg tagatagaat ttttccatct    240
agtgtaagct taggattgtt ttctttttcc cagtgacatg tacagtttca cntactccac    300
ttaaaaaaaa tcgttagctc agataaagtg tgtggcacat gaaatgaatt ttgccaattc    360
accaccgaaa tccctgcttt atatctcttc agtggaacac taaaccaact tctttcccaa    420
gtacactgat ttgatcttta caaattatat gaatgtatta aattatcaca tgtgccctga    480
aactgtgtac atctattatg yatcattaga gagatggaaa aaaaaaaaag aaactgctta    540
gtaaagtaga aaaaatagtt ttaaagtaat tttgtaaggc taatggaaga cttactgtat    600
aaaacaaaaa ggattttaac cacattcaaa ttattgactg ttttggggct tttcaggaat    660
cacttaaaaa gcaccnaagt tcacagccag gcacggtggc tcatgcctgt aatcccagca    720
ctttgggagg ctgaggtggg cagatcactt gaggtcagga gtttgagaca agcctggtca    780
tcatggcaaa atctcatctc tactaaaaat acaaaaatta gacctggtgg catgtgcctg    840
taatcccagc tactgaggag tctgaggcat gagaaacgct tgaacctggg aggcggaggt    900
tgcagtgagc caagatcgtg ccactgcatt ccagcctggg gaacagagca agtctttgtc    960
tcaaaaaaaa aaaaaaaaaa agcactaagt tcatgacagg t                       1001
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<210> 185
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-468-491 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-468-491.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-468-491.mis2, potential complement

<220>
<221> primer_bind
<222> 10..29
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 517..537
<223> downstream amplification primer, complement

<220>

<221> misc_binding
<222> 489..513
<223> 12-468-491 potential probe

<220>
<221> misc_feature
<222> 189,573,901,905
<223> n=a, g, c or t

<400> 185
ccaaagaccg catagtttct ctgatatggt tccaaaggga tattctttcc actgaaacac 60
tgtatgtata ccagtaaatg cttcctaatg gtagatgata aatatttttg ttgcttgtag 120
atagaatttt tccatctagt gtaagcttag gattgttttc tttttcccag tgacatgtac 180
agtttcacnt actccactta aaaaaaatcg ttagctcaga taaagtgtgt ggcacatgaa 240
atgaattttg ccaattcacc accgaaatcc ctgctttata tctcttcagt ggaacactaa 300
accaacttct ttcccaagta cactgatttg atctttacaa attatatgaa tgtattaaat 360
tatcacatgt gccctgaaac tgtgtacatc tattatgtat cattagagag atggaaaaaa 420
aaaaaagaaa ctgcttagta aagtagaaaa aatagtttta aagtaatttt gtaaggctaa 480
tggaagactt actgtataaa rcaaaaagga ttttaaccac attcaaatta ttgactgttt 540
tggggctttt caggaatcac ttaaaaagca ccnaagttca cagccaggca cggtggctca 600
tgcctgtaat cccagcactt tgggaggctg aggtgggcag atcacttgag gtcaggagtt 660
tgagacaagc ctggtcatca tggcaaaatc tcatctctac taaaaataca aaaattagac 720
ctggtggcat gtgcctgtaa tcccagctac tgaggagtct gaggcatgag aaacgcttga 780
acctgggagg cggaggttgc agtgagccaa gatcgtgcca ctgcattcca gcctggggaa 840
cagagcaagt ctttgtctca aaaaaaaaaa aaaaaaaagc actaagttca tgacaggtta 900
nggtnagccc ctcccacccc cccccaaagt catgtgactt caaatctggg ttgtagataa 960
agtttagatt agatgtttca gtttctaaca tatatgttcc t 1001

<210> 186
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-469-132 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-469-132.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-469-132.mis2, potential complement

<220>
<221> primer_bind
<222> 370..387
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 812..832
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-469-132 potential probe

<220>
<221> misc_feature
<222> 16,226,688,735
<223> n=a, g, c or t

<400> 186
gcccgcggtc cccgtncccc gccgggcacc cgtgtctggc cgcccgcgct gcctttgtct 60
tgccctacgc ccccggccct atcgcggtcc gcgttctcca ctgcgcccgg gggtcctcga 120
gcgcctcccg gccccgggag catcgtccct gctttcgcct agtccgcgtc cagggccatc 180
ctcctgacta gactcctttc ttgttcattc attcttttgg gttttncccc ttcattccat 240
aaacacggat tgggcgctgg gagggcgtga gcatgaaaaa gtgacattag gtgctgcgag 300
tcttcaacct agtgtatctg cagaccggca actaccatga tccaccttac aggctcaaaa 360
ttcgcttttg cggtcaatat gaaagagatt taagttttcc tagtaggcct gctgctttta 420
gaaatcaggt cttcaggatg tccacttctg ccctacctca tgcaggtgtc ttttccttaa 480
acctctccaa cttctcatct yccctcccct ccaaaacaca cacacttcat agctataaat 540
tgaaaccagt aaattacggc tcagtttcct acatgggggga ggaaccttcc ctttcctgtt 600
taattctaag tgggaatgca tttagagttt caacattagg atttgcttgt gtctttccat 660
ggcctaggtc cagcaactaa actttacnaa accagtgttc tgcctagaga tgaaatgtct 720
ctagattctc agtanggttg aaccattgtt tattggaatg atctggaatg cagcaatgtt 780
aaaactgttg atttagtgtc atctgccaaa actttttgtg ccttcccttt ctgtttttga 840
aaattacgtg tgtatgcagt acacattaaa tgacttcttg agaagtccat ctctgttttt 900
gtttttagct tttgccttag atggcttgcc acctgtgtaa attgtttatc ttttggccag 960
tgttgttatc aatcttggcc taagtgctga cgtgctgtta c 1001

<210> 187
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-469-245 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-469-245.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-469-245.mis2, potential complement

<220>
<221> primer_bind
<222> 257..274
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 699..719
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-469-245 potential probe

<220>
<221> misc_feature
<222> 113,575,622,936
<223> n=a, g, c or t

<400> 187
tcctcgagcg cctcccggcc ccgggagcat cgtccctgct ttcgcctagt ccgcgtccag 60
ggccatcctc ctgactagac tcctttcttg ttcattcatt cttttgggtt ttnccccttc 120
attccataaa cacggattgg gcgctgggag ggcgtgagca tgaaaaagtg acattaggtg 180
ctgcgagtct tcaacctagt gtatctgcag accggcaact accatgatcc accttacagg 240
ctcaaaattc gcttttgcgg tcaatatgaa agagatttaa gttttcctag taggcctgct 300
gcttttagaa atcaggtctt caggatgtcc acttctgccc tacctcatgc aggtgtcttt 360
tcccttaaacc tctccaactt ctcatcttcc ctcccctcca aaacacacac acttcatagc 420
tataaattga aaccagtaaa ttacggctca gtttcctaca tgggggagga accttcccctt 480
tcctgtttaa ttctaagtgg raatgcattt agagtttcaa cattaggatt tgcttgtgtc 540
tttccatggc ctaggtccag caactaaact ttacnaaacc agtgttctgc ctagagatga 600
aatgtctcta gattctcagt anggttgaac cattgtttat tggaatgatc tggaatgcag 660
caatgttaaa actgttgatt tagtgtcatc tgccaaaact ttttgtgcct tccctttctg 720
tttttgaaaa ttacgtgtgt atgcagtaca cattaaatga cttcttgaga agtccatctc 780
tgtttttgtt tttagctttt gccttagatg gcttgccacc tgtgtaaatt gtttatcttt 840
tggccagtgt tgttatcaat cttggcctaa gtgctgacgt gctgttacac cagtgcagaa 900
tatctccttt caaaaagtta gttttttttt tttttnctaa gattgggatt ctacctccta 960
cagctgaaga aattgtgctg ttttaaatta ggaaagtatg a 1001

<210> 188
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-472-435 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-472-435.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-472-435.mis2, potential complement

<220>
<221> primer_bind
<222> 68..86
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 533..553
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-472-435 potential probe

<400> 188
gatttgttaa atgtgaagtt tgaatgtggc cattttccct cccccatact tcatgtcctc 60
acattagaga gaggatgatt taagtgaatc aaacccaagg aactggattc ttcctggtat 120
atttcactgt aagataggca caggtacatg tgctctgtat gggttgcata aacatgcttt 180
ttgatcagaa atataactgc atggagcttt ttttagcatg taagtgacac tttgaatttg 240
caggagctga cttttgtttg tttttagatg gctttgagtg ctgcatctcc cttttaccga 300
ggctatgtgt cagacattga ttgtcgctgg ggagtgattt ctgcatctgt agatgataga 360
actcgggagg agcgaggact ggaggtggga attgtttttc cttaatagcc cttttaagtc 420

aagcaggtaa aatggatctt ttgtaactac ttgcaatttc aggatgtctc cctgcaattt 480
ttatctgaaa tggggaaaaa ratttggtct aggtggggag ttaattttta tcgtatgttg 540
atgtctgtat ttgttttagc ttcatttaaa attagtagtc cgatttttct atattttgga 600
agtgctgatg gctgttttta ccaaaaggct tttggtgcc acatgagtgt tttgtatatg 660
gtgctttctg ctgtggaaag tataatttgt tgtcagagat tctttttcca tgtaaaaggt 720
taggcattga ctaataaggg tgagatggca cctcttgttt gcatgttgaa ctgtaaagta 780
acccttgcat ctctccaaca aggggtgtgc atcagaacca cccatggaaa tctttgaaaa 840
tagacaccca gaccctatcc tagacctact aaataagaat ctctaggatg ggacccgaac 900
aagggtgttt ttaaaggagc cctcataagt ggttttgata ttctcaacca gggctatact 960
actactgctc tggtcttcat gtaattgttc ataaattgtt g 1001

<210> 189
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-473-311 : polymorphic base A or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-473-311.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-473-311.mis2, potential complement

<220>
<221> primer_bind
<222> 192..210
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 740..758
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-473-311 potential probe

<400> 189
taatttttat cgtatgttga tgtctgtatt tgttttagct tcatttaaaa ttagtagtcc 60
gatttttcta tattttggaa gtgctgatgg ctgtttttac caaaaggctt tttggtgcca 120
catgagtgtt ttgtatatgg tgctttctgc tgtggaaagt ataatttgtt gtcagagatt 180
ctttttccat gtaaaaggtt aggcattgac taataagggt gagatggcac ctcttgtttg 240
catgttgaac tgtaaagtaa cccttgcatc tctccaacaa ggggtgtgca tcagaaccac 300
ccatggaaat ctttgaaaat agacacccag accctatcct agacctacta aataagaatc 360
tctaggatgg gacccgaaca agggtgtttt taaaggagcc ctcataagtg gttttgatat 420
tctcaaccag ggctatacta ctactgctct ggtcttcatg taattgttca taaattgttg 480
aacatgcttt ctaagtagaa mtaaacttta aaggataatt attttgatag gtttatctta 540
cgttatagat ttatttattt atttgctttt aaccttagta tttattttcc ctagcttaat 600
aagaatgaaa gtgatctgct tttaaaagat aaaagtatat ttaaatcata ccagaaaaaa 660
agggtattta aattgccttc agattttaaa aaacataatt ttccttaata atacttttta 720
gggctcacta acttttttc tgtatcttat gttgaggttt ttatataatt atcatatata 780
aaaatatatt ccactcattt tatatagcat attcatttat atatattttt aatctttagc 840
cattgaagaa caataactat aggatcagta aatcccgata tgactcaata gacagctatt 900
tatctaagtg tggtgagaaa tataatgaca tcgacttgac gatagataaa gagatctacg 960

aacagctgtt gcaggaaggt gggtttctac tccatctttc t 1001

<210> 190
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-473-483 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-473-483.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-473-483.mis2, potential complement

<220>
<221> primer_bind
<222> 20..38
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 568..586
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-473-483 potential probe

<400> 190
cagagattct ttttccatgt aaaaggttag gcattgacta ataagggtga gatggcacct 60
cttgtttgca tgttgaactg taaagtaacc cttgcatctc tccaacaagg ggtgtgcatc 120
agaaccaccc atggaaatct ttgaaaatag acacccagac cctatcctag acctactaaa 180
taagaatctc taggatggga cccgaacaag ggtgttttta aaggagccct cataagtggt 240
tttgatattc tcaaccaggg ctatactact actgctctgg tcttcatgta attgttcata 300
aattgttgaa catgctttct aagtagaaat aaactttaaa ggataattat tttgataggt 360
ttatcttacg ttatagattt atttatttat ttgcttttaa ccttagtatt tattttccct 420
agcttaataa gaatgaaagt gatctgcttt taaaagataa aagtatattt aaatcatacc 480
agaaaaaaag ggtatttaaa ytgccttcag attttaaaaa acataatttt ccttaataat 540
actttttagg gctcactaac ttttttctg tatcttatgt tgaggttttt atataattat 600
catatataaa aatatattcc actcatttta tatagcatat tcatttatat atattttaa 660
tctttagcca ttgaagaaca ataactatag gatcagtaaa tcccgatatg actcaataga 720
cagctattta tctaagtgtg gtgagaaata taatgacatc gacttgacga tagataaaga 780
gatctacgaa cagctgttgc aggaaggtgg gtttctactc catctttctg ggtttgaatg 840
tacgccttta gttcttcaaa gctcttttac actttttgc tgactcctgg tctggtttct 900
atttttagtg caaagtcttt aacttctctc atgaggctac ttgttcctaa agtttcaggt 960
tccaaatact tgtgagattt tcttgatttt tagcaaaagg a 1001

<210> 191
<211> 998
<212> DNA
<213> Homo Sapiens

<220>
<221> allele

<222> 501
<223> 12-475-85 : polymorphic base T or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-475-85.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-475-85.mis2, potential complement

<220>
<221> primer_bind
<222> 566..585
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 108..126
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-475-85 potential probe

<220>
<221> misc_feature
<222> 555,666,713
<223> n=a, g, c or t

<400> 191
acaccattga atatgcttgg taaaattctc ggtctgcagg acaaatgcta acaagtttag 60
taatgtgact gcagccttcc cagctaatct gctggcaagc gagccctgtg aaaaggcaga 120
tgcaggacga gccctttcta tgaaaatcag gctgacctca tttgatagtt atgcagcctg 180
tgtcgatctc ttcccagggc agcaggtagc aggccagaat cagaacccca agtcaggagc 240
tttaacttat ctgagatttt catcctttag catgaatttc aaatatggca gggaaggaga 300
ttgaattcac aaaaacctaa atcttccaaa tcccacaggt tacagttact ctgttggtgg 360
gatccactat aacacccagg tacgattcct gaatgggaac ctgatgctgc ctttgtgaga 420
tgtggttatg acacagtgtc tgcactcaga ttcgtatgat ggtggaatgg cattaaactt 480
ggaggtcttg aagccctgtc ktcctgtccc tggaggcata ggtgaccccc agtgagcact 540
agcagtcact ttggnactta gaattcctgt atttagcatt gactctcact tagtctcttt 600
agaaaactct ctttttctc tctgttaggt tgattagtct aacttcagtt cctaggaact 660
aaaatncctg aatttctcat aggcagtctg aatttagggc agcctaattt atnaacatgc 720
cttagaagga aatcatgtgt gcattcttgc ttgctcagcc caagaagtgt atcaggccct 780
gagcggggca ccgcccactg gggatgtgt tctctgtctt gtccccatgc taaagcccta 840
aactctcctg cacctagagg gaaccgctgc agaaattctc catgattctc acccactaca 900
gtgccccagc tctggctact gcagggcagt tgatccaaag cagcttctgt ctggggatca 960
ggatactgtt tcttgtcaac cacgtggtga ctagaact 998

<210> 192
<211> 985
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 485
<223> 12-475-446 : polymorphic base G or A

<220>

<221> misc_binding
<222> 465..484
<223> 12-475-446.mis1, potential

<220>
<221> misc_binding
<222> 486..505
<223> 12-475-446.mis2, potential complement

<220>
<221> primer_bind
<222> 911..930
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 453..471
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 473..497
<223> 12-475-446 potential probe

<220>
<221> misc_feature
<222> 47,196,202..203,900
<223> n=a, g, c or t

<400> 192
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gcctgcactc ttagctgctc ccccacctat taccgcccaa ataggcagga ggaaaagagc     120
tctgtgacag ttttaatagg ctccaaacag agatgagatt gagggtggcg aggaagagaa     180
gaaagaatag agaaanggga tnnggtggta atgcaggaag taggcttttt gtttttttaat     240
gaaaatatga atatgtcatc agccacagat ccacgcttaa gcattttttg gtaccccata     300
gcaggtaatt ctcttctagt gaaatgccag cactctttca aaacgacacc attgaatatg     360
cttggtaaaa ttctcggtct gcaggacaaa tgctaacaag tttagtaatg tgactgcagc     420
cttcccagct aatctgctgg caagcgagcc ctgtgaaaag gcagatgcag gacgagccct     480
ttctrtgaaa atcaggctga cctcatttga tagttatgca gcctgtgtcg atctcttccc     540
agggcagcag gtagcaggcc agaatcagaa ccccaagtca ggagctttaa cttatctgag     600
attttcatcc tttagcatga atttcaaata tggcagggaa ggagattgaa ttcacaaaaa     660
cctaaatctt ccaaatccca caggttacag ttactctgtt ggtgggatcc actataacac     720
ccaggtacga ttcctgaatg ggaacctgat gctgcctttg tgagatgtgg ttatgacaca     780
gtgtctgcac tcagattcgt atgatggtgg aatggcatta aacttggagg tcttgaagcc     840
ctgtcgtcct gtccctggag gcataggtga cccccagtga gcactagcag tcactttggn     900
acttagaatt cctgtattta gcattgactc tcacttagtc tctttagaaa actctctttt     960
ttctctctgt taggttgatt agtct                                           985
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<210> 193
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-477-100 : polymorphic base G or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-477-100.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-477-100.mis2, potential complement

<220>
<221> primer_bind
<222> 580..600
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 62..82
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-477-100 potential probe

<220>
<221> misc_feature
<222> 368
<223> n=a, g, c or t

<400> 193
tcagttactg tgacctacca tatcatggtt gaattcctcc atgttaagac cctactgtct 60
agaagtatgg tgttagcaga tgtactcatt gattggtact gtctgtagtt tcattttgaa 120
gcataaacct gagtaacatt cagtaagact ctgtatgttc agaaaagatg tcacaatatt 180
aattgagcct ctaacatcac tatttatgtt tctgaacatt tttacatact gtcaaggcat 240
ctgaatatat tcttaaagtt agaaaactgt atatgaagca ttactgatat tgctggtatt 300
actggaaaga ccatatccta acgagcttgc taattagtac tctgtttcta catttcatga 360
tataatcnag gtgtttttaa aaaaacattt taacagcttt attgagttat aattaacata 420
aagttaactg cacatattta aaatgtacaa tttggtaagt tttgatatat gtatacatca 480
taaaatcacc tctgataata rgtatattca ttatctccaa aaatgtcatc atgccccttt 540
ggtaatttct tcctctggcc atcccatgca gctgatttgc tttctgtagt ttgcattttc 600
tagattttca tatttaagaa atcatagttt gcatttgata tctagtttca tatacctagg 660
aaatcatcca gcatatcctc ttttggtctg ccttcttaga gtctacataa atattttgag 720
atccatccat gttgttacat gtgtcagtag ttcattcctt ttcgtcgctg agtaatattt 780
cattccatgg ttataccagt ttgtttatac attcaccatt tgtgttgcat tcagtttttc 840
actattataa aaaaattata tgaacattaa catacaagtt tgtatgtatg gactaatgct 900
tttcttcatc ttattaccct aggagtagcg tgttgttaac tttttaagga aactataata 960
ccaaactttt ccagggtggt tataccattt tgcattctca c 1001

<210> 194
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-477-331 : polymorphic base G or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-477-331.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-477-331.mis2, potential complement

<220>
<221> primer_bind
<222> 812..832
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 294..314
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-477-331 potential probe

<220>
<221> misc_feature
<222> 600
<223> n=a, g, c or t

<400> 194
gtgtaacaaa ggaggaaagg tgagaaatac cattggatag tatgtgaagg ttattgtgca 60
gtttagtgtt gtaaatgcag tgaataggtt tagccagctt gtagaagtct ttgtctagtt 120
ctcaaaaagt agaggttatg ttgtacttta aaagcatgag aaaagtagaa tcgaaaaaaa 180
gtgtattagt cttctatacc tatctcctac agaaaaaatc ttttaagact tatcagttac 240
tgtgacctac catatcatgg ttgaattcct ccatgttaag accctactgt ctagaagtat 300
ggtgttagca gatgtactca ttgattggta ctgtctgtag tttcattttg aagcataaac 360
ctgagtaaca ttcagtaaga ctctgtatgt tcagaaaaga tgtcacaata ttaattgagc 420
ctctaacatc actatttatg tttctgaaca tttttacata ctgtcaaggc atctgaatat 480
attcttaaag ttagaaaact rtatatgaag cattactgat attgctggta ttactggaaa 540
gaccatatcc taacgagctt gctaattagt actctgtttc tacatttcat gatataatcn 600
aggtgttttt aaaaaaacat tttaacagct ttattgagtt ataattaaca taaagttaac 660
tgcacatatt taaaatgtac aatttggtaa gttttgatat atgtatacat cataaaatca 720
cctctgataa taagtatatt cattatctcc aaaaatgtca tcatgcccct ttggtaattt 780
cttcctctgg ccatccccatg cagctgattt gctttctgta gtttgcattt tctagatttt 840
catatttaag aaatcatagt ttgcatttga tatctagttt catataccta ggaaatcatc 900
cagcatatcc tcttttggtc tgccttctta gagtctacat aaatattttg agatccatcc 960
atgttgttac atgtgtcagt agttcattcc ttttcgtcgc t 1001

<210> 195
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-477-332 : polymorphic base T or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-477-332.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-477-332.mis2, potential complement

<220>
<221> primer_bind
<222> 813..833

<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 295..315
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-477-332 potential probe

<220>
<221> misc_feature
<222> 601
<223> n=a, g, c or t

<400> 195
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tctcaaaaag tagaggttat gttgtacttt aaaagcatga gaaaagtaga atcgaaaaaa 180
agtgtattag tcttctatac ctatctccta cagaaaaaat cttttaagac ttatcagtta 240
ctgtgaccta ccatatcatg gttgaattcc tccatgttaa gaccctactg tctagaagta 300
tggtgttagc agatgtactc attgattggt actgtctgta gtttcatttt gaagcataaa 360
cctgagtaac attcagtaag actctgtatg ttcagaaaag atgtcacaat attaattgag 420
cctctaacat cactatttat gtttctgaac atttttacat actgtcaagg catctgaata 480
tattcttaaa gttagaaaac ygtatatgaa gcattactga tattgctggt attactggaa 540
agaccatatc ctaacgagct tgctaattag tactctgttt ctacatttca tgatataatc 600
naggtgtttt taaaaaaaca ttttaacagc tttattgagt tataattaac ataaagttaa 660
ctgcacatat ttaaaatgta caatttggta agttttgata tatgtataca tcataaaatc 720
acctctgata ataagtatat tcattatctc caaaaatgtc atcatgcccc tttggtaatt 780
tcttcctctg gccatcccat gcagctgatt tgctttctgt agtttgcatt ttctagattt 840
tcatatttaa gaaatcatag tttgcatttg atatctagtt tcatatacct aggaaatcat 900
ccagcatatc ctcttttggt ctgccttctt agagtctaca taaatatttt gagatccatc 960
catgttgtta catgtgtcag tagttcattc cttttcgtcg c 1001

<210> 196
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-477-44 : polymorphic base C or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-477-44.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-477-44.mis2, potential complement

<220>
<221> primer_bind
<222> 524..544
<223> upstream amplification primer, complement

<220>
<221> primer_bind

<222> 6..26
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-477-44 potential probe

<220>
<221> misc_feature
<222> 312
<223> n=a, g, c or t

<400> 196
gtctagaagt atggtgttag cagatgtact cattgattgg tactgtctgt agtttcattt 60
tgaagcataa acctgagtaa cattcagtaa gactctgtat gttcagaaaa gatgtcacaa 120
tattaattga gcctctaaca tcactattta tgtttctgaa catttttaca tactgtcaag 180
gcatctgaat atattcttaa agttagaaaa ctgtatatga agcattactg atattgctgg 240
tattactgga aagaccatat cctaacgagc ttgctaatta gtactctgtt tctacatttc 300
atgatataat cnaggtgttt ttaaaaaaac attttaacag ctttattgag ttataattaa 360
cataaagtta actgcacata tttaaaatgt acaatttggt aagttttgat atatgtatac 420
atcataaaat cacctctgat aataagtata ttcattatct ccaaaaatgt catcatgccc 480
ctttggtaat ttcttcctct sgccatccca tgcagctgat ttgctttctg tagtttgcat 540
tttctagatt ttcatattta agaaatcata gtttgcattt gatatctagt ttcatatacc 600
taggaaatca tccagcatat cctcttttgg tctgccttct tagagtctac ataaatattt 660
tgagatccat ccatgttgtt acatgtgtca gtagttcatt ccttttcgtc gctgagtaat 720
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tttcactatt ataaaaaaat tatatgaaca ttaacataca agtttgtatg tatggactaa 840
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aataccaaac ttttccaggg tggttatacc attttgcatt ctcactagca gagtatgcca 960
gttcagttca tccacattct tgttaacacc ggtatgggca g 1001

<210> 197
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-478-223 : polymorphic base G or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-478-223.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-478-223.mis2, potential complement

<220>
<221> primer_bind
<222> 704..723
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 234..254
<223> downstream amplification primer

<220>

<221> misc_binding
<222> 489..513
<223> 12-478-223 potential probe

<220>
<221> misc_feature
<222> 35,194,272,317,458
<223> n=a, g, c or t

<400> 197
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gcctcccagg ctcaagctgt ttagatcgta tttctaagtt gcgcttcaaa aacgcattga 120
cacaggctca ggctaggctt cttaaaataa gatatagagc acaaattaat tatttcttaa 180
taggcattac aaangattca ggttccttct ataggtcata gcgtattctg taacacaaaa 240
agcaaagttg tcgcatctct ctatcttttt tnagctgtca ctggacattg attcaacagc 300
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gggagaaagg aaggcattat rgtcaaaaga acagtgtaac aaaggaggaa aggtgagaaa 540
taccattgga tagtatgtga aggttattgt gcagtttagt gttgtaaatg cagtgaatag 600
gtttagccag cttgtagaag tctttgtcta gttctcaaaa agtagaggtt atgttgtact 660
ttaaaagcat gagaaaagta gaatcgaaaa aaagtgtatt agtcttctat acctatctcc 720
tacagaaaaa atcttttaag acttatcagt tactgtgacc taccatatca tggttgaatt 780
cctccatgtt aagaccctac tgtctagaag tatggtgtta gcagatgtac tcattgattg 840
gtactgtctg tagtttcatt ttgaagcata aacctgagta acattcagta agactctgta 900
tgttcagaaa agatgtcaca atattaattg agcctctaac atcactattt atgtttctga 960
acatttttac atactgtcaa ggcatctgaa tatattctta a 1001

<210> 198
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-478-320 : polymorphic base G or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-478-320.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-478-320.mis2, potential complement

<220>
<221> primer_bind
<222> 801..820
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 331..351
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-478-320 potential probe

<220>
<221> misc_feature
<222> 132,291,369,414,555
<223> n=a, g, c or t

<400> 198
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cattaacagt aattttttat tgtatttctt ttcttttttt taatattatg tatttatgta     60
tttatttatt tatttattta ttttgagaca gggtctttct tgctctgtca cccaggctag    120
agtgcagtga cnaccatcac agtgtgctgc agccgcagcc tcccaggctc aagctgttta    180
gatcgtattt ctaagttgcg cttcaaaaac gcattgacac aggctcaggc taggcttctt    240
aaaataagat atagagcaca aattaattat ttcttaatag gcattacaaa ngattcaggt    300
tccttctata ggtcatagcg tattctgtaa cacaaaaagc aaagttgtcg catctctcta    360
tctttttttna gctgtcactg gacattgatt caacagcatt tattgtccgt taanccccta    420
cccaccccca gaagttccct tgtgcccttt gcacgtgtgt gcatgcgtgt atgctagaga    480
gagaggggga gagcacttca rttgattctg gttttccttc agacaccacc tttgagaaac    540
tgccttaaag agtgntgtgg tcattaatta gatgaagggg agaaaggaag gcattatggt    600
caaaagaaca gtgtaacaaa ggaggaaagg tgagaaatac cattggatag tatgtgaagg    660
ttattgtgca gtttagtgtt gtaaatgcag tgaataggtt tagccagctt gtagaagtct    720
ttgtctagtt ctcaaaaagt agaggttatg ttgtacttta aaagcatgag aaaagtagaa    780
tcgaaaaaaa gtgtattagt cttctatacc tatctcctac agaaaaaatc ttttaagact    840
tatcagttac tgtgacctac catatcatgg ttgaattcct ccatgttaag accctactgt    900
ctagaagtat ggtgttagca gatgtactca ttgattggta ctgtctgtag tttcattttg    960
aagcataaac ctgagtaaca ttcagtaaga ctctgtatgt t                       1001
```

<210> 199
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-479-289 : polymorphic base G or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-479-289.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-479-289.mis2, potential complement

<220>
<221> primer_bind
<222> 213..230
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 678..698
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-479-289 potential probe

<220>
<221> misc_feature
<222> 444,957..958
<223> n=a, g, c or t

<400> 199
ctctcctgtt actcccccctt ctctcactcc actccagcca tactagcctc cttactgttc 60
tttgaccact ctagcttccc tccctgcctg aggcctttgt atcagctgtt ccctctgcct 120
ggaatggctg aatttcctta cctccttcaa atccttgctt aatccctcct tctcaaagag 180
acctaaacac cctggccacc ttctttaata taatattctg accatgcacc taacctcaca 240
ccctgatccc ctgctctaat ctgtcttttt cataatgttt atcaacttct gactttctat 300
atagttattt attgtgcatg ttgtgtgcct ccccttgcta aaatgtaagc tccacaaggg 360
caggcatgct tgtttgttat agtcagtgat gtatcctaag cacctagaac agtacttgcc 420
tgatggtgag tgctcaatga acantttgca gaaaaatgaa tgaatgaatg ccaggcattc 480
ataagcccac aaaaaaaatc katgtgtcat tctacacctt cactgtagcc taatgcttca 540
tgctccaaaa agaaagaaga ggcatcattt tctctgtttc ctgtgctcca cctctcgcac 600
attccccact ctcctagctg ctgtctttcc cctgactttt ttgtctagta acaagaactc 660
cctgcctggt gaaagtcggc attttcttct caatttactt ctaaatatta gtgcttttgt 720
ttaccctgtg aagcagatgg taacagttaa tgtaataacc agactgtctc ctctctcttg 780
tttgacacag tagatgtcat gagccatatt ttcccttggt tatatttgtt aaatagaaga 840
caggagatct gctatatggt caacattagg tctggtcact gcttttatat tgttaacact 900
gtgtttcctt tcatatattt acatcatttg gaaacatttg ccctagttcc agcaatnnag 960
gctaagagat aaggatccaa atgaaagaaa gaggataaaa a 1001

<210> 200
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-482-237 : polymorphic base G or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-482-237.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-482-237.mis2, potential complement

<220>
<221> primer_bind
<222> 720..737
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 223..243
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-482-237 potential probe

<220>
<221> misc_feature
<222> 552,561,757,831,845
<223> n=a, g, c or t

<400> 200
ttctcttggg actcatatca ctaatctagg caagttaaga atgttttctc tgtttgggct 60
gagacaatat tgagaaagtt actccaccta atcctatagg aaattaattg atttttgtgc 120

```
agtattaaaa ttgagattaa tgtgttataa ataaaaagca gcctgctctg tgctacagaa     180
aactagatca gggagaggcc acatttattt taatttctaa aagtgtaaac ctttcatagt     240
atcatgtgaa attctttagt atgaatagac atttcaaagt aggaggaaaa aaacctattt     300
tctcaaaata tatgaaatgt tagcagaatt tgatacagct ttagacaaaa ctgctaaaac     360
attttctttt tggaacatag aacaatttaa ttattacagt atccacagtc atcaaatata     420
tatatattta aatcatcaaa tatatatgtt taaaatatag ttgtgtgtgt gatgttatgt     480
atgtataatg tcatgtacac raaagcacat acagtttcta ctttgtactt actggtcccc     540
taaaagtgct tnggagatta nccatgtcaa acagtggttt tcctatttgt gatgtcatca     600
ttagacatat ctaacatggg agtccatctt taaaaatctg agccatatgt aattttatta     660
catctgtatt agaatctcat attcagtttt ctacttttta aaacacagct cctcttttag     720
tcttgtcagt caggttgtcc tatgttactg tgggtgnttt aaaaattaag tagcatcact     780
atggctaaca cctctttggg tgctccaagt ttgggaagtg aatgccatcc naacttgatg     840
gttgnagatt tcttttaaaa aaaaatttgt cattaccatt ttgctgtgag aggaaacagt     900
cttctgggca gaaggcattg agtccctaac tttaaaacag tttataacct agagggtgac     960
tacttggcat gatctctgtg ggtggatgc agtgatctgc g                        1001
```

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<210> 201
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-482-285 : polymorphic base T or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-482-285.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-482-285.mis2, potential complement

<220>
<221> primer_bind
<222> 768..785
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 271..291
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-482-285 potential probe

<220>
<221> misc_feature
<222> 600,609,805,879,893
<223> n=a, g, c or t

<400> 201
cccgcaactc tcactgtctt tctctatttt attaaagtct tgaaattttt ctcttgggac      60
tcatatcact aatctaggca agttaagaat gttttctctg tttgggctga gacaatattg     120
agaaagttac tccacctaat cctataggaa attaattgat ttttgtgcag tattaaaatt     180
gagattaatg tgttataaat aaaaagcagc ctgctctgtg ctacagaaaa ctagatcagg     240
gagaggccac atttatttta atttctaaaa gtgtaaacct ttcatagtat catgtgaaat     300
tctttagtat gaatagacat ttcaaagtag gaggaaaaaa acctattttc tcaaaatata     360
```

```
tgaaatgtta gcagaatttg atacagcttt agacaaaact gctaaaacat tttctttttg    420
gaacatagaa caatttaatt attacagtat ccacagtcat caaatatata tatatttaaa    480
tcatcaaata tatatgttta waatatagtt gtgtgtgtga tgttatgtat gtataatgtc    540
atgtacacaa aagcacatac agtttctact ttgtacttac tggtccccta aaagtgcttn    600
ggagattanc catgtcaaac agtggttttc ctatttgtga tgtcatcatt agacatatct    660
aacatgggag tccatcttta aaaatctgag ccatatgtaa ttttattaca tctgtattag    720
aatctcatat tcagttttct actttttaaa acacagctcc tcttttagtc ttgtcagtca    780
ggttgtccta tgttactgtg ggtgntttaa aaattaagta gcatcactat ggctaacacc    840
tctttgggtg ctccaagttt gggaagtgaa tgccatccna acttgatggt tgnagatttc    900
ttttaaaaaa aaatttgtca ttaccatttt gctgtgagag gaaacagtct tctgggcaga    960
aggcattgag tccctaactt taaaacagtt tataacctag a                       1001
```

<210> 202
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-482-482 : polymorphic base T or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-482-482.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-482-482.mis2, potential complement

<220>
<221> primer_bind
<222> 965..982
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 468..488
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-482-482 potential probe

<220>
<221> misc_feature
<222> 67,797,806
<223> n=a, g, c or t

<400> 202

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tctgcagtaa gagaaatgtt ctactctata ctatccatta gggagtagga aactgatttt     60
tttattntta tgttaagtaa ttttaaatcc acacagccac atgtgcttag tgactagcat    120
aatggacaac acaatttttt gtgttccttt ggtgacaggt gacattttct ccctgtatga    180
gagtcctccc agtttacccc gcaactctca ctgtctttct ctattttatt aaagtcttga    240
aatttttctc ttgggactca tatcactaat ctaggcaagt taagaatgtt ttctctgttt    300
gggctgagac aatattgaga aagttactcc acctaatcct ataggaaatt aattgatttt    360
tgtgcagtat taaaattgag attaatgtgt tataaataaa aagcagcctg ctctgtgcta    420
cagaaaacta gatcagggag aggccacatt tattttaatt tctaaaagtg taaacctttc    480
atagtatcat gtgaaattct wtagtatgaa tagacatttc aaagtaggag gaaaaaaacc    540
tattttctca aaatatatga aatgttagca gaatttgata cagctttaga caaaactgct    600
```

```
aaaacatttt ctttttggaa catagaacaa tttaattatt acagtatcca cagtcatcaa    660
atatatatat atttaaatca tcaaatatat atgtttaaaa tatagttgtg tgtgtgatgt    720
tatgtatgta taatgtcatg tacacaaaag cacatacagt ttctactttg tacttactgg    780
tcccctaaaa gtgcttngga gattanccat gtcaaacagt ggttttccta tttgtgatgt    840
catcattaga catatctaac atgggagtcc atctttaaaa atctgagcca tatgtaattt    900
tattacatct gtattagaat ctcatattca gttttctact ttttaaaaca cagctcctct    960
tttagtcttg tcagtcaggt tgtcctatgt tactgtgggt g                       1001
```

<210> 203
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 499
<223> 12-483-322 : polymorphic base T or A

<220>
<221> misc_binding
<222> 479..498
<223> 12-483-322.mis1, potential

<220>
<221> misc_binding
<222> 500..519
<223> 12-483-322.mis2, potential complement

<220>
<221> primer_bind
<222> 802..820
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 311..331
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 487..511
<223> 12-483-322 potential probe

<220>
<221> misc_feature
<222> 253,301..302,345,368,400,565,570,968,973,978
<223> n=a, g, c or t

<400> 203

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agacactttg aaatgtcttt gcttaaaaac aattgtttta agtgcactgc aaaagcatta     60
catggtctag cctcataata attctccctt tttggagacc caggattcag tgtgggctct    120
gcccagattt cagagatcta ggcaaaaaag aaataatccc tatatgaata aaattggtct    180
cctcatacaa tcccatgata gagttctata attttatgtt tgatttggca tccatcttta    240
ttctccctct agncaccact agacttttc tgtctgtacc ttgagatata aattttgcta     300
nntgattttt catctaagag ttgtttcctt caatatgcag gtttnagggc tatttagctg    360
acaactgncc aggttaatga aacaggttat catgagtttn gcaagtctaa gacaggggaa    420
aacaaaagga ggtcttagga atctataaga tgtacttcta tcagtatgcc taatacatct    480
atgtatctat gtgttatgwa cacgtttcac tactaaaaac atataaaaga gctgtaatta    540
attggcttgc agaaaaataa aggtngcttn aaatccaatg ctttatcaga gaaaagaaaa    600
gactagccaa atgcttttc aagtttatgt gatttaagta aaatctttaa taaataagct     660
agctttaaaa ttactggcaa agtaatatta gaaatgtctt aagaattgcc agcatacatt    720
ttcgtttgca tttatggatc aagtcatttc atatttatcc ctgccaaata ctgtaaggtg    780
tcaaagtttg gcatagggtt acaaaactat aaacccagcc taaaacagaa tgatttttgt    840
```

```
ttgtgttaat ttttaataaa taagacattg atattggttt aatgaaaata gctacatctt     900
gaattattta gtaaaattac tgtaacttct aatcttgtgg ccttagggag tctagtccac     960
aggcaatnaa ggntttcntt ttgggaaatg actgttatca t                         1001
```

<210> 204
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-484-46 : polymorphic base G or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-484-46.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-484-46.mis2, potential complement

<220>
<221> primer_bind
<222> 528..546
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 86..106
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-484-46 potential probe

<400> 204

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tgtgagcaag aagtgtgggg agtggttgta aaggggcaca gtatttacac aacatctgtt      60
ttgtaaacac aaagccctct gaaaagggga tactagaaat gaggtgtctt tggcaggtgc     120
agtgatggca agactgcaca caattaattc ttgaaaacaa atcccatcta tttagttctt     180
caatttgttg tagattaggc tgtcctgggt tcacactgcc cgaggtcaaa cccaacccag     240
tggaaggagg agcttccaag tccctcttct ttccagatga agcaataaac aagcaccctc     300
gcttcaggtg agtatggctt tgtgttgaaa tgcagatgcc cttcactaga cccctgactt     360
ctgagagtat agtatttctg tctagaaatc ctttttgagc attaactgag ttttggctct     420
cttcctaagt aaccagagaa gatagcagat gtgcacctgt tcacatcttc agtacccccca    480
ggcttcttgg ttgttgatgc rtgcaccagg cttgatttgt caattctcca agtcgtcaca     540
aagttattcg ctgagccact gcgaataact cttttaatag ggagattatt ttcagtccta     600
ggtctgtaaa tgcctactgg gattttttttt tctcttagtt atttctcctt ttttgtcctc    660
tctaaccatc agtatctgtg atttgcccat cttactctat ataacttata aaataggtgc     720
agtacctgat atatataata ggcactctct tccattaact tcaagttctg ttggtttgtt     780
gttcaattct gaggttttaa gttgctttaa ggctctcact agtctgatct tagctttgta     840
caatgcatgc tcatctgtca tcctgagcct aggctcctga tccagagtgg gaacatggag     900
acttctcagc gttcattcct ttaacaggcc ctcacgtttg ctatgtgcag agccttttgg     960
ggaagacaga tatttgtaga cgtagtttct aacttcatat g                         1001
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<210> 205
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-490-312 : polymorphic base A or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-490-312.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-490-312.mis2, potential complement

<220>
<221> primer_bind
<222> 189..209
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 621..641
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-490-312 potential probe

<220>
<221> misc_feature
<222> 437,543,597,604,664,732,872,932
<223> n=a, g, c or t

<400> 205
cgctgagtca cggggaggcg gtgccgcgcg cgggggaggc gggcccgcgc agtcacgtgg 60
cgggggctgt atcacaacaa ctgcgcggcg tgcgccgccc gcggcccaca ccgcttcctc 120
ccgcgacagg ccggctctcc gagcatgctc agcttggcct cacgactgca cggcgtcccc 180
ccatgcggat ctccacggtc caggttttcc ggacggctct gggggcgggg cctgtgttgg 240
tccgcggggc tgcgaggcga ggttgcggtg ccagggcgcc gctgggcaga gatgggttcc 300
tggagagcgg gtctcgcgtt tttccgcgga agacactact gggaatcggc ctttggtcat 360
ggtctaggga agagctgatt ctgcaagata tgagctcctt ctttcccctt cagctatcgt 420
tacagccctg atggagnctg tctgctgaaa actcacttcc agatgtcgaa acctggccct 480
gggtgcagtc tacagaatga watcgagcag tagtggacct atgcaggcaa agcattgtca 540
ganggggagt aactcttgtt aaatatgact tcagttgatc cgtgatggga tttttgnttt 600
tttnctttgt aacagaaaag gctaaagaca ctgagagatc aaggtttaaa ttgggcataa 660
ctgnccctgt ggtgcagcag cgccggcgcc ctttttggga ttgtccaaag ctctgggacc 720
cccgctgggg gnagctggtt cagaattcgg gggggtagga tagggtgagg gaggtcccctt 780
atgtgagtgt gagccgggat ctaggacaga gtaactccaa ttacagtgtt aaactcttac 840
taggttcagt gtcgcgtagg gctttggcta gnactagaat ttagtctatt attgaaccgc 900
ccaggtccat gattcctaac aggtgcatgg gnaaaagtgt atggtgtgca gcaggtgtat 960
gggaaaactg ctttgcaaag tgtaaatcaa ggtctacatc a 1001

<210> 206
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-491-295 : polymorphic base G or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-491-295.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-491-295.mis2, potential complement

<220>
<221> primer_bind
<222> 777..795
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 266..286
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-491-295 potential probe

<220>
<221> misc_feature
<222> 128,300,307,312,357
<223> n=a, g, c or t

<400> 206
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tgcaggcaga aatgaaaaaa gaaatcctga aactttaaga atcggggata atatcagata     60
agtatgttgc ttaaatttga ctaatttaaa ccatttttat aaattagtca ctcagcatga    120
agacatcnaa aaattcttcc taaattctaa acactatgta catttgaatg ctgagttagt    180
cccaggattc atccccaaaa tatcactgac cagtatgatt taatattagt atttgccctc    240
tcaggggcat ccttgctgca ggatatcaca agggtagaag gtaaagcagc tgcacaaaan    300
catcttntgc tncttgtttg ttactctgag atgatcctct gcctgaaaat atctaangca    360
gatacttttc tcagctttgc aatgcaaatg atatttaaca gttccctagg aatgttttgt    420
gtgcttatca aatttcagct aaacacattt atttatatga taaatatgat aaccaaaagg    480
ttccatgtat tatcttttca rtattcatgt tatactgtac aagcactgta ttatacaaat    540
actgtataat atagtattgt aaggtacaaa aatacaataa actaaccata cttcaactct    600
gcggggttgc tgtgggagag ctctgcaggg ttgctgtgca agccccaggt aagtgattaa    660
gtcagacaat aactacatca gtgcttctca aattttcatg tgcctgcaga ttatcggttg    720
ggggcgggga gtttttaata tgcattctga cttagtaggc ctggtgtcag gccagagatt    780
ctgcgtctct cccaagcttt caggtgatac agatgctgac tggtggacca cattttgagt    840
agcaagatgc taaagcttct tacaactcta aactttcaaa atcctttata aaaggatagc    900
tataatgtat atgtgaaatg gactatggaa acataaaata ataaaagctt actattgtca    960
gtcacttggg aagtgtcact tttggaagtt agtcacttcc c                       1001
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<210> 207
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-493-417 : polymorphic base G or C

<220>
<221> misc_binding
<222> 481..500

<223> 12-493-417.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-493-417.mis2, potential complement

<220>
<221> primer_bind
<222> 90..109
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 514..534
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-493-417 potential probe

<220>
<221> misc_feature
<222> 590,704,1000
<223> n=a, g, c or t

<400> 207
aatgttaatt tttctcacct ttattttcaa taggtggaat acatgttggt atcttttgat 60
catgaaaata aaaaagtccg gttggtcctg tctggggaga aagttcttga aactctgcaa 120
gagaaggggg aaaggacaaa cccaaagtaa gctctcatgt gctgatttag tgtttctgaa 180
actgctaaaa cttctagaat atagagtttt ttctcaatta ttggaggcag gatagcctaa 240
cagttaagag tacaggctct ggtttcaggt tgccatagtt tcaaatcatg gttcctttac 300
tcaatagctg aataaccttg ggcaagttac ttaactttc tgtgcctcag ttctctcatc 360
tgtaaagtaa agatcatagc aatacctacc taaggtgttg gaattaaata cattaatata 420
tgaagcactt tgtacagtaa actaaatata aagcctgttt tttattaaaa catttttggg 480
aaaaaatgta ttgcagaagc statactgg gatcacaaac catgatgcaa gatataagtt 540
gcagatgggc tttgtttggc tttgtttggc tggcatgatt tttttttgan gacggagtct 600
cactctgtcg tccgggctgg agtgcagtgg cacgatctca gctcactgca agctccacct 660
cctggcttca cgccattctc ctgcctcacc ctcccgagta gctngggact acaggcgccc 720
gccaccacgc ctggctaatt ttttgtattt ttagtagaga cgggggtttc accgtgttag 780
ccaggatggt ctccatttcc tgacctcatg atctgcccgc ctcagcctcc caaagtgctg 840
ggattacaag catgagccac cgcacccggc ctggtgtgtt tttaaggtat tcctacattt 900
aagtagacag agacggggag gggaggggaa tatatactcc tctgctcatt ttccactcat 960
tcgttttggg gaagctgcat ttgagtttgg agggcagcan t 1001

<210> 208
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-494-373 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-494-373.mis1, potential

<220>
<221> misc_binding

<222> 502..521
<223> 12-494-373.mis2, potential complement

<220>
<221> primer_bind
<222> 127..144
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 571..591
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-494-373 potential probe

<220>
<221> misc_feature
<222> 2,4,8,15,19,33,36,296,311,640,899
<223> n=a, g, c or t

<400> 208
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antncagncc gggcnatana gttagatcct gtntcnaaaa aaaaaaaaaa agaaaagaaa      60
agaaaacaaa agtcttgggt tctagtccca ctttactgct gattaacatt ttaacttgaa     120
gagtgattca atcactcggt tgccccactt gaaaaaaaaa aaaagctgga gtacatatct     180
agaatcctta ccacacgaac attctatatt tttggttctt tgactctaaa atggtcagct     240
taaaagagtg ttttccatcc ctcttttggc tgttagagcc atccctggtg actttnaccc     300
ctttcccctg naacctttca tatgtttatt gagcatccac tccagttgtg cactggtgtt     360
tgttttcacg ggttactgg taccctccac cctcacccct ctttctccct gcagaaagct      420
tttctaatac tttcagccgt ggtcaatttc aggtgatagc aatggtaatc atttattgag     480
tacttaccaa atgctagaga ytgacacagg ctatgtcatt ttttcaatac caagccctgt     540
gaaatgggta ctatcagacc atttttacac ctgtggctta gaagacttaa atgtctagtg     600
taagggcggt tgtagtggta ggcagaggca ggtctcaaan ccctcgccta cctaactcag     660
acacacttgg caatactata tatctcttta agcctttcag aggatatgtt ttaggaggtg     720
gattgttcca ttttatatat atatgaacat gatagacaga cagatagata gataaataga     780
tagagataat tttaaacgtg ctcactttca tttatgaaaa tttacatttg ataactaaaa     840
gagccttgca attccagcat ctccctcatg gtggcagtag aagactaagt catgtacanc     900
gcagcctcca gcaccaacaa ctaacccaga agaaacctcc ttaataaatc agcttttggt     960
caagattggt gttacgtaaa atgcaaaatt aggaccctcg g                        1001
```

<210> 209
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-495-166 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-495-166.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-495-166.mis2, potential complement

<220>

<221> primer_bind
<222> 336..355
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 784..802
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-495-166 potential probe

<220>
<221> misc_feature
<222> 146,405,641,702,965
<223> n=a, g, c or t

<400> 209
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tagagactga cacaggctat gtcatttttt caataccaag ccctgtgaaa tgggtactat     60
cagaccattt ttacacctgt ggcttagaag acttaaatgt ctagtgtaag ggcggttgta    120
gtggtaggca gaggcaggtc tcaaanccct cgcctaccta actcagacac acttggcaat    180
actatatatc tctttaagcc tttcagagga tatgttttag gaggtggatt gttccatttt    240
atatatatat gaacatgata gacagacaga tagatagata aatagataga gataatttta    300
aacgtgctca ctttcattta tgaaaattta catttgataa ctaaaagagc cttgcaattc    360
cagcatctcc ctcatggtgg cagtagaaga ctaagtcatg tacancgcag cctccagcac    420
caacaactaa cccagaagaa acctccttaa taaatcagct tttggtcaag attggtgtta    480
cgtaaaatgc aaaattagga ycctcggaag gggaaaaaaa gagtctcaag tatctaggtt    540
attgacccca gaaacaaaag aaatttgaca aacttgcaaa acagagacaa caacttccta    600
tgggggtaaa aaaaacaaag caactacttg ttgctgccca ncccgtttag taactggcct    660
tggtagtctt ccagcagcaa gcacaatagc cttgtccaca gnatgctttt cccatttcct    720
cggtcccctt gaaaccaagc ttttgagaac aaatagttca tttctccttt cttaatttgc    780
tctgaaggtt tttaacacag cgataactgg catatagaaa tttcacatat ttttcttgat    840
cactatggcc tatcaacccc cgcctgatga ttaaatgaag gacgatgtat ccaaggttct    900
taaagaactt ggttgcaacg aatgaacaca aaaaacacca gacaataaac atgtattgaa    960
ttatnatctg ggtacagtag acaccattgg gcagacttca g                       1001
```

<210> 210
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-495-272 : polymorphic base A or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-495-272.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-495-272.mis2, potential complement

<220>
<221> primer_bind
<222> 230..249
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 678..696
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-495-272 potential probe

<220>
<221> misc_feature
<222> 40,299,535,596,859
<223> n=a, g, c or t

<400> 210
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taagggcggt tgtagtggta ggcagaggca ggtctcaaan ccctcgccta cctaactcag     60
acacacttgg caatactata tatctcttta agcctttcag aggatatgtt ttaggaggtg    120
gattgttcca ttttatatat atatgaacat gatagacaga cagatagata gataaataga    180
tagagataat tttaaacgtg ctcactttca tttatgaaaa tttacatttg ataactaaaa    240
gagccttgca attccagcat ctccctcatg gtggcagtag aagactaagt catgtacanc    300
gcagcctcca gcaccaacaa ctaacccaga agaaacctcc ttaataaatc agcttttggt    360
caagattggt gttacgtaaa atgcaaaatt aggaccctcg gaaggggaaa aaaagagtct    420
caagtatcta ggttattgac cccagaaaca aaagaaattt gacaaacttg caaaacagag    480
acaacaactt cctatggggg waaaaaaaac aaagcaacta cttgttgctg cccancccgt    540
ttagtaactg gccttggtag tcttccagca gcaagcacaa tagccttgtc cacagnatgc    600
ttttcccatt tcctcggtcc ccttgaaacc aagcttttga gaacaaatag ttcatttctc    660
ctttcttaat ttgctctgaa ggtttttaac acagcgataa ctggcatata gaaatttcac    720
atatttttct tgatcactat ggcctatcaa cccccgcctg atgattaaat gaaggacgat    780
gtatccaagg ttcttaaaga acttggttgc aacgaatgaa cacaaaaaac accagacaat    840
aaacatgtat tgaattatna tctgggtaca gtagacacca ttgggcagac ttcagaatta    900
gcccccggaa gttttgcttt tgcttgactc ttggtcatag ctgattggac tagaagtgaa    960
cacctgactc aggaggagga agttcattgg ctgaccagga g                       1001
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<210> 211
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-495-424 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-495-424.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-495-424.mis2, potential complement

<220>
<221> primer_bind
<222> 78..97
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 526..544
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-495-424 potential probe

<220>
<221> misc_feature
<222> 147,383,444,707
<223> n=a, g, c or t

<400> 211
tagacagaca gatagatgata taaatagata gagataattt taaacgtgct cactttcatt 60
tatgaaaatt tacatttgat aactaaaaga gccttgcaat tccagcatct ccctcatggt 120
ggcagtagaa gactaagtca tgtacancgc agcctccagc accaacaact aacccagaag 180
aaacctcctt aataaatcag cttttggtca agattggtgt tacgtaaaat gcaaaattag 240
gaccctcgga aggggaaaaa aagagtctca agtatctagg ttattgaccc cagaaacaaa 300
agaaatttga caaacttgca aaacagagac aacaacttcc tatgggggta aaaaaaacaa 360
agcaactact tgttgctgcc cancccgttt agtaactggc cttggtagtc ttccagcagc 420
aagcacaata gccttgtcca cagnatgctt ttcccatttc ctcggtcccc ttgaaaccaa 480
gcttttgaga acaaatagtt yatttctcct ttcttaattt gctctgaagg tttttaacac 540
agcgataact ggcatataga aatttcacat atttttcttg atcactatgg cctatcaacc 600
cccgcctgat gattaaatga aggacgatgt atccaaggtt cttaaagaac ttggttgcaa 660
cgaatgaaca caaaaaacac cagacaataa acatgtattg aattatnatc tgggtacagt 720
agacaccatt gggcagactt cagaattagc ccccggaagt tttgcttttg cttgactctt 780
ggtcatagct gattggacta gaagtgaaca cctgactcag gaggaggaag ttcattggct 840
gaccaggagc caattagggt ctctctcttg agaactctga ctaagagaca gagatgcagg 900
ttatttagtc cagttgcggg tgtagcatta gacagatata aaacccaaga actcttggta 960
ctgaggcctg gttgttcaac tttcctcgga ttttaggggg t 1001

<210> 212
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-500-220 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-500-220.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-500-220.mis2, potential complement

<220>
<221> primer_bind
<222> 283..303
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 711..731
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513

<223> 12-500-220 potential probe

<400> 212
tcccatctct tgaaaaaaaa aagcaactgg aaagaattac tattttttaa aaaatacttt 60
taaacctttt ttagagacag ggtctcacta tgttgctcag gctggtctcg aactcctggg 120
ctgaaatgat cgtcctcctg ctgcctcagc cttccaggta gctggaatta cagacacaaa 180
ccaccatgct cagctttgga aagagttctt aaaggaattc taattagtgg cctcagacaa 240
attctagaga ggttcagtca catccataaa acaagtatta tagattgtgc ttatttaatg 300
gtgagtattc tcaccagtag agcagatgtt gaatatccaa ggtagtgatt taaaagacca 360
aatgaagatt aatcccagca ggatggtgaa gaaatggaaa ttatggaaat cctgaagcat 420
ggaaagctct ggaaaattca atgtttgtgt aataatttag aagaggagaa tagtttatat 480
aggaaagata tacaataatc raagaaataa tagaattttt ccttaataag tcttccttaa 540
ggatgagaca aatatttaac tcaaatgtag gcatttatta atctcaaaga gaaaattaac 600
tgtccggaca ggagaaaaaa ttaggagaca tgaaaagggg ggaaaatcaa ctgatattac 660
ttttcatttg caacattaaa tgctagatgg aaagaagttt tcagaatctc gagaggtaaa 720
gaattaacaa ccacagaatt atcttctcag ccaaattatt ctttaaattt caggtgattc 780
taacaaaact gaatggatca agttagggct aaaagtatgc cagaagtctt atctagtgtc 840
ttggtttgtt tgggctgctg taacaaaaat accttacagt gggtggctta taaacaacag 900
gaatgtattg ctcacagttc tggaggctgg gaagttcacg atcaagtcac cggcagtttc 960
ggtgtgtggt gagagctttt gctctctggt tcatacatgg t 1001

<210> 213
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-501-155 : polymorphic base T or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-501-155.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-501-155.mis2, potential complement

<220>
<221> primer_bind
<222> 636..655
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 168..188
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-501-155 potential probe

<400> 213
acagctctca tgagctttac catctgaaca cagctaagaa tttgggattt taggaacaga 60
actgtaaatc ttaaaacaag caaaaagtgc tttctccttg gtagaaatac ctgtggccaa 120
gcccagacct tcagatccta acttgggata caactgattg ttacttaacc tgctgctaac 180
ctaaagacta gttttctgct catctagtcc cctgtgtgaa taagaggttt cctcctggtc 240
ccaggatgcc tctgctgctc agctcatctc tgaggctgtc tgtgagcctt cagttcagaa 300
attgagggaa aatccattgc cttggatgtc tccttccaaa tcaccaccca aaacaaaaat 360

```
taggagacgt agaaatccag gatgtgttgt gggttaggcc atattctgag gagttggaag    420
gtttcttggg gacctgaagt ctcgtgaaga gaaaatgtgg aaataagtgt ccttcaagcc    480
attgtagtgc ttgacatggg kgaaagaggc cagggggagg gggacctgtg gtgccagggc    540
ctttcagagc ttggctagat gagggggtcc ttctcagaac tgtaaataag ctgctcagtt    600
gcatgatttt cagaggccct gctaatgagc tttttgtttg ggttaagcct cccctgcttt    660
ccctgaagat aagccactga gttctatcag ctgctgtctt ctctccatta tgctttcgta    720
taaatattta acatttccta taaacaattc tggaagtaca tgccaagtga tacttatgga    780
agtgtaagaa gatgtttcag ttcaggctgc tataactacc acagactgag tgacttacac    840
aactgacatt tgttactgtt agggaggctg gaagtgcaag agcaaggcac tggcggattc    900
agctcctggt gagcgctctt catggtttgc agatggttgt cttgctgcgt cccatgtgtt    960
ggagagatca tttctcttgt atctctcctt atctaaggac a                       1001
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<210> 214
<211> 998
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-503-52 : polymorphic base T or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-503-52.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-503-52.mis2, potential complement

<220>
<221> primer_bind
<222> 535..552
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 80..100
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-503-52 potential probe

<220>
<221> misc_feature
<222> 105,135,165,402,424,522,569,587,843,873
<223> n=a, g, c or t

<400> 214

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gaatcatgta ttctgtcatt tgatattaca tcttttaata tttgataagt gtctttaatt     60
tgcatacaaa atgtcttgat tccatttaat cttgatgccc atcanggtat ccacgatgta    120
attcttagaa cagancatat aatattacat ctgtctattg aattnctcca aaaaatgtat    180
atatcctctg tacaatacta aaaatggtta tcatatttct attcacagaa gcaatgtttt    240
catgtattaa actaagacta tgagctgagt acttcacatg tttgacataa tcatttttgg    300
tggaaataat ggccacacat ctttgtatac acaagccata tttgctctat tatcatttcc    360
caggcaatta gcatttttat gtcaatatta tctgtttcca anttcattaa taatttcacg    420
aggntagatc atatctagtt ttttctttca catttcaata aagtcagtat aacttttttc    480
tgttgatata acatcattct kaatgtgaac atacttaata antgttacat acttgttcac    540
aatcggctac atctggtata taataaaana tcaaggtatt ttgcttncct ttttttaat     600
```

```
tgagacattc ttgctctgtc gcccaggctg gagtgcagtg gtgtgttctc agctcactgc    660
aacctccatc tccagggtgc aagtgattcg cccacctcag cctcccgagt agctgggact    720
acaggtgtgt gccaccacac cagctaattt ttgtattttt agtagagagg ggtttcacca    780
cattggccat gctggtctcg aactcctgac gtcaagtgac ccacccgcct ccgactccca    840
aangtgctgg gattacaggc atgagccact gcngccagct tgctcacata cttatttcaa    900
gcttttgaaa tgtctaacat ttccctttct tcacttttgt cttcacaatt caaaacagat    960
tctttagtta actctgaatt tggtaattgt tctattct                            998
```

<210> 215
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-503-62 : polymorphic base T or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-503-62.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-503-62.mis2, potential complement

<220>
<221> primer_bind
<222> 545..562
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 90..110
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-503-62 potential probe

<220>
<221> misc_feature
<222> 115,145,175,412,434,532,579,597,853,883
<223> n=a, g, c or t

<400> 215

```
ttcaattata gaatcatgta ttctgtcatt tgatattaca tcttttaata tttgataagt     60
gtctttaatt tgcatacaaa atgtcttgat tccatttaat cttgatgccc atcanggtat    120
ccacgatgta attcttagaa cagancatat aatattacat ctgtctattg aattnctcca    180
aaaaatgtat atatcctctg tacaatacta aaaatggtta tcatatttct attcacagaa    240
gcaatgtttt catgtattaa actaagacta tgagctgagt acttcacatg tttgacataa    300
tcatttttgg tggaaataat ggccacacat ctttgtatac acaagccata tttgctctat    360
tatcatttcc caggcaatta gcatttttat gtcaatatta tctgtttcca anttcattaa    420
taatttcacg aggntagatc atatctagtt ttttctttca catttcaata aagtcagtat    480
aactttttc tgttgatata wcatcattct taatgtgaac atacttaata antgttacat     540
acttgttcac aatcggctac atctggtata taataaaana tcaaggtatt ttgcttncct    600
ttttttaat tgagacattc ttgctctgtc gcccaggctg gagtgcagtg gtgtgttctc     660
agctcactgc aacctccatc tccagggtgc aagtgattcg cccacctcag cctcccgagt    720
agctgggact acaggtgtgt gccaccacac cagctaattt ttgtattttt agtagagagg    780
ggtttcacca cattggccat gctggtctcg aactcctgac gtcaagtgac ccacccgcct    840
```

```
ccgactccca aangtgctgg gattacaggc atgagccact gcngccagct tgctcacata    900
cttatttcaa gcttttgaaa tgtctaacat ttccctttct tcacttttgt cttcacaatt    960
caaaacagat tctttagtta actctgaatt tggtaattgt t                       1001
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<210> 216
<211> 1013
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 499
<223> 12-504-54 : polymorphic base A or G

<220>
<221> misc_binding
<222> 479..498
<223> 12-504-54.mis1, potential

<220>
<221> misc_binding
<222> 500..519
<223> 12-504-54.mis2, potential complement

<220>
<221> primer_bind
<222> 446..463
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 993..1013
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 487..511
<223> 12-504-54 potential probe

<220>
<221> misc_feature
<222> 108,180..181,663,712,768
<223> n=a, g, c or t

<400> 216

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tgtttgagac agtctcactc tgtcacccag gctagagtac agtggtgcaa tctcagctcg     60
ctgcaaactc cacctcccag gttcaagtga ttctcctgcc tcagcctncc cgagtagctg    120
ggattacaga tggccaccac catgcccaac tatttttgt atttttcgta gagacagggn    180
ntttcaccat gttggcctga gtggtcttga actcctgacc tcaagtgatc tgcccacctc    240
ggcctcccaa agtgctggaa ttataggcat gagccatcgt gcccagcgtg gttgtgctta    300
ttttaaattc ttaatttgtt tgttccagta tttctgcttg atatcgtgta tgttcagtgt    360
gtgtttttct ttttgcagtg gttctaacct caggtatttt aagctgtgag ctgatgttcc    420
cctggagtta tcaggtacca atgtgacata ccaataccag gtcctacttt ctgtgttcct    480
tatggtttta agattaagra gttgagtccc agagagtccc ttaggtgttg gaacgatagt    540
caacaagcca tctgttgccc ctccactagg cattactctg ctagggattc tcctctaaag    600
cctttgaaag ggagccggta gtcatctcat aagtgatgca ccatttacca cacatgagga    660
ggnactggag gagtgagtgc tcagggaagc tggtcagcct cccctttta gncgtgggtg     720
attgctgctg cctcctgact cacagtggtt atgggacagg caatggtncc aaaggaaaga    780
ggagagaaaa ggagagcaga acctagcagc actctaccta ttattctaac tctgcattcc    840
tccccaccca aagtttatga tggcctttag tgtctccagg agtttctcac agttttttc     900
tagggctgat tccccagggc atctgtggcc tgtgcctgat cttgtctgta cttcaggggc    960
cagcagtggg ggataggtta ctgaaagttt ttgagttttg ctgtgagaag att          1013
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<210> 217
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-504-96 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-504-96.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-504-96.mis2, potential complement

<220>
<221> primer_bind
<222> 406..423
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 953..973
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-504-96 potential probe

<220>
<221> misc_feature
<222> 68,140..141,623,672,728
<223> n=a, g, c or t

<400> 217
agtggtgcaa tctcagctcg ctgcaaactc cacctcccag gttcaagtga ttctcctgcc 60
tcagcctncc cgagtagctg ggattacaga tggccaccac catgcccaac tattttttgt 120
atttttcgta gagacagggn ntttcaccat gttggcctga gtggtcttga actcctgacc 180
tcaagtgatc tgcccacctc ggcctcccaa agtgctggaa ttataggcat gagccatcgt 240
gcccagcgtg gttgtgctta ttttaaattc ttaatttgtt tgttccagta tttctgcttg 300
atatcgtgta tgttcagtgt gtgtttttct ttttgcagtg gttctaacct caggtatttt 360
aagctgtgag ctgatgttcc cctggagtta tcaggtacca atgtgacata ccaataccag 420
gtcctacttt ctgtgttcct tatggtttta agattaagga gttgagtccc agagagtccc 480
ttaggtgttg gaacgatagt yaacaagcca tctgttgccc ctccactagg cattactctg 540
ctagggattc tcctctaaag cctttgaaag ggagccggta gtcatctcat aagtgatgca 600
ccatttacca cacatgagga ggnactggag gagtgagtgc tcagggaagc tggtcagcct 660
cccctttta gncgtgggtg attgctgctg cctcctgact cacagtggtt atgggacagg 720
caatggtncc aaaggaaaga ggagagaaaa ggagagcaga acctagcagc actctaccta 780
ttattctaac tctgcattcc tccccaccca aagtttatga tggcctttag tgtctccagg 840
agtttctcac agttttttc tagggctgat tccccagggc atctgtggcc tgtgcctgat 900
cttgtctgta cttcaggggc cagcagtggg ggataggtta ctgaaagttt ttgagttttg 960
ctgtgagaag attaatcttt cagcagagtg caataaaagg a 1001

<210> 218
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-504-428 : polymorphic base G or C

<220>
<221> misc_binding
<222> 482..500
<223> 12-504-428.mis1

<220>
<221> misc_binding
<222> 502..521
<223> 12-504-428.mis2, potential complement

<220>
<221> primer_bind
<222> 75..92
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 622..642
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-504-428 potential probe

<220>
<221> misc_feature
<222> 292,341,397
<223> n=a, g, c or t

<400> 218
tttgcagtgg ttctaacctc aggtatttta agctgtgagc tgatgttccc ctggagttat 60
caggtaccaa tgtgacatac caataccagg tcctactttc tgtgttcctt atggttttaa 120
gattaaggag ttgagtccca gagagtccct taggtgttgg aacgatagtc aacaagccat 180
ctgttgcccc tccactaggc attactctgc tagggattct cctctaaagc ctttgaaagg 240
gagccggtag tcatctcata agtgatgcac catttaccac acatgaggag gnactggagg 300
agtgagtgct cagggaagct ggtcagcctc cccttttag ncgtgggtga ttgctgctgc 360
ctcctgactc acagtggtta tgggacaggc aatggtncca aaggaaagag gagagaaaag 420
gagagcagaa cctagcagca ctctacctat tattctaact ctgcattcct ccccacccaa 480
agtttatgat ggcctttagt stctccagga gtttctcaca gttttttct agggctgatt 540
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aataaaagga ggaaggaaac cctgttacta gtttaagtaa gcaataatgg agatctggat 720
taatagtttg tatgttgaag tgagaagatt tttttttaa gtataaatga tttatttgtt 780
agttgagccc aagcttgaag aagctgctct tttattttgc ctcttttttt tcttacatat 840
gtttattctt agccttttct tttcttttct ttcttttttt tttttttgc agtgaattct 900
acaaactaag cactggaaga atgtcgagat gttacagtga aaaaggaagc taaatgaggc 960
cagattggag agcaaattgt tattatttaa aacttatgga c 1001

<210> 219
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 474

<223> 12-507-53 : polymorphic base C or T

<220>
<221> misc_binding
<222> 454..473
<223> 12-507-53.mis1, potential

<220>
<221> misc_binding
<222> 475..493
<223> 12-507-53.mis2, complement

<220>
<221> primer_bind
<222> 422..441
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 982..1001
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 462..486
<223> 12-507-53 potential probe

<220>
<221> misc_feature
<222> 153,560,925,934
<223> n=a, g, c or t

<400> 219
agtgtagcta ctccccctgt gctcccaccc ccaccatata ccagtggttc ttaaacttta 60
acatgcatca taatcaccca gagagtttgt taaaacaggg attgctgggc tccacctcca 120
gagtttctga ttcagtaaat ctggggcaag ccnttgataa tgtgtttcct aacaagtccc 180
caactcatag tgacactact agtccaggga tcaactctga gaatcactgc catataccaa 240
tatttctcag tactgactgc acctggggat tttaaagaga atacaactgc caaaaattac 300
cagtgctcag gtctgttccc actgattctg atttaattgg ttgggaatga ggccaggata 360
cctgtatttt ataaaagttc ttcaggagat tctaaggtat acttaggttc aagaagcact 420
tccttacact caatctccac ccgtcattca gagaaactca tgtagtttct gttycacctt 480
ccattaaagc cttcaatgtt aagctattat caagatattt ttatatagac tgggatgcct 540
attagtctta gtcaccaccn aaaatgtaag tcactaagta tttatcctct cccttactct 600
tactatttct ccatgatttc tctccactaa tccatacctg ctcctacttt gccttccacc 660
atgagtaaaa gttccttgag gcctccccag aagcagacgc cgccatgctt cctgtacagc 720
ctgcagagcc atgagccaat taaaccactt ttcttataaa ttacccagtc tcaggtattt 780
ctttatggca atgcaagaaa ggactgatac aggtaataaa tcattcattc attcaaataa 840
agttaccata gtgttgggga tacagaaaag agacagcccc ttaaggagct caaagtcctc 900
agaataccct tcctttattg tgatnttagt gccnactttt gaagacaaaa aagaagtaag 960
agtcttattt cgtgaacatg tgcaaatgta tgactcatta c 1001

<210> 220
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-507-92 : polymorphic base A or G

<220>
<221> misc_binding

<222> 481..500
<223> 12-507-92.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-507-92.mis2, potential complement

<220>
<221> primer_bind
<222> 410..429
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 970..990
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-507-92 potential probe

<220>
<221> misc_feature
<222> 141,548,913,922
<223> n=a, g, c or t

<400> 220
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atcacccaga gagtttgtta aaacagggat tgctgggctc cacctccaga gtttctgatt    120
cagtaaatct ggggcaagcc nttgataatg tgtttcctaa caagtcccca actcatagtg    180
acactactag tccagggatc aactctgaga atcactgcca tataccaata tttctcagta    240
ctgactgcac ctggggattt taaagagaat acaactgcca aaaattacca gtgctcaggt    300
ctgttcccac tgattctgat ttaattggtt gggaatgagg ccaggatacc tgtattttat    360
aaaagttctt caggagattc taaggtatac ttaggttcaa gaagcacttc cttacactca    420
atctccaccc gtcattcaga gaaactcatg tagtttctgt ttcaccttcc attaaagcct    480
tcaatgttaa gctattatca rgatattttt atatagactg ggatgcctat tagtcttagt    540
caccaccnaa aatgtaagtc actaagtatt tatcctctcc cttactctta ctatttctcc    600
atgatttctc tccactaatc catacctgct cctactttgc cttccaccat gagtaaaagt    660
tccttgaggc ctcccccagaa gcagacgccg ccatgcttcc tgtacagcct gcagagccat    720
gagccaatta aaccactttt cttataaatt acccagtctc aggtatttct ttatggcaat    780
gcaagaaagg actgatacag gtaataaatc attcattcat tcaaataaag ttaccatagt    840
gttggggata cagaaaagag acagcccctt aaggagctca aagtcctcag aatacccttc    900
ctttattgtg atnttagtgc cnacttttga agacaaaaaa gaagtaagag tcttatttcg    960
tgaacatgtg gcaaatgtat gactcattac gtttatggtt c                        1001
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<210> 221
<211> 1000
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 500
<223> 12-507-159 : polymorphic base G or T

<220>
<221> misc_binding
<222> 480..499
<223> 12-507-159.mis1, potential

<220>

<221> misc_binding
<222> 501..520
<223> 12-507-159.mis2, potential complement

<220>
<221> primer_bind
<222> 341..360
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 901..921
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 488..512
<223> 12-507-159 potential probe

<220>
<221> misc_feature
<222> 72,479,844,853
<223> n=a, g, c or t

<400> 221
agagtttgtt aaaacaggga ttgctgggct ccacctccag agtttctgat tcagtaaatc 60
tggggcaagc cnttgataat gtgtttccta acaagtcccc aactcatagt gacactacta 120
gtccagggat caactctgag aatcactgcc atataccaat atttctcagt actgactgca 180
cctggggatt ttaaagagaa tacaactgcc aaaaattacc agtgctcagg tctgttccca 240
ctgattctga tttaattggt tgggaatgag gccaggatac ctgtatttta taaaagttct 300
tcaggagatt ctaaggtata cttaggttca agaagcactt ccttacactc aatctccacc 360
cgtcattcag agaaactcat gtagtttctg tttcaccttc cattaaagcc ttcaatgtta 420
agctattatc aagatatttt tatatagact gggatgccta ttagtcttag tcaccaccna 480
aaatgtaagt cactaagtak ttatcctctc ccttactctt actatttctc catgatttct 540
ctccactaat ccatacctgc tcctactttg ccttccacca tgagtaaaag ttccttgagg 600
cctcccccaga agcagacgcc gccatgcttc ctgtacagcc tgcagagcca tgagccaatt 660
aaaccacttt tcttataaat tacccagtct caggtatttc tttatggcaa tgcaagaaag 720
gactgataca ggtaataaat cattcattca ttcaaataaa gttaccatag tgttggggat 780
acagaaaaga gacagcccct taaggagctc aaagtcctca gaatacсctt cctttattgt 840
gatnttagtg ccnacttttg aagacaaaaa agaagtaaga gtcttatttc gtgaacatgt 900
ggcaaatgta tgactcatta cgtttatggt tccactaagt ttaaattagg aggaagttcc 960
taataagtat ttttaagcaa aaaatagttg tgatcgattg 1000

<210> 222
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-507-177 : polymorphic base G or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-507-177.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-507-177.mis2, potential complement

<220>
<221> primer_bind
<222> 324..343
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 884..904
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-507-177 potential probe

<220>
<221> misc_feature
<222> 55,462,827,836
<223> n=a, g, c or t

<400> 222
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aatgtgtttc ctaacaagtc cccaactcat agtgacacta ctagtccagg gatcaactct    120
gagaatcact gccatatacc aatatttctc agtactgact gcacctgggg attttaaaga    180
gaatacaact gccaaaaatt accagtgctc aggtctgttc ccactgattc tgatttaatt    240
ggttgggaat gaggccagga tacctgtatt ttataaaagt tcttcaggag attctaaggt    300
atacttaggt tcaagaagca cttccttaca ctcaatctcc acccgtcatt cagagaaact    360
catgtagttt ctgtttcacc ttccattaaa gccttcaatg ttaagctatt atcaagatat    420
ttttatatag actgggatgc ctattagtct tagtcaccac cnaaaatgta agtcactaag    480
tatttatcct ctcccttact sttactattt ctccatgatt tctctccact aatccatacc    540
tgctcctact ttgccttcca ccatgagtaa aagttccttg aggcctcccc agaagcagac    600
gccgccatgc ttcctgtaca gcctgcagag ccatgagcca attaaaccac ttttcttata    660
aattacccag tctcaggtat ttctttatgg caatgcaaga aaggactgat acaggtaata    720
aatcattcat tcattcaaat aaagttacca tagtgttggg gatacagaaa agagacagcc    780
ccttaaggag ctcaaagtcc tcagaatacc cttcctttat tgtgatntta gtgccnactt    840
ttgaagacaa aaaagaagta agagtcttat ttcgtgaaca tgtggcaaat gtatgactca    900
ttacgtttat ggttccacta agtttaaatt aggaggaagt tcctaataag tatttttaag    960
caaaaaatag ttgtgatcga ttgtaaaatt agacacaaat t                       1001
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<210> 223
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-508-29 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-508-29.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-508-29.mis2, potential complement

<220>
<221> primer_bind
<222> 473..491
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 907..925
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-508-29 potential probe

<220>
<221> misc_feature
<222> 847
<223> n=a, g, c or t

<400> 223
cctaattaag cattgttttt acctctagga gtagatatta agaaattagt atttcataaa 60
atacccagcc attcctcaaa ttgttttttt tttttttttt tgaggcggag tcttgctctg 120
tcacccaggc cagagtgcag tgccgcgatc tcggctcact gcaagctctg cctcctgagt 180
tcacgccatt ctcctgcctc agcctcctta gtagctggga ctacaggcgc ccgccagcat 240
gcctagctaa tttttgtat ttttagtaga gatggggctt caccgtgtta gccaggatgg 300
tcttgatctc ctgaccttgt gatccgcccg cctcggcctc ccaaagtgct gggattacag 360
gcatgagcca ccgtgccctg cctgccattc ctcaaattct aagctccctg aaactcttac 420
ccttaaggta gagtatcaaa agtttttaaa agcaagaaaa gaaaattttt atcttatgct 480
agtggtaaat gccatttaaa racttaaatc ctaaaagctt gtatttaccc ttaaacttca 540
ttgtcacagg tatttctctg tctgctgtat attcagcatt gtactgagta cttacatcgc 600
ctcagttaaa attctttgtt tttgttggcc taatttcaga ttaacataaa agtacctcac 660
ccttgtttaa acctgcatta aatgacttgg attactgtgt ctggagtttt cctagcaaca 720
ctatttcaca cacaaagcaa agtacatact agccttttgt atgtgtcttt gtccttggtt 780
caacagctca gggatagtag tgtattaatg acttttattc tggtctttta tatgtgtctt 840
tgtcctntga tttgacagct gagaatagtg gtttttattc tagtaggata aaatttagcc 900
ttttagcact agaagtctaa gagattttaa ttttcatttg taaaaatagt gcacatttaa 960
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<210> 224
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-509-42 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-509-42.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-509-42.mis2, potential complement

<220>
<221> primer_bind
<222> 460..479
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 889..909

<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-509-42 potential probe

<220>
<221> misc_feature
<222> 678,728,796,824
<223> n=a, g, c or t

<400> 224
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actttttatt atcaccaatc atctcggtta ttgcgtcaaa ccccatttca gctctagttt 120
gacttttaaa tatgcagtta cgattcagaa tgctcatata gacaggctct aatcggaaat 180
aaacataaat gtgttgaggt ggtgggggtg tttaacaaaa agctaaaagt ttgaagaacc 240
tctttgagga ctagtgcaga aagatcaagg tgactgcaga gaaggagcac ttcagaaggc 300
attacatttt agtttgaaaa accgtcagga aattcttgag gcttccaact gatgattatt 360
ctattgaaaa gtaaatttgg ttttctttct catttggtaa atattctgat gtttttctgt 420
ttcatttgct taatgagatc atgaagtgat tatactttaa ttgaggagag tttggtttgt 480
taacatttta aatgtcatcc rtttggcatt taaaactgat atttaaaact cagaatgagc 540
tttaactttt tgttcttttg ccctacccat gttttaaact tgtgggctaa gagtgaattt 600
gaaaactaag gatttcaatt tttttcaaag ttaggaaact aacaattaaa gttattgcaa 660
cttagtttat ataattgnct acaagttctt gctcatttgg taaaaaataa atgatgcact 720
cagtaagnca aggaagtatc tcttagactt tctttaggaa gcatgttttc tagttaagca 780
aataacttaa ttccangtag cagatgccag gcagatgagt tggnagtcta agtgagtgaa 840
ggaggaagta ctgaagaagg aacatttcct cctagctggg agagttagga atgctacaca 900
gagtaagtgg gttccgtcct gggcctgagg gatgggccag ttcatctgtt aaaatctatg 960
actgtaacta ttgttacagc ccagcttcca tgatataatg t 1001

<210> 225
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-509-126 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-509-126.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-509-126.mis2, potential complement

<220>
<221> primer_bind
<222> 376..395
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 805..825
<223> downstream amplification primer, complement

<220>
<221> misc_binding

<222> 489..513
<223> 12-509-126 potential probe

<220>
<221> misc_feature
<222> 594,644,712,740
<223> n=a, g, c or t

<400> 225
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tcagaatgct catatagaca ggctctaatc ggaaataaac ataaatgtgt tgaggtggtg    120
ggggtgttta acaaaaagct aaaagtttga agaacctctt tgaggactag tgcagaaaga    180
tcaaggtgac tgcagagaag gagcacttca gaaggcatta cattttagtt tgaaaaaccg    240
tcaggaaatt cttgaggctt ccaactgatg attattctat tgaaaagtaa atttggtttt    300
ctttctcatt tggtaaatat tctgatgttt ttctgtttca tttgcttaat gagatcatga    360
agtgattata ctttaattga ggagagtttg gtttgttaac attttaaatg tcatccgttt    420
ggcatttaaa actgatattt aaaactcaga atgagcttta actttttgtt cttttgccct    480
acccatgttt taaacttgtg rgctaagagt gaatttgaaa actaaggatt tcaatttttt    540
tcaaagttag gaaactaaca attaaagtta ttgcaactta gtttatataa ttgnctacaa    600
gttcttgctc atttggtaaa aataaatga tgcactcagt aagncaagga agtatctctt     660
agactttctt taggaagcat gttttctagt taagcaaata acttaattcc angtagcaga    720
tgccaggcag atgagttggn agtctaagtg agtgaaggag gaagtactga agaaggaaca    780
tttcctccta gctgggagag ttaggaatgc tacacagagt aagtgggttc cgtcctgggc    840
ctgagggatg ggccagttca tctgttaaaa tctatgactg taactattgt tacagcccag    900
cttccatgat ataatgttag gaccccttcc atgaaatgaa agcataatca atttgagata    960
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<210> 226
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-510-59 : polymorphic base G or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-510-59.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-510-59.mis2, potential complement

<220>
<221> primer_bind
<222> 539..559
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 107..127
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-510-59 potential probe

<220>

<221> misc_feature
<222> 7..8,169,196,281,468,470,821
<223> n=a, g, c or t

<400> 226
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tagacagaga tagtgaataa atacatatta ataatgtttt aaaactttna aaaattgata    180
taaactttca tatcancaaa atgtataaat cttaaatata aactcaatga atcacttgag    240
tgagcttaag tgtaagctca aacaataact taatagtttt ncataagtgc tagaaatctt    300
atccaggaat aattgaaatt ttaccaatga gcataatatc ccaaataaaa taaatgggct    360
ttggtttgaa ttgtcatttt gaagaccatt actcagatat ttgaaagttg ttagtttggg    420
gcaaggtcat cacaccatgg cctgtgggac taggggctaa taatggtntn ttatattttt    480
gaaaggttta agacaaaaac rgaagaagaa aaagaaggag aaagagaagg aacagagact    540
atatgtggac ttcaatgctg aaacatactt attatcttgt ttcttataga aaaatttgct    600
aaccctggag ctacagagta aaagtcaact ggaagccaag acagtgattt cttttctttg    660
ttctttagcc tagtaagcca gatgtgtcaa caggttcttt ttgactggca ttaacatctt    720
gctcaataat aaaaggcctt aaatttttac taacttatat cagccccacc tagtgaaatt    780
aaatacaagg aatagttagc tgaaacactg tgtaccagaa nccattaagt caggacagtc    840
tgaggttgtt gacctcaatt ttgatatgaa ctggattttt tagacacgta ggaatagtta    900
tggctatatt taactatttt catggctatg gtgtatgttt ttaagacttt cccatagata    960
ttgtcattat ctactggctg gggcctttag aacagatggg a                       1001
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<210> 227
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-511-74 : polymorphic base T or C

<220>
<221> misc_binding
<222> 502..521
<223> 12-511-74.mis1, potential complement

<220>
<221> misc_binding
<222> 483..500
<223> 12-511-74.mis2

<220>
<221> primer_bind
<222> 558..575
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 125..145
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-511-74 potential probe

<220>
<221> misc_feature
<222> 102,561,637
<223> n=a, g, c or t

<400> 227
tgcagccctg ccctcagcca aggatctgta gggaactccc acttagactt ctaggaactc 60
atctttgcag ctcccctcctt actggtacca tgccctgcaa anttccaaac tttttgcatc 120
cctgaacttc agtctctgcc tcttcagctc agggagactg ctgtgctctg tttgggctcc 180
acttcatggc ctctgttgtt caaaaagttg cccccaaacc tggggcaaat gtgctgctca 240
cttcataggc ttcctttctc tgaaggagca cagttctatg ctgccttgct tccaacgtcc 300
gaaaatagct gtcatttatt ttgtcattta aaaaccttga attacagtaa gggaaagcat 360
attcataaat gaaatgatgt aaagacttta agtctaccta acatctagtt tttttctttt 420
ttgctaattg gactattcct cttttcattc atgtccttta agtttgttta tggaaaaaaa 480
ttatgacgac cacactcttc ygtggttata ggaactttca cacccattac aacattatgc 540
atttatattc tgacgacctt ngatgggaca cacaaaacct gattcttgca actttgccat 600
gaactttgtg atttccagag actggtaacc acttagnccc cacaaacttc taattctcta 660
cacagattat ctctctttcc ttgactctta tggtttgtaa ataaatgtct tttacacaca 720
actctgaagc gcgtcagatt ttatggtacc ccatagggct ataatgccta tagaaatggg 780
accaaattga aattttggaa atctctcttg gctttgtaga ctagttggtc gtaacttccc 840
aagtcacact tctgatacac ctgtgaggga ttactgcttt gtgccacact agatgacctg 900
caaggttttc taaccataga taaagccagt ctgtgattct catggacaaa ttttatgtgt 960
ttgttggaac caggcatcca gaggttcctc atttgtctg t 1001

<210> 228
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-325-311 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 10-325-311.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-325-311.mis2, potential complement

<220>
<221> primer_bind
<222> 191..208
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 596..613
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-325-311 potential probe

<400> 228
gcggaggggt catcttcacc atctacaatg tgacaacagg tgggcccaca tgtgaactgc 60
catggggaag atgggcttgt ccacaccact gcgtaacccc ttctccagcc agtcccatca 120
actcaagccc gtttctgggt gttcttgggc cccctgccct gccccatttg cctcagctgt 180
gcaaagccct tgtgtcaact cctgtccctg tgttagccca gagtccatct cataatgcag 240
agatggaaac tgaggcctag agcaggccag gggctgtctg cagggtccat gaccactcac 300
ctgccctgcc ctactccagg gaaggtggag gtcatcaatg cccgggagac ggtgccggcc 360
agccacgccc cgagcctgct ggaccagtgt gcacaggctc tgccactggg cacaggtgac 420
gccccatgga ggtcccccac tcccaccccc caggccacta ggactaatca gaacaccccc 480

gcaaaggagc agcgcctcac rgacaggctg tgactccctg gcacgggggg acacggagcc 540
tgtggggaac cccagcccc aacctgcagg gattgagaag gtccccttg ggaacgggct 600
ctctgaggtg atccagggag agggaccagg ctggacaaag gcctggaggg ttcagtggag 660
atgggttggc ggggcagggt ggggctcctg gggccagttt gtgtagggcc ccttgggctt 720
ggccatggac tttgtgggga gccacaggtg atttgagcag ggagggacgt ggtcgggtgt 780
gggctccaga aagctcactc tggctgctgt aactgggggg ccacatgtag ggtgatggc 840
aaacctggga aggcctggaa gccacagggt tgagagctgg gatgtgccat gcaggggccc 900
agtggatcgg ggtgcccggg gagctccgtg gctatgccga ggcccaccgc cgccatggcc 960
gcctgccctg ggcgcagctg ttccagccca ccatcgcgct g 1001

<210> 229
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-327-120 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 10-327-120.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-327-120.mis2, potential complement

<220>
<221> primer_bind
<222> 382..400
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 805..824
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-327-120 potential probe

<400> 229
ggccactagg actaatcaga acaccccgc aaaggagcag cgcctcacgg acaggctgtg 60
actccctggc acggggggac acggagcctg tggggaaccc ccagccccaa cctgcaggga 120
ttgagaaggt cccccttggg aacgggctct ctgaggtgat ccagggagag ggaccaggct 180
ggacaaaggc ctggagggtt cagtggagat gggttggcgg ggcagggtgg ggctcctggg 240
gccagtttgt gtagggcccc ttgggcttgg ccatggactt tgtggggagc cacaggtgat 300
ttgagcaggg agggacgtgg tcgggtgtgg gctccagaaa gctcactctg gctgctgtaa 360
ctgggggcc acatgtaggg gtgatggcaa acctgggaag gcctggaagc cacagggttg 420
agagctggga tgtgccatgc aggggcccag tggatcgggg tgcccgggga gctccgtggc 480
tatgccgagg cccaccgccg ycatggccgc ctgccctggg cgcagctgtt ccagcccacc 540
atcgcgctgc tccgaggggg gcatgtggtg gcccctgtcc tcagccgttt cctgcacaac 600
agcatcctgc ggccttcctt gcaggcgtca accctgcggt gagccccaca tggtggccct 660
gggttcctgg gttcaaggcc atatcctgtc tgggcccagt ccacacccca gctctgcctc 720
agtccctctt acactggagg attgaccctc ggggtgctgg ccaggacaaa gagtactttt 780
catggccctt ccagctcccc gtggcagagc ctaacttggg gttaggctgc ggggagttta 840
ttgcccaagt gataggactc caaggtgtgg atttgggctc tgccacccgc cctgggcccc 900
cggcctcctt cttcctctct ctggcatggc aggagggctt caactgccac tctcacctgc 960
cccacccagc ccactgacag gccctcccag gagtgagatg a 1001

<210> 230
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-331-179 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 10-331-179.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-331-179.mis2, potential complement

<220>
<221> primer_bind
<222> 326..345
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 728..747
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-331-179 potential probe

<400> 230
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gccaggagtt caataccagc ctgaacaaca tggcgaaatc ctgtctacta aaaatacaaa     60
aataattagc tgtacgtggt ggcgaacaca tgtagtctca gctactcagg agactaagga    120
ccaagaatca cttgaaccca ggaggcagag attgcagtga gctgagactg cgccattgca    180
ctccagcctg ggcaatagag tgagactctg tctaaaaaaa aaaaaaaaaa aaaaaaaatc    240
cttaacttac ttttccactt aaggtattag tcactcttgt gctgtataag gtaatatcca    300
caggttttgg gaattaggat gtgggtggat ctttctgtgg tggggggtgg gggcaacatt    360
caacccatta catagggtga ccccaaccaa cctgtgcccc aacctctctc cagggttcaa    420
cttctcaaca gagtctatgg ccaggcctga agggagggtg aacgtgtacc accaccttgt    480
agagacgctc aagtttgcca rggggcagag gtggaggctg gggaccctc gaagccaccc     540
gaagctccag gtgaggttgc tgaggttgct gggctggtgg gccgtcctcc tccctggctc    600
aggacttggc atgaaatgag ggtcaggcct ggtagggggа agttggaggg atatgtatgt    660
ggttctaggc cagggcagga ctgaaaggga tcccggggtg gcaggtacag gggtcaggtg    720
caggagtggc accatatctc aaaggacctg gagggtgagc agagtctaga cctagctggg    780
cttgagggag acctggccac aaggtagagg acagactgga ggtggccccc atgggggctg    840
atctcatcct gcccttggtt ctgcggattc tgcctggccc ctcactgacc ctgccacctg    900
cccacccacc ccagaatgcc tcccgggacc tgctgggga gaccctggcc cagctcatcc      960
gccaacagat cgatggccgg ggggaccacc agctcagcca c                        1001
```

<210> 231
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501

<223> 10-331-357 : polymorphic base G or T

<220>
<221> misc_binding
<222> 481..500
<223> 10-331-357.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-331-357.mis2, potential complement

<220>
<221> primer_bind
<222> 148..167
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 550..569
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-331-357 potential probe

<400> 231
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cactccagcc tgggcaatag agtgagactc tgtctaaaaa aaaaaaaaaa aaaaaaaaaa      60
tccttaactt acttttccac ttaaggtatt agtcactctt gtgctgtata aggtaatatc     120
cacaggtttt gggaattagg atgtgggtgg atctttctgt ggtggggggt gggggcaaca     180
ttcaacccat tacatagggt gaccccaacc aacctgtgcc ccaacctctc tccagggttc     240
aacttctcaa cagagtctat ggccaggcct gaagggaggg tgaacgtgta ccaccacctt     300
gtagagacgc tcaagtttgc caaggggcag aggtggaggc tgggggaccc tcgaagccac     360
ccgaagctcc aggtgaggtt gctgaggttg ctgggctggt gggccgtcct cctccctggc     420
tcaggacttg gcatgaaatg agggtcaggc ctggtagggg gaagttggag ggatatgtat     480
gtggttctag gccagggcag kactgaaagg gatcccgggg tggcaggtac aggggtcagg     540
tgcaggagtg gcaccatatc tcaaaggacc tggagggtga gcagagtcta gacctagctg     600
ggcttgaggg agacctggcc acaaggtaga ggacagactg gaggtggccc ccatgggggc     660
tgatctcatc ctgcccttgg ttctgcggat tctgcctggc ccctcactga ccctgccacc     720
tgcccaccca ccccagaatg cctcccggga cctgctgggg gagaccctgg cccagctcat     780
ccgccaacag atcgatggcc ggggggacca ccagctcagc cactacagct tggccgaggc     840
ctggggccac gggacaggca cgtcccatgt gtctgtgctg ggggaggatg gcagcgccgt     900
ggctgccacc agcaccatca acacaccgtg cgtagggcct gggggaaggc ggatggcttc     960
actcctcctc tcctagacct gcacaccccc agccccatgt c                        1001
```

<210> 232
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-334-263 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 10-334-263.mis1, potential

<220>
<221> misc_binding

<222> 502..521
<223> 10-334-263.mis2, potential complement

<220>
<221> primer_bind
<222> 240..257
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 658..675
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-334-263 potential probe

<400> 232
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tgcacacccc cagccccatg tcccctcact tgtccccacg gggcagcacc ttgcttttgc     60
ccttttctc ctcctctatt tcaaaagagg cccccacccc tgacatctct ggctggaaag    120
gctgctgctg gggtggcccc gacccaagat ttacctggga atgggtagcc tcactcagaa    180
gggtgccctg atgtgggggc acaggtgggt ctttggggac ccctcctggg tggtgccagg    240
gagagaatag cggcttcagc atgcttcggg gcagctgtaa aacgaggggg tcctgcaaag    300
cgtgcagggt aagtggtgtc tggtgggagc cccgggtcct agcccaggct cttctgcctc    360
cacggctgca gctttggagc gatggtgtat tcaccacgga caggcatcat cctcaacaac    420
gagctcctgg acttatgcga gcgatgcccc cggggttccg gcaccacccc ctcacctggt    480
gagaacaaag cttcccaccc rgggtccaca agggcccccc accaggggag aggagggagg    540
gggctgggct ggggttgcat gctaacccct ggatgggtca ctgcacttgc caagacgctg    600
tttgctcagc agtgagtgga gacagggtgg gtggagctcc cggaaggtgc tggcccccag    660
ttccaggcga gcgttcccca tcctccatgg tgccctccat cttgatcaac aaagcccagg    720
ggtcgaagct agtgattggc ggggctggcg gggagctcat catctctgct gtggcccagg    780
tgagtctggg gctcctggct cgagtgtctc ctctctgggc agcatactgt ctgactgtct    840
ctggagtggg gatgtgaggg ctgatgtagg gtagcagggt gccccctttc tccctgaaac    900
cctcatctct cccccaggcc atcatgagca agctgtggct tggctttgac ctgagagcgg    960
ccattgcagc ccccatcctg catgtcaaca gcaagggctg t                       1001
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<210> 233
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-321-226 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 10-321-226.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-321-226.mis2, potential complement

<220>
<221> primer_bind
<222> 276..293
<223> upstream amplification primer

<220>

<221> primer_bind
<222> 692..711
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-321-226 potential probe

<400> 233
gcacaggtgg gtctttgggg acccctcctg ggtggtgcca gggagagaat agcggcttca 60
gcatgcttcg gggcagctgt aaaacgaggg ggtcctgcaa agcgtgcagg gtaagtggtg 120
tctggtggga gccccgggtc ctagcccagg ctcttctgcc tccacggctg cagctttgga 180
gcgatggtgt attcaccacg gacaggcatc atcctcaaca acgagctcct ggacttatgc 240
gagcgatgcc cccggggttc cggcaccacc ccctcacctg gtgagaacaa agcttcccac 300
ccagggtcca caagggcccc ccaccagggg agaggaggga gggggctggg ctggggttgc 360
atgctaaccc ctggatgggt cactgcactt gccaagacgc tgtttgctca gcagtgagtg 420
gagacagggt gggtggagct cccggaaggt gctggccccc agttccaggc gagcgttccc 480
catcctccat ggtgccctcc rtcttgatca acaaagccca ggggtcgaag ctagtgattg 540
gcggggctgg cggggagctc atcatctctg ctgtggccca ggtgagtctg gggctcctgg 600
ctcgagtgtc tcctctctgg gcagcatact gtctgactgt ctctggagtg gggatgtgag 660
ggctgatgta gggtagcagg gtgccccctt tctccctgaa accctcatct ctcccccagg 720
ccatcatgag caagctgtgg cttggctttg acctgagagc ggccattgca gcccccatcc 780
tgcatgtcaa cagcaagggc tgtgtggagt acgagcccaa cttcagccag gtgaggctga 840
ggtccgagct ggatgcctag ggcagagccc actccccaaa tccgtgctgc tcaaagccac 900
ctgggaggaa ctcagtcact gagattctta ggccaggtac acttcaactt tgggggccat 960
aggagttggg gaccttgatg ggtgaggctg tcagtggcct c 1001

<210> 234
<211> 858
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-183-98 : polymorphic base G or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-183-98.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-183-98.mis2, potential complement

<220>
<221> primer_bind
<222> 581..598
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 136..155
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-183-98 potential probe

<400> 234
ctgagacccc agagggtccc tcccagcatc ttcaaagcaa caggattttg tgcctgcaga 60
tccttctttg cagcacacac caccccaccct gaccaggacc cctagaatgc ccagcatccc 120
tgggagggcc ctgtggtagt ttcagctccc tctgggggcc cagaatgaac ctggcctgtg 180
gtgaggatgt aagcaccaat ggccaattgg gtccaaagga agacaccggt tcaaacactg 240
aaaccaatca gattctccca cggccttcct gccatcagac gacactggtg caggggtggt 300
tgctatgtac agggcagagc cacccaatcc ccacgcagga gctgtgtcct gccatgctgg 360
cctcctcctg gccatcacat caggccaagc aggggagagg aatgggaatg cccatgcacc 420
cctatcaact ctgcagacac agaaccatgc acagctcttg ggaggagtca gatgagctgc 480
tcaaagcccg ggagggaccc rcacagtggt cagcatagca gggacggtgc tttagccaag 540
gcagggatgg caggtgactc actcaggatc ttcaaggagg ccgctgcatt tccgtgctct 600
ttccagataa gaaggacatg tcggtgatga tgagcgagac ggacatgaac gccatcgcag 660
gcacgctgaa gctgtacttc cgtgagctgc ctgagcccct cttcactgac gagttctacc 720
ccagcttcgc agagggcatc ggtgagcatt ggaggccttg gcctcgtggg agacgtctcc 780
tccatgtgca ctgctgccct tggaggctgt gaaaagtgag gtgtgggaac ctgagctgtg 840
acccctctgc catggtcg 858

<210> 235
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-185-78 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-185-78.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-185-78.mis2, potential complement

<220>
<221> primer_bind
<222> 424..444
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 855..875
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-185-78 potential probe

<220>
<221> misc_feature
<222> 661,672,954
<223> n=a, g, c or t

<400> 235
gctgagaaag ccacagttct ggcagctggc agagctgaaa gagaagggaa aatctatgca 60
cagggcccctt ggatttccac ccatattccc caggaaagga tacagttcca ggaagggctc 120
tctctgatct cccggaatga aatctgagat gaaccacagg gccttattgc ttacctgtac 180
ctcctttttg tagtttccag ctggcctggc acagactgac aaccccaaat ggatggtcga 240
aatccactgt tctccagtcc ctctcaaacc tcaccggcaa gaaggaaaga aactaaaccc 300

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cgagggccca ttatattcca gcggggtcct agggattcca cactcattca gttcctttac    360
atcataagaa gtgggtatta taatatcaga tccactgtaa aaggtgatcc cgaagcaaat    420
ggtagagcag gagtctgaat aggggcacct ccaacagcca catccacccc accacagctc    480
ccaggggttt ctttctaatc ycaagggtgg cctataccct gggactatag ggggccttgg    540
tgtgctaaat cttcagagac atttttaaac ggtcaagacg cctcttggcg actggaagaa    600
gttcctgacc tcgcggcatt ccctccttcc catcccact accacaccaa tcctatgcca     660
ngcctgtctg tngtcaggga agaagtccag ctggacaact ctggcagcct cctgtcgccc    720
tcccctgcca gcaatccttc tgtgccacag ctgtgtgtcc acactctaaa gcacacatcc    780
caccaggcca ctctcctgta aaataatgcc tcactgtccc aggccaaata ccccagcgcc    840
gatacctgct tcttcaaatc caggctccaa cccatccctc catctcattt ccattttacg    900
tgcacacata gtcacacact ctcacatacc cacactttgg ctcctactgt tccntacccc    960
tgaaaacccc ttaccacttt cctccctgag aaataactgc t                        1001
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<210> 236
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-186-154 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-186-154.mis1, potential

<220>
<221> misc_binding
<222> 502..520
<223> 12-186-154.mis2, complement

<220>
<221> primer_bind
<222> 348..368
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 784..803
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-186-154 potential probe

<220>
<221> misc_feature
<222> 3
<223> n=a, g, c or t

<400> 236

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ttntttttct tttttttgag acggagtctc gctctgttgc ccaggctggc gtgcagtggc     60
acgatcttgg ctcactgcaa gctctgcctc ccgagttcac gccattcccc tgcctcatcc    120
tcccgcctca tcctcccaag tagctgggac tacaggcacc caccaccacg ctcggctaat    180
tttttgtatt tttagtagag acagggtttc accgtgttag ccaggatggt ctcgatctcc    240
tgaccttgtg atccgcccgc cttggcctcc caaagtgctg ggattatagg cgtgagccac    300
cgcgcccggc cccctcccttg actcttgact gaaggacctt tgtctttgtg aacatcaatt   360
ctcaggacct ttcaccctgg ggacgtgaaa tgctgagaat ttgggagatg acagtctggg    420
gactgggatt aatggaatcc agtgacccac aaacctaagg ttctcagctc ccttggggag    480
ttggaatgtc agctattcag rtctagggct ttccatggag taaatcctaa actctgggtt    540
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ggagacttta agcctccaag gaccttcaca gctaaggccc agggactagg gcgaggagag 600
tctttgatcc tcagagtctt ggagtttggc cagtggactc tgaggaatgg agtctctgag 660
cactgaaggt ccaactttgg cttcagcagt aaaggatctt ggccttcaag tctaaggaca 720
gtgggcaatt agtaggtcag gcatggggaa ctcatagcca aacgtgcagg gctccaaaga 780
cctcatttgc cctgtcagca gctcaggcca tgtggcatca cccgatgcat ctagatgtct 840
ccggaatctc aggccctgca gggtgaggtt ctcgggccat tagtttttt tgttttgttt 900
tgttttgttt ttttggcttg ttgttgttga gacaaagttt cactctgtca cccaggctgg 960
agtgcagtgg cgcgatctca gcttattgca acctccacct c 1001

<210> 237
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-186-397 : polymorphic base C or T

<220>
<221> misc_binding
<222> 482..500
<223> 12-186-397.mis1

<220>
<221> misc_binding
<222> 502..521
<223> 12-186-397.mis2, potential complement

<220>
<221> primer_bind
<222> 105..125
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 541..560
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-186-397 potential probe

<400> 237
ccttgtgatc cgcccgcctt ggcctcccaa agtgctggga ttataggcgt gagccaccgc 60
gcccggcccc tcccttgact cttgactgaa ggacctttgt ctttgtgaac atcaattctc 120
aggacctttc accctgggga cgtgaaatgc tgagaatttg ggagatgaca gtctggggac 180
tgggattaat ggaatccagt gacccacaaa cctaaggttc tcagctccct tggggagttg 240
gaatgtcagc tattcaggtc tagggctttc catggagtaa atcctaaact ctgggttgga 300
gactttaagc ctccaaggac cttcacagct aaggcccagg gactagggcg aggagagtct 360
ttgatcctca gagtcttgga gtttggccag tggactctga ggaatggagt ctctgagcac 420
tgaaggtcca actttggctt cagcagtaaa ggatcttggc cttcaagtct aaggacagtg 480
ggcaattagt aggtcaggca yggggaactc atagccaaac gtgcagggct ccaaagacct 540
catttgccct gtcagcagct caggccatgt ggcatcaccc gatgcatcta gatgtctccg 600
gaatctcagg ccctgcaggg tgaggttctc gggccattag tttttttgt tttgttttgt 660
tttgtttttt tggcttgttg ttgttgagac aaagtttcac tctgtcaccc aggctggagt 720
gcagtggcgc gatctcagct tattgcaacc tccacctcct gggttcaagc aattctcatg 780
tctcagcctc ccaagtagct gggattacaa gtgtgtgcca ccaagcctgg ctaattttg 840
tatttttagc agaaacagcg tttctccatg ttggccaggc tggtctcaaa ctcctgacct 900
caggtgatct gcccaccttg gcctcccaaa gtgctgggat tacaggcatg accaccgcgc 960
ctggctaggg agcagtgttt ttaaggacaa cttggcgggt t 1001

<210> 238
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-187-65 : polymorphic base C or T

<220>
<221> misc_binding
<222> 482..500
<223> 12-187-65.mis1

<220>
<221> misc_binding
<222> 502..521
<223> 12-187-65.mis2, potential complement

<220>
<221> primer_bind
<222> 437..456
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 839..859
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-187-65 potential probe

<400> 238
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cctatatttt tatttattta tttatttatt tttctgagat ggagtctcac tctgtcacct     60
aggctggagt gcagtggtgc aatcttggct cactgcaacc tccgcctccc aggttcaagg    120
gattcttgtg cctcagcctc ccgagtaaat gggattacaa gcacccgcca ctgcatctgg    180
ctaatttttg tatttttagt agagacaagg tttcaccacg ttggccaggc tggtctcgaa    240
ctcctaacct caaatgatct gccggcctca gcttcccaaa gtgctgggat tacaggtgtg    300
agccaccgtg cccggccggc atcctatatt tttatattct aactctggca accttaaata    360
taagtgacaa atgaaaccaa aaataatggg caaaggtcta aacacatcag tgatcataaa    420
aaggaattga gaacattgtc agaacactgt cctgccttaa acactcttct ggaaagttcc    480
acaggttaag tgtgtcgtgt ygtcaggacc tgagatctct tctgccaatt aagctcccac    540
accatagaat aaggaggaaa atttgcacat ctgctttatg aagccagcgt agcactgacc    600
ccaaacttgg caaagaaaac cgcagactaa ttgtgtttat gatgcaaagc aaaatcctaa    660
caaaattgga gaatatataa ttaaaaaaga gaatccagta gtacattaaa aagaacaaca    720
tgacttacct accctagtgg agccaacgct aatattgcaa ggaagatctt ctcagtatgt    780
ccctgaccgt gactcttagc tcttaccttt caccagagga gaaaaaaatc actccatcga    840
gactgaagac gcatttgaca atatttaaca cccattcttt tttttttttt tttttaaaga    900
caggtctcac tctgttgccc atgctggagt ggagtggtgc gatcacagct cactgcagcc    960
ttgacctcct aggctcaaga gatcctcctg cctcagcttt t                       1001
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<210> 239
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-187-66 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-187-66.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-187-66.mis2, potential complement

<220>
<221> primer_bind
<222> 436..455
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 838..858
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-187-66 potential probe

<400> 239
ctatattttt atttatttat ttatttattt ttctgagatg gagtctcact ctgtcaccta 60
ggctggagtg cagtggtgca atcttggctc actgcaacct ccgcctccca ggttcaaggg 120
attcttgtgc ctcagcctcc cgagtaaatg ggattacaag cacccgccac tgcatctggc 180
taatttttgt atttttagta gagacaaggt ttcaccacgt tggccaggct ggtctcgaac 240
tcctaacctc aaatgatctg ccggcctcag cttcccaaag tgctgggatt acaggtgtga 300
gccaccgtgc ccggccggca tcctatattt ttatattcta actctggcaa ccttaaatat 360
aagtgacaaa tgaaaccaaa aataatgggc aaaggtctaa acacatcagt gatcataaaa 420
aggaattgag aacattgtca gaacactgtc ctgccttaaa cactcttctg gaaagttcca 480
caggttaagt gtgtcgtgtt rtcaggacct gagatctctt ctgccaatta agctcccaca 540
ccatagaata aggaggaaaa tttgcacatc tgctttatga agccagcgta gcactgaccc 600
caaacttggc aaagaaaacc gcagactaat tgtgtttatg atgcaaagca aaatcctaac 660
aaaattggag aatatataat taaaaaagag aatccagtag tacattaaaa agaacaacat 720
gacttaccta ccctagtgga gccaacgcta atattgcaag gaagatcttc tcagtatgtc 780
cctgaccgtg actcttagct cttacctttc accagaggag aaaaaaatca ctccatcgag 840
actgaagacg catttgacaa tatttaacac ccattctttt tttttttttt ttttaaagac 900
aggtctcact ctgttgccca tgctggagtg gagtggtgcg atcacagctc actgcagcct 960
tgacctccta ggctcaagag atcctcctgc ctcagctttt g 1001

<210> 240
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-189-348 : polymorphic base G or A

<220>
<221> misc_binding
<222> 502..520
<223> 12-189-348.mis1, complement

<220>
<221> misc_binding
<222> 481..500

<223> 12-189-348.mis2, potential

<220>
<221> primer_bind
<222> 832..849
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 384..402
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-189-348 potential probe

<220>
<221> misc_feature
<222> 69,615
<223> n=a, g, c or t

<400> 240
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cgaggcaggt ggatcaagtg aggtcagaag tttgagacca gcctagccaa catggtgaaa     60
ccctgtctnc taccaaaaat ataaaaaatt agctgggtgt ggtggtgcgt gcctgtaatc    120
ccagctaatt gggaggctga ggcagaagaa tcgcttgaac ccgggaggca gaggttgcaa    180
tgagccgata tcgtgccgct gcactccagc ctgggcaaca aagtgagact ccatctcaaa    240
aaaaaaaaaa aaggactagg acaaaaatac ctactttcaa ggagttcaca gtctacagga    300
ataaacagga catgtaaatg aacaaaatag gtccccatcc tttatgaacc tactttaaaa    360
aacaaaaaac agggcaagta tatgtacagg atacaatgga agcagaaaga tccccaattc    420
tgccttactt tgggcaacaa agtaggaggt acacctcgaa ggtatgagag taaacacagg    480
ttcaactgaa gaactctaat racttggcta gaatacagta tggctagaat acagaaatgt    540
caaaatgagg acttgtcggc aagggccaga agaccagtca agccctgggc ttcatgtgac    600
acaggacggt gaatnaaaag ccgtgcagtc ctataacctg acttgcagtt cccaaagact    660
aacctgcgct gctgtactga agatacagaa tgggagggtc agggatgagg aaaacagaat    720
gggcatctaa ttccctgtaa tgtctttgct ctcccttaat ctaagcttta tgttcaaaat    780
aaaagtacca ctctcactcc acaactcccc cagtatctga agaccaccat ggcgattccc    840
taaattggcc ctccttccaa gtcagcacca cacattcccc atccactcct ccagatttca    900
gtaccctgtg tccactggca tcaaagtatg acaggcacct cggaagtggg cacagataca    960
agacagatct ggtctggcaa gcacagagct cagcaagact a                       1001
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<210> 241
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-192-63 : polymorphic base C or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-192-63.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-192-63.mis2, potential complement

<220>
<221> primer_bind

<222> 544..563
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 75..94
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-192-63 potential probe

<400> 241
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caagtttccc ctgctgccac gcaggcgagg ggagcctttg atgctgccac ctcccttaga      60
gctggggtac cgggtcactg ttgaagacct ggaccgggag aaggaggcgg ccttccagcg     120
catcaacagt gcactgcagg ttgaggacaa ggccatctcg gactgcagac cctcacggcc     180
ttcccacact ttgtcctcac ttgcaacagg ggcttctggt ctgcctgccg tttctaaagc     240
acccagtatg gatgcacagc aggagacaca caagtcccaa gactgcctgg gcctactgga     300
cccttagca tctgctgcag gggtcccctc tacagctccc atgtctggga agaagcacag     360
accaccaggc cccctgttct cctcctcaga tccccttcct gccacctctt ctgattccca     420
ggactcagcc caggtcacct cgctgattcc tgccccccttc ccagctgcaa gcatggatgc    480
gggcatgaga agaacaaggc stggcacttc tgctcctgca gctgccgcag cagcccctcc     540
ccgctccaca ttgaacccca cgttggggtc actactggag tggatggagg cccttcacat     600
ttctgggcct cagccacagc tgcagcaggt gcccagaggt cagaaccaga gatcccagac     660
ctcctggacc agctcgtgcc ccaaatgaaa tgccatctcg agcccctaca gctctacggg     720
aggcctcccg gaacaaaagc ggaagagggg ccagcctcat cccactgcca gctgaccctc     780
agttcctcaa acacagtgag tgaggacgga cctcaggctg tctcttcggg tcacacccag     840
tgtgaaaaga cggcagatac agcaccaggg cagacactcg cctccagggg tggctccccc     900
agatcccagg cctctaggcc ccgtatatgc aagtttcccc tgctgccacg caggcgaggg     960
gagcctttga tgctgccacc tcccttagag atggggtacc g                        1001
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<210> 242
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 502
<223> 12-192-64 : polymorphic base T or C

<220>
<221> misc_binding
<222> 482..501
<223> 12-192-64.mis1, potential

<220>
<221> misc_binding
<222> 503..522
<223> 12-192-64.mis2, potential complement

<220>
<221> primer_bind
<222> 545..564
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 76..95
<223> downstream amplification primer

<220>

<221> misc_binding
<222> 490..514
<223> 12-192-64 potential probe

<400> 242
acaagtttcc cctgctgcca cgcaggcgag gggagccttt gatgctgcca cctccccttag 60
agctggggta ccgggtcact gttgaagacc tggaccggga gaaggaggcg gccttccagc 120
gcatcaacag tgcactgcag gttgaggaca aggccatctc ggactgcaga ccctcacggc 180
cttcccacac tttgtcctca cttgcaacag gggcttctgg tctgcctgcc gtttctaaag 240
cacccagtat ggatgcacag caggagacac acaagtccca agactgcctg ggcctactgg 300
accccttagc atctgctgca ggggtcccct ctacagctcc catgtctggg aagaagcaca 360
gaccaccagg ccccctgttc tcctcctcag atccccttcc tgccacctct tctgattccc 420
aggactcagc ccaggtcacc tcgctgattc ctgcccccctt cccagctgca agcatggatg 480
cgggcatgag aagaacaagg cytggcactt ctgctcctgc agctgccgca gcagcccctc 540
cccgctccac attgaacccc acgttggggt cactactgga gtggatggag gcccttcaca 600
tttctgggcc tcagccacag ctgcagcagg tgcccagagg tcagaaccag agatcccaga 660
cctcctggac cagctcgtgc cccaaatgaa atgccatctc gagcccctac agctctacgg 720
gaggcctccc ggaacaaaag cggaagaggg gccagcctca tcccactgcc agctgaccct 780
cagttcctca aacacagtga gtgaggacgg acctcaggct gtctcttcgg gtcacaccca 840
gtgtgaaaag acggcagata cagcaccagg gcagacactc gcctccaggg gtggctcccc 900
cagatcccag gcctctaggc cccgtatatg caagtttccc ctgctgccac gcaggcgagg 960
ggagcctttg atgctgccac ctccccttaga gatggggtac c 1001

<210> 243
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-192-268 : polymorphic base C or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-192-268.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-192-268.mis2, potential complement

<220>
<221> primer_bind
<222> 749..768
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 280..299
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-192-268 potential probe

<400> 243
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cctcaaagac agtgagtgag gacaggcctc aggctgtctc ttcaggtcac acccagtgtg 120
aaaaggcagc agatatagca ccagggcaga cactcaccct caggaatgac tcctccacat 180
ccgaggcctc taggcccagt acacacaagt ttcccctgct gccacgcagg cgaggggagc 240

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ctttgatgct gccacctccc ttagagctgg ggtaccgggt cactgttgaa gacctggacc    300
gggagaagga ggcggccttc cagcgcatca acagtgcact gcaggttgag gacaaggcca    360
tctcggactg cagaccctca cggccttccc acactttgtc ctcacttgca acaggggctt    420
ctggtctgcc tgccgtttct aaagcaccca gtatggatgc acagcaggag acacacaagt    480
cccaagactg cctgggccta stggacccct tagcatctgc tgcaggggtc ccctctacag    540
ctcccatgtc tgggaagaag cacagaccac caggccccct gttctcctcc tcagatcccc    600
ttcctgccac ctcttctgat tcccaggact cagcccaggt cacctcgctg attcctgccc    660
ccttcccagc tgcaagcatg gatgcgggca tgagaagaac aaggcatggc acttctgctc    720
ctgcagctgc cgcagcagcc cctccccgct ccacattgaa ccccacgttg gggtcactac    780
tggagtggat ggaggccctt cacatttctg ggcctcagcc acagctgcag caggtgccca    840
gaggtcagaa ccagagatcc cagacctcct ggaccagctc gtgccccaaa tgaaatgcca    900
tctcgagccc ctacagctct acgggaggcc tcccggaaca aaagcggaag aggggccagc    960
ctcatcccac tgccagctga ccctcagttc ctcaaacaca g                        1001
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<210> 244
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-192-334 : polymorphic base G or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-192-334.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-192-334.mis2, potential complement

<220>
<221> primer_bind
<222> 815..834
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 346..365
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-192-334 potential probe

<400> 244

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tcagttcctc aaagacagtg agtgaggaca ggcctcaggc tgtctcttca ggtcacaccc    180
agtgtgaaaa ggcagcagat atagcaccag ggcagacact caccctcagg aatgactcct    240
ccacatccga ggcctctagg cccagtacac acaagtttcc cctgctgcca cgcaggcgag    300
gggagccttt gatgctgcca cctcccttag agctggggta ccgggtcact gttgaagacc    360
tggaccggga gaaggaggcg gccttccagc gcatcaacag tgcactgcag gttgaggaca    420
aggccatctc ggactgcaga ccctcacggc cttcccacac tttgtcctca cttgcaacag    480
gggcttctgg tctgcctgcc rtttctaaag cacccagtat ggatgcacag caggagacac    540
acaagtccca agactgcctg ggcctactgg acccсttagc atctgctgca ggggtcccct    600
ctacagctcc catgtctggg aagaagcaca gaccaccagg ccccctgttc tcctcctcag    660
atccccttcc tgccacctct tctgattccc aggactcagc ccaggtcacc tcgctgattc    720
ctgccccctt cccagctgca agcatggatg cgggcatgag aagaacaagg catggcactt    780
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ctgctcctgc agctgccgca gcagcccctc cccgctccac attgaacccc acgttggggt 840
cactactgga gtggatggag gcccttcaca tttctgggcc tcagccacag ctgcagcagg 900
tgcccagagg tcagaaccag agatcccaga cctcctggac cagctcgtgc cccaaatgaa 960
atgccatctc gagcccctac agctctacgg gaggcctccc g 1001

<210> 245
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-192-352 : polymorphic base G or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-192-352.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-192-352.mis2, potential complement

<220>
<221> primer_bind
<222> 833..852
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 364..383
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-192-352 potential probe

<400> 245
ataacccgac atcccagacc tcctggacga gctcctgcac caaccgaaat gccatctcca 60
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cccactgcca gctgaccctc agttcctcaa agacagtgag tgaggacagg cctcaggctg 180
tctcttcagg tcacacccag tgtgaaaagg cagcagatat agcaccaggg cagacactca 240
ccctcaggaa tgactcctcc acatccgagg cctctaggcc cagtacacac aagtttcccc 300
tgctgccacg caggcgaggg gagcctttga tgctgccacc tcccttagag ctggggtacc 360
gggtcactgt tgaagacctg gaccgggaga aggaggcggc cttccagcgc atcaacagtg 420
cactgcaggt tgaggacaag gccatctcgg actgcagacc ctcacggcct tcccacactt 480
tgtcctcact tgcaacaggg rcttctggtc tgcctgccgt ttctaaagca cccagtatgg 540
atgcacagca ggagacacac aagtcccaag actgcctggg cctactggac cccttagcat 600
ctgctgcagg ggtcccctct acagctccca tgtctgggaa gaagcacaga ccaccaggcc 660
ccctgttctc ctcctcagat ccccttcctg ccacctcttc tgattcccag gactcagccc 720
aggtcacctc gctgattcct gccccctttcc cagctgcaag catggatgcg ggcatgagaa 780
gaacaaggca tggcacttct gctcctgcag ctgccgcagc agcccctccc cgctccacat 840
tgaaccccac gttggggtca ctactggagt ggatggaggc ccttcacatt tctgggcctc 900
agccacagct gcagcaggtg cccagaggtc agaaccagag atcccagacc tcctggacca 960
gctcgtgccc caaatgaaat gccatctcga gcccctacag c 1001

<210> 246
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-194-135 : polymorphic base G or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-194-135.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-194-135.mis2, potential complement

<220>
<221> primer_bind
<222> 363..381
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 878..893
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-194-135 potential probe

<220>
<221> misc_feature
<222> 223,412,431,439..440,565..566,894
<223> n=a, g, c or t

<400> 246
gcgggtggat cacctgaggt taggagttcg ataccagcct ggccaacatg gtgaaacccc 60
gtctctacaa aaaatataaa aattagtcgg gcgtggtggc acacgcttgt gatcccagcg 120
gctcgggagg ccgagacagg agaattgctt aggaggcaga gggtgcagtg aaccgaggtc 180
tcgccactgc actccagcct gggcgacaga gtgagactct gtnctcaaaa aaaaaaaaaa 240
acagctatta caatatacat gtatgttgta aaataaccaa accaacatag aagggtatat 300
agtgaaagga gaagtattgt tgtgggtaaa attgtttcaa taaatggcta atccagtatt 360
tttttcctcc aaaaaaacac cttttcccct ttgatttagt gtataccaca cnagagtcgc 420
ttagccgatt ncagtgacnn ttttttgata gctggagaat gcttcctaat ggttgcaggt 480
gtgtaggggt tttcttgaca ktttcagtaa gaaagtgaat gttgtgccat aggaaagctt 540
tatcacaggt gcacgttggt agccnnaact aaataacgtg agtgtcaagt acagtatcta 600
gtgagtggag aataactgta ataattacaa ttacagttgt agttaaagtg aagtttgtat 660
caaaatttct gtttcaaagg tgaactttta ggaggtgtat ctgcggtgtt tcttcctcag 720
atgtgatttc tctgaagcag tggttctcta taactgactt gacacacagt gcatctgata 780
tttcgaatga cttaagtgat agtatcaaaa ttactatcat atacatattt aaatcacatg 840
actaacctgt gtgtggtatt atgcaaactg ctcagctcag taagggaaca gaanataaga 900
aaaaaaggac aatattggga gtcttttata caattcaatt tattcaattg aaggactatc 960
ttttctttaa aaaagttctg ctttcttggt gttaaaataa a 1001

<210> 247
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501

<223> 12-194-325 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-194-325.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-194-325.mis2, potential complement

<220>
<221> primer_bind
<222> 171..189
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 686..707
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-194-325 potential probe

<220>
<221> misc_feature
<222> 31,220,239,247..248,373..374,702
<223> n=a, g, c or t

<400> 247
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tccagcctgg gcgacagagt gagactctgt nctcaaaaaa aaaaaaaaac agctattaca      60
atatacatgt atgttgtaaa ataaccaaac caacatagaa gggtatatag tgaaaggaga     120
agtattgttg tgggtaaaat tgtttcaata aatggctaat ccagtatttt tttcctccaa     180
aaaaacacct tttccccttt gatttagtgt ataccacacn agagtcgctt agccgattnc     240
agtgacnntt ttttgatagc tggagaatgc ttcctaatgg ttgcaggtgt gtaggggttt     300
tcttgacatt ttcagtaaga aagtgaatgt tgtgccatag gaaagcttta tcacaggtgc     360
acgttggtag ccnnaactaa ataacgtgag tgtcaagtac agtatctagt gagtggagaa     420
taactgtaat aattacaatt acagttgtag ttaaagtgaa gtttgtatca aaatttctgt     480
ttcaaaggtg aacttttagg rggtgtatct gcggtgtttc ttcctcagat gtgatttctc     540
tgaagcagtg gttctctata actgacttga cacacagtgc atctgatatt tcgaatgact     600
taagtgatag tatcaaaatt actatcatat acatatttaa atcacatgac taacctgtgt     660
gtggtattat gcaaactgct cagctcagta agggaacaga anataagaaa aaaaggacaa     720
tattgggagt cttttataca attcaattta ttcaattgaa ggactatctt ttctttaaaa     780
aagttctgct ttcttggtgt taaaataaag catcttttat gaaatgatgg tgatagtaaa     840
tggtgatata tggtaaacgt aaatagtaaa tgcaagggta gttattgtga tttttaaaaa     900
taaagagagc cgagaatctc ttgttttcct gctgctgtta gggagttcag gaaaaagttc     960
ctggggcttt tgctgttaag aagattcaaa tatagagtat t                        1001
```

<210> 248
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-194-337 : polymorphic base A or G

<220>
<221> misc_binding

<222> 481..500
<223> 12-194-337.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-194-337.mis2, potential complement

<220>
<221> primer_bind
<222> 159..177
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 674..695
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-194-337 potential probe

<220>
<221> misc_feature
<222> 19,208,227,235..236,361..362,690
<223> n=a, g, c or t

<400> 248
gacagagtga gactctgtnc tcaaaaaaaa aaaaaaacag ctattacaat atacatgtat 60
gttgtaaaat aaccaaacca acatagaagg gtatatagtg aaaggagaag tattgttgtg 120
ggtaaaattg tttcaataaa tggctaatcc agtatttttt tcctccaaaa aaacaccttt 180
tcccctttga tttagtgtat accacacnag agtcgcttag ccgattncag tgacnntttt 240
ttgatagctg gagaatgctt cctaatggtt gcaggtgtgt aggggttttc ttgacatttt 300
cagtaagaaa gtgaatgttg tgccatagga aagctttatc acaggtgcac gttggtagcc 360
nnaactaaat aacgtgagtg tcaagtacag tatctagtga gtggagaata actgtaataa 420
ttacaattac agttgtagtt aaagtgaagt ttgtatcaaa atttctgttt caaaggtgaa 480
cttttaggag gtgtatctgc rgtgtttctt cctcagatgt gatttctctg aagcagtggt 540
tctctataac tgacttgaca cacagtgcat ctgatatttc gaatgactta agtgatagta 600
tcaaaattac tatcatatac atatttaaat cacatgacta acctgtgtgt ggtattatgc 660
aaactgctca gctcagtaag ggaacagaan ataagaaaaa aaggacaata ttgggagtct 720
tttatacaat tcaatttatt caattgaagg actatctttt ctttaaaaaa gttctgcttt 780
cttggtgtta aaataaagca tcttttatga aatgatggtg atagtaaatg gtgatatatg 840
gtaaacgtaa atagtaaatg caagggtagt tattgtgatt tttaaaaata aagagagccg 900
agaatctctt gttttcctgc tgctgttagg gagttcagga aaaagttcct ggggcttttg 960
ctgttaagaa gattcaaata tagagtattt cttaagagta a 1001

<210> 249
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-194-479 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-194-479.mis1, potential

<220>

<221> misc_binding
<222> 502..521
<223> 12-194-479.mis2, potential complement

<220>
<221> primer_bind
<222> 17..35
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 532..553
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-194-479 potential probe

<220>
<221> misc_feature
<222> 66,85,93..94,219..220,548
<223> n=a, g, c or t

<400> 249
```
gctaatccag tattttttc ctccaaaaaa acacctttc ccctttgatt tagtgtatac     60
cacacnagag tcgcttagcc gattncagtg acnnttttt gatagctgga gaatgcttcc    120
taatggttgc aggtgtgtag gggttttctt gacattttca gtaagaaagt gaatgttgtg   180
ccataggaaa gctttatcac aggtgcacgt tggtagccnn aactaaataa cgtgagtgtc   240
aagtacagta tctagtgagt ggagaataac tgtaataatt acaattacag ttgtagttaa   300
agtgaagttt gtatcaaaat ttctgtttca aaggtgaact tttaggaggt gtatctgcgg   360
tgtttcttcc tcagatgtga tttctctgaa gcagtggttc tctataactg acttgacaca   420
cagtgcatct gatatttcga atgacttaag tgatagtatc aaaattacta tcatatacat   480
atttaaatca catgactaac ytgtgtgtgg tattatgcaa actgctcagc tcagtaaggg   540
aacagaanat aagaaaaaaa ggacaatatt gggagtcttt tatacaattc aatttattca   600
attgaaggac tatcttttct ttaaaaaagt tctgctttct tggtgttaaa ataaagcatc   660
ttttatgaaa tgatggtgat agtaaatggt gatatatggt aaacgtaaat agtaaatgca   720
agggtagtta ttgtgatttt taaaaataaa gagagccgag aatctcttgt tttcctgctg   780
ctgttaggga gttcaggaaa aagttcctgg ggcttttgct gttaagaaga ttcaaatata   840
gagtatttct taagagtaaa tatgagttta ttttgagatc attggtcaca gtctactgag   900
aaatccactg agaaagctgt taaatttgca tggcattaaa gatgttccta ttctgatcat   960
tgttaaatag atcttttta ttagatataa ttgtttttga g                       1001
```

<210> 250
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-442-133 : polymorphic base G or C

<220>
<221> misc_binding
<222> 482..500
<223> 10-442-133.mis1

<220>
<221> misc_binding
<222> 502..521
<223> 10-442-133.mis2, potential complement

<220>
<221> primer_bind
<222> 369..386
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 777..794
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-442-133 potential probe

<400> 250
```
ggcagagttg ggaaatgcag cctgcacagg tgtgttcagg tggccggtga tatgtcaccc      60
ccgcggccta gacttcagtc ctgcatctgt cgtgaggagt aggaagtggg gagagcagcc     120
cagaggccag gagctcggaa gcccccaggt cccagtggcc gccctgactg cctggcctct     180
ccccggcaaa ctccaggcac aatgacctcc cctggcagct gctggatatg ttcaacaacc     240
ggctgcagga cgagagggcc aacctgacca ccttggccgg cacacacacc aacatcccca     300
agctgagggc cggctttgtg ggaggccagg taccgcctgc cctgccttgt gcttgccctg     360
tgtggggtca tcccgtctcc tacctcaggc ctggctacag tgggaccatc cctgtggtgt     420
tcctccaggg tccctcggtg cccaggccga gggagggctt cccagcgggt gggaaaccag     480
actcccacag gcatgcgggg sgtgggctga gacctggctg catcagctcc tggcaccccc     540
tgcggcccac agttctggtc cgtgtacacg ccctgcgaca cccagaacaa agacgccgtg     600
cggaggacgc tggagcagat ggacgtggtc caccgcatgt gccggatgta cccggagacc     660
ttcctgtatg tcaccagcag tgcaggtggg gtcctgacct gggtcctcca ggtcctgcgt     720
cttctcaccc agccctcatc ctgagcagca ggtgccggtc aggacacctc accctccaga     780
taccaggtgc ccactcccct gcaccctgac tctccccgca ggcattcggc aggccttccg     840
ggaagggaag gtggccagcc tgatcggcgt ggaggcggc cactccattg acagcagttt      900
gggcgtcctg cgggcactct atcagctggg catgcggtac ctgaccctca cccacagctg     960
caacacgccc tggtgcgtga ctccccatgg gaggcccccg g                        1001
```

<210> 251
<211> 984
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 484
<223> 10-444-248 : polymorphic base A or G

<220>
<221> misc_binding
<222> 464..483
<223> 10-444-248.mis1, potential

<220>
<221> misc_binding
<222> 485..503
<223> 10-444-248.mis2, complement

<220>
<221> primer_bind
<222> 237..253
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 567..586
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 472..496
<223> 10-444-248 potential probe

<400> 251
gcattcggca ggccttccgg gaagggaagg tggccagcct gatcggcgtg gagggcggcc 60
actccattga cagcagtttg ggcgtcctgc gggcactcta tcagctgggc atgcggtacc 120
tgaccctcac ccacagctgc aacacgccct ggtgcgtgac tccccatggg aggcccccgg 180
gctgtggtca ggagggaggg ggcagacact ccctgccacc ctccagagcc catcccctct 240
gcctgtgagt cccaggccgg gcctcgcctg ctgggctgat gggaggccga gaccaccgct 300
cacctcttgg gcacctgcct tttgcttctc cagggctgac aactggctgg tggacacggg 360
agacagcgag ccccagagcc aaggcttgtc accctttggg caggtgagtg gggtgggagc 420
ggccagtcac ccccgaggag aaggcagagg ccctggaggg tgaccagaac aatgcatctc 480
ctcrcgtggg acctcagtgt ccttgtctgt aaaatggagc tggcagccat ccccccaggg 540
tgggtgctga gccctgagtg gccccggact tccagccacg aaggatgatg actcacatct 600
ggtccagccc gtccacctcc gcagccccga ccctggggc tgtgagggtg gacggagccc 660
tgtcttccca gcgtgtggtg aaggagctga accgtctggg ggtcctcatc gacttggctc 720
acgtgtctgt ggccaccatg aaggccaccc tgcagctgtc cagagccccg gtcatcttca 780
gccactcctc ggcctacagc gtgtgcgcaa gccggcgcaa cgtgcctgac gacgtcctga 840
ggctggtggt gagggccgag ggggcgacct ccacccccgcc tccctgggca ggccctccca 900
gctctcagct tcaccctgtc ttccttcttg tgcagaaaca gacagacagc ctggtgatgg 960
tgaacttcta caacaattac attt 984

<210> 252
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-445-281 : polymorphic base C or T

<220>
<221> misc_binding
<222> 482..500
<223> 10-445-281.mis1

<220>
<221> misc_binding
<222> 502..521
<223> 10-445-281.mis2, potential complement

<220>
<221> primer_bind
<222> 221..238
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 624..641
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-445-281 potential probe

<220>
<221> misc_feature
<222> 926,936,957,960,972

<223> n=a, g, c or t

<400> 252
cgggagacag cgagccccag agccaaggct tgtcaccctt tgggcaggtg agtggggtgg 60
gagcggccag tcacccccga ggagaaggca gaggccctgg agggtgacca gaacaatgca 120
tctcctcgcg tgggacctca gtgtccttgt ctgtaaaatg gagctggcag ccatcccccc 180
agggtgggtg ctgagccctg agtggccccg gacttccagc cacgaaggat gatgactcac 240
atctggtcca gcccgtccac ctccgcagcc ccgaccctgg gggctgtgag ggtggacgga 300
gccctgtctt cccagcgtgt ggtgaaggag ctgaaccgtc tgggggtcct catcgacttg 360
gctcacgtgt ctgtggccac catgaaggcc accctgcagc tgtccagagc cccggtcatc 420
ttcagccact cctcggccta cagcgtgtgc gcaagccggc gcaacgtgcc tgacgacgtc 480
ctgaggctgg tggtgagggc ygaggggcg acctccaccc cgcctccctg ggcaggccct 540
cccagctctc agcttcaccc tgtcttcctt cttgtgcaga aacagacaga cagcctggtg 600
atggtgaact tctacaacaa ttacatttcc tgcaccaaca aggccaacct gtcccaagtg 660
gccggtaggt ggggtgtgag cggccaaggg ggccgaaggg ggagggcctc actcgggacc 720
catacctgct gctccctgga cagaccatct ggatcacatc aaggaggtgg caggagccag 780
agccgtgggt tttggtgggg actttgatgg tgttccaagg taaggggctg agagctctgt 840
cctgtggatg agccgggagg ttcatggcct cgtcagaggg atgaggtggc tggaggaggg 900
acctgtgtcc tagtgtgggg gcccangttc tcctgncctc aacacagggt ccctganggn 960
ctggaggacg tntccaagta tccagacctg atcgctgagc t 1001

<210> 253
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-668-362 : polymorphic base T or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-668-362.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-668-362.mis2, potential complement

<220>
<221> primer_bind
<222> 844..861
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 390..410
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-668-362 potential probe

<400> 253
cctgcgcctc tcgtgcacct ccacatctgg tttgaggtca ggtcatttcc tgtctgtggg 60
cccagctgct gtgacaccca aggggagggc cggcgtcccc gaagccaggt cagccgtgca 120
cccggcagag ccccgcagat tggccccagc agagcttggg gtggggggag ctcggtgtca 180
ccaacaggcc cttgaggaca ctcgtgtgga gaatccctgg gacacgtgga ggacccccaa 240
gtcctgagcc ccgtactccg tactgcaggg agcaggccag gagccacggg ccttggggca 300
cagggtcctt ctcagggaca ggttcaggca ctggctggaa caggctggac ccctctaccc 360

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agcacatgtg ggcatgcgtc tgggttccga gggtggggaa atgtggaaag gctcctgctg    420
gccggcttag gcctgctgcc cttggagcct tccatataca gagagtccca cctccagcaa    480
gggttggcct ggactctcca wccccctgct gtgcccagga ctcccccagg gacaaggcaa    540
ccagaggccc agacccctcc ccagcaaaga gaagcaccac gggagctgtc tcccaagagc    600
ccttgacctg ggcccagct ggcctagggc cgggccccgg ggctgttgta gagcagagtg     660
tccatctgtg cacgctgtag ccacaagcgc cgctgggcgt cgccaagcag cacacgcagc    720
gagtggcctg gacggcaggc gggcagggct gcacagtggg cagcatgcag ctggcgacag    780
gtgtcgcagc agagggtggg cagggcgcca ggggacaggc agctgtgtgc ctggtagcct    840
gggggctccg agacagacct ataggctgag gctggtaccc cctctgcccg aatacgcctc    900
gggctggccg ctgcagagct ttcaggggtg gccaggtccc caggcctact cagctcacgg    960
cgcagagaga ggaaggagaa ggcggaaggt tcaggttcca g                       1001
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<210> 254
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-670-48 : polymorphic base G or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-670-48.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-670-48.mis2, potential complement

<220>
<221> primer_bind
<222> 454..474
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 883..901
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-670-48 potential probe

<220>
<221> misc_feature
<222> 49,105,142,317
<223> n=a, g, c or t

<400> 254

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cttttctgga cattccatgg aaagggaact gcaacatgag tggtctttnc ctctggcttg     60
tctcactcag tgtcccacct ttgggactcc ttcacggtgt ggcangggag tcagcagcct    120
gctcctcact gtcgctcagc cngtcactgc atggagagcg tgcacacttc atttatctg     180
ctgaaactct gttctcactc ttgctctgct gttttccctt catgtccacc ttcctccccc    240
accctctggt gtgacagaca ctgctggggc ccttccaaca ggcggtcctc cttccccac     300
ttccgttact ggcagangtc ctgcccactc ccatgcttca cagctccctc cagcccctgg    360
tgaatttgca ccattgaatg agtcctgcag aggctgggca ggcgaagcct tcctgggaaa    420
ggtttccttg ctaatatgaa gcaaggagca atgcctttgc agtagatgca gtcctgcctg    480
cgtgtggggg gctgtacact satcgggggc tgtggacact gagagtggtc aagaagagac    540
acgcaaagtc tttgatgtca ctgttgtgct aacaagccaa cctggaagct ccacctctga    600
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```
ccccttcattc gtgagacatt aaatccctgt gttaaagctg cgtttagtga gcttttctgt     660
aactttcagc taaaagcacc gtgacagaca ggtagcattt tccaaactgc cacccaaggg     720
tgatgctatt cctgcagggt tccatcctcc ggtggggggt tgcgccctcc tgtgaggggt     780
tccaccctcc agtgggaggt tccaaagttg ggaattcaaa tccaagtctt tcttccaagt     840
ccaaggccca gagcctccta ctttcagccc ttgatcctac aagcgtgtca gtgtgaagca     900
gtccaggccc agctcctctg cctagcaggc cagtcatccc cctgacattc tttcttgtct     960
gacccgagtg gttctctcct tattattttt ttttttttct g                         1001
```

<210> 255
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-670-91 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-670-91.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-670-91.mis2, potential complement

<220>
<221> primer_bind
<222> 411..431
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 840..858
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-670-91 potential probe

<220>
<221> misc_feature
<222> 6,62,99,274
<223> n=a, g, c or t

<400> 255

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tctttncctc tggcttgtct cactcagtgt cccacctttg ggactccttc acggtgtggc      60
angggagtca gcagcctgct cctcactgtc gctcagccng tcactgcatg gagagcgtgc     120
acacttcatt ttatctgctg aaactctgtt ctcactcttg ctctgctgtt ttcccttcat     180
gtccaccttc ctcccccacc ctctggtgtg acagacactg ctggggccct tccaacaggc     240
ggtcctcctt cccccacttc cgttactggc agangtcctg cccactccca tgcttcacag     300
ctccctccag cccctggtga atttgcacca ttgaatgagt cctgcagagg ctgggcaggc     360
gaagccttcc tgggaaaggt ttccttgcta atatgaagca aggagcaatg cctttgcagt     420
agatgcagtc ctgcctgcgt gtggggggct gtacactcat cgggggctgt ggacactgag     480
agtggtcaag aagagacacg yaaagtcttt gatgtcactg ttgtgctaac aagccaacct     540
ggaagctcca cctctgaccc ttcattcgtg agacattaaa tccctgtgtt aaagctgcgt     600
ttagtgagct tttctgtaac tttcagctaa aagcaccgtg acagacaggt agcattttcc     660
aaactgccac ccaagggtga tgctattcct gcagggttcc atcctccggt ggggggttgc     720
gccctcctgt gaggggttcc accctccagt gggaggttcc aaagttggga attcaaatcc     780
aagtctttct tccaagtcca aggcccagag cctcctactt tcagcccttg atcctacaag     840
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cgtgtcagtg tgaagcagtc caggcccagc tcctctgcct agcaggccag tcatccccct 900
gacattcttt cttgtctgac ccgagtggtt ctctccttat tattttttt tttttctgag 960
acagagtctc actctgtagc ccaggctgga gtgcagtggt g 1001

<210> 256
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-670-157 : polymorphic base C or T.

<220>
<221> misc_binding
<222> 482..500
<223> 12-670-157.mis1

<220>
<221> misc_binding
<222> 502..521
<223> 12-670-157.mis2, potential complement

<220>
<221> primer_bind
<222> 345..365
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 774..792
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-670-157 potential probe

<220>
<221> misc_feature
<222> 33,208
<223> n=a, g, c or t

<400> 256
gtcagcagcc tgctcctcac tgtcgctcag ccngtcactg catggagagc gtgcacactt 60
cattttatct gctgaaactc tgttctcact cttgctctgc tgttttccct tcatgtccac 120
cttcctcccc caccctctgg tgtgacagac actgctgggg cccttccaac aggcggtcct 180
ccttccccca cttccgttac tggcagangt cctgcccact cccatgcttc acagctccct 240
ccagcccctg gtgaatttgc accattgaat gagtcctgca gaggctgggc aggcgaagcc 300
ttcctgggaa aggtttcctt gctaatatga agcaaggagc aatgcctttg cagtagatgc 360
agtcctgcct gcgtgtgggg ggctgtacac tcatcggggg ctgtggacac tgagagtggt 420
caagaagaga cacgcaaagt ctttgatgtc actgttgtgc taacaagcca acctggaagc 480
tccacctctg acccttcatt ygtgagacat taaatccctg tgttaaagct gcgtttagtg 540
agcttttctg taactttcag ctaaaagcac cgtgacagac aggtagcatt ttccaaactg 600
ccacccaagg gtgatgctat tcctgcaggg ttccatcctc cggtgggggg ttgcgccctc 660
ctgtgagggg ttccaccctc cagtgggagg ttccaaagtt gggaattcaa atccaagtct 720
ttcttccaag tccaaggccc agagcctcct actttcagcc cttgatccta caagcgtgtc 780
agtgtgaagc agtccaggcc cagctcctct gcctagcagg ccagtcatcc ccctgacatt 840
ctttcttgtc tgacccgagt ggttctctcc ttattatttt tttttttttc tgagacagag 900
tctcactctg tagcccaggc tggagtgcag tggtgcgatc tcgctcaccg ctacttctgc 960
ctcccgggtc ccggttcaag gttcgagcaa ttctcctgcc t 1001

<210> 257
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-671-148 : polymorphic base C or T

<220>
<221> misc_binding
<222> 482..500
<223> 12-671-148.mis1

<220>
<221> misc_binding
<222> 502..521
<223> 12-671-148.mis2, potential complement

<220>
<221> primer_bind
<222> 354..372
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 784..804
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-671-148 potential probe

<220>
<221> misc_feature
<222> 31,33,37,88,270,348,764
<223> n=a, g, c or t

<400> 257
agcggcctcc ctcagctggt gtcggagtgc ncngccntgg aggagttcat ccacgagggg 60
tagaccctgg cgggtcaggg tgggggtnct ctgtgcgaag agcagggacc tcatccctca 120
acctaaacgg tggttgtcag tagcagctgg ggagggtagc gtgtggctcc gtcacagcca 180
tgccttcggg cagcccctgt gggtccacct gtgcagagtg cctgctgcca catgtcccgt 240
ggcccttcgc ttagctcagc ctctcccagn acagcaggag ctgggggctg tcccctgagc 300
agcatctgcc tggggagggg ataaggatcc agtgccatcc ctggctcnta ccgtccaagg 360
acgagcacat agtgggtggg aaaggcctcc tctagcccag ccgccctgac agccccacct 420
gcccaccctc agcacccagg tcctgaactg ggagggcaga cactaccttc tggagggccg 480
ggggtgtcct tctgttcgtt yagatgacac cggctgcccc tgccatccat gcaggtacct 540
gatcggagag gagggctact gcctcacatc actgcagagt gccctgagct acgtggagct 600
gctgccccgg ggaggcctgg ccaagtagta cagctagagc ccagggtccc tgcagggcct 660
ggcctcgcct cccagggctg tctctcctac acctggagcc atgggatcta ctgaggacca 720
tcctggagcc tcacgctgct ctgcacatgg tgggggcttg tccnactgtg gtgtgctctc 780
cagctcttca ccttcctcac ctcacatctg accctggagc ttggggttgg cacctctgcc 840
ccgacagaat ggggctgaat cagctccagg aggaaccagg ccctgctctc ctgtgtaggc 900
ctcagagagg ccaagaaggg aagctttggg cttcggtggg tgcaggctca gcgatgaaca 960
tctggctggg gcagctcctg gggagcatca gggaagaggg g 1001

<210> 258
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 253
<223> 12-679-245 : polymorphic base A or G

<220>
<221> misc_binding
<222> 233..252
<223> 12-679-245.mis1, potential

<220>
<221> misc_binding
<222> 254..273
<223> 12-679-245.mis2, potential complement

<220>
<221> primer_bind
<222> 9..29
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 439..458
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 241..265
<223> 12-679-245 potential probe

<220>
<221> misc_feature
<222> 257..258,678,798
<223> n=a, g, c or t

<400> 258
tgcccactta cttcctttct gggtaaggct caaaggactc gtccgaagac tgggcatttt 60
gcttcttgtc attttcatct tcactcaaga cgtctctagg aattaagaga gaatcttcag 120
caaagccctg ggcctgggca gtgacagacc caacacgacc tcctgcctaa agataccaaa 180
tggacccccca tgtcccacat ttgagttctt ctgaaaatgt cttaaatcta aaatccccaa 240
atttccaatc ccrtttnncg aacacaaagg gccagccagg ctcacaagcc agcaatcccc 300
acaagccatg tgctctgggc accaggacac tggacttgga aacagccctt tccacagcgg 360
cccagaaggg gtggaggcgc tcaaaggtag cttcctgcta agcagacttt gagaaatcga 420
ccacctcacc ccataactgc gaaccctatg caactgatgg gtttgccatg agtcacttct 480
aagttcacaa aagtggctgg gtgcagaggc taactcctgt aatcccagca cttcgggagg 540
ctgacgtagg tggatcgcat gaggtcagga gttcaagacc agcctggcca ataccgtgaa 600
accccgtctc tactaaaaat acaaaaattg gccgggtgcg gtggctcaca cctgtaatcc 660
cagcactttg ggaggcanga ggcgggcgga tcacgaggtc aggagatcaa gaccatcccg 720
gctaacaaag tgaaaccccg tctctactaa aaatacaaaa aattagccgg gcgtggtggc 780
gggtgcctgt agtcccangc gactcagaag ctgaggccgg agaatggcgt gaacccggga 840
ggcagagctt gcagtaggcc gagattgtgc cactgcactc cagcctgggc aacacagcga 900
gactccgtct caaataaaaa aaaaataaat aaatacaaaa cttagctggg tgtggtggcg 960
ggcgcctgta atcccagcta ctcgggaggc tgaggcggga g 1001

<210> 259
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 379

<223> 12-679-371 : polymorphic base A or G

<220>
<221> misc_binding
<222> 359..378
<223> 12-679-371.mis1, potential

<220>
<221> misc_binding
<222> 380..399
<223> 12-679-371.mis2, potential complement

<220>
<221> primer_bind
<222> 9..29
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 439..458
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 367..391
<223> 12-679-371 potential probe

<220>
<221> misc_feature
<222> 257..258,678,798
<223> n=a, g, c or t

<400> 259
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tgcccactta cttcctttct gggtaaggct caaaggactc gtccgaagac tgggcatttt     60
gcttcttgtc attttcatct tcactcaaga cgtctctagg aattaagaga gaatcttcag    120
caaagccctg ggcctgggca gtgacagacc caacacgacc tcctgcctaa agataccaaa    180
tggacccccca tgtcccacat ttgagttctt ctgaaaatgt cttaaatcta aaatccccaa   240
atttccaatc ccatttnncg aacacaaagg gccagccagg ctcacaagcc agcaatcccc    300
acaagccatg tgctctgggc accaggacac tggacttgga aacagccctt tccacagcgg    360
cccagaaggg gtggaggcrc tcaaaggtag cttcctgcta agcagacttt gagaaatcga    420
ccacctcacc ccataactgc gaaccctatg caactgatgg gtttgccatg agtcacttct    480
aagttcacaa aagtggctgg gtgcagaggc taactcctgt aatcccagca cttcgggagg    540
ctgacgtagg tggatcgcat gaggtcagga gttcaagacc agcctggcca ataccgtgaa    600
accccgtctc tactaaaaat acaaaaattg gccgggtgcg gtggctcaca cctgtaatcc    660
cagcactttg ggaggcanga ggcgggcgga tcacgaggtc aggagatcaa gaccatcccg    720
gctaacaaag tgaaaccccg tctctactaa aaatacaaaa aattagccgg gcgtggtggc    780
gggtgcctgt agtcccangc gactcagaag ctgaggccgg agaatggcgt gaacccggga    840
ggcagagctt gcagtaggcc gagattgtgc cactgcactc cagcctgggc aacacagcga    900
gactccgtct caaataaaaa aaaaataaat aaatacaaaa cttagctggg tgtggtggcg    960
ggcgcctgta atcccagcta ctcgggaggc tgaggcggga g                       1001
```

<210> 260
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 434
<223> 12-679-426 : polymorphic base C or T

<220>
<221> misc_binding

<222> 414..433
<223> 12-679-426.mis1, potential

<220>
<221> misc_binding
<222> 435..454
<223> 12-679-426.mis2, potential complement

<220>
<221> primer_bind
<222> 9..29
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 439..458
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 422..446
<223> 12-679-426 potential probe

<220>
<221> misc_feature
<222> 257..258,678,798
<223> n=a, g, c or t

<400> 260
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tgcccactta cttcctttct gggtaaggct caaaggactc gtccgaagac tgggcatttt     60
gcttcttgtc attttcatct tcactcaaga cgtctctagg aattaagaga gaatcttcag    120
caaagccctg ggcctgggca gtgacagacc caacacgacc tcctgcctaa agataccaaa    180
tggacccccca tgtcccacat ttgagttctt ctgaaaatgt cttaaatcta aaatccccaa   240
atttccaatc ccatttnncg aacacaaagg gccagccagg ctcacaagcc agcaatcccc    300
acaagccatg tgctctgggc accaggacac tggacttgga aacagccctt tccacagcgg    360
cccagaaggg gtggaggcgc tcaaaggtag cttcctgcta agcagacttt gagaaatcga    420
ccacctcacc ccayaactgc gaaccctatg caactgatgg gtttgccatg agtcacttct    480
aagttcacaa aagtggctgg gtgcagaggc taactcctgt aatcccagca cttcgggagg    540
ctgacgtagg tggatcgcat gaggtcagga gttcaagacc agcctggcca ataccgtgaa    600
accccgtctc tactaaaaat acaaaaattg gccgggtgcg gtggctcaca cctgtaatcc    660
cagcactttg ggaggcanga ggcgggcgga tcacgaggtc aggagatcaa gaccatcccg    720
gctaacaaag tgaaaccccg tctctactaa aaatacaaaa aattagccgg gcgtggtggc    780
gggtgcctgt agtcccangc gactcagaag ctgaggccgg agaatggcgt gaacccggga    840
ggcagagctt gcagtaggcc gagattgtgc cactgcactc cagcctgggc aacacagcga    900
gactccgtct caaataaaaa aaaaataaat aaatacaaaa cttagctggg tgtggtggcg    960
ggcgcctgta atcccagcta ctcgggaggc tgaggcggga g                       1001
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<210> 261
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 12-680-331 : polymorphic base C or T

<220>
<221> misc_binding
<222> 483..502
<223> 12-680-331.mis1, potential

<220>

<221> misc_binding
<222> 504..523
<223> 12-680-331.mis2, potential complement

<220>
<221> primer_bind
<222> 173..192
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 645..665
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 12-680-331 potential probe

<400> 261
ggtaagagga tcctctaggt gggggggggg ggttccccag gtgaggggac ctccaggtaa 60
gaggatcctc taggtggggg agtcccccag gtgaagggcc ctccaggtaa gagggtcctc 120
caggtgagag ggtcctccag cggagggggt cccccaggta agagggtcct ccagttggga 180
gtccttcagg tggggtggtc ctccaggtga gagagtcttc caggtgagag ggtcctccag 240
gtgagaggtg aaggtgaagg tcctccaggt gagggtcagg tcacttggtc cagggatgtg 300
gcttcagcaa gcatttgggt gcctcctctg tgttcaggac atggggactc cgggagactg 360
aaggaagcaa gtggcaatgt ccatgccgtc aagttctgtc acagaaataa gcaggagtga 420
gtgaaagaca ggagagaagc tctgtgaggg gtggcattca agcttagctt ctgggcagga 480
agaggcagct atgtcagcat tcyctaacaa ggtttggcaa agtagatacc tcccctcact 540
catggaagac ctgacttccc aggctggtag aagcttctct cacaggcacc tgcctctcca 600
atctctttca cagcccagcc ctggaaggtg gaaaaagaaa agttgacatg gaatgtttag 660
gaagcaccat tggtccaggt ccaggatcgg ggcagccagc atgtcctcta atctggcttc 720
actgttgaaa tccagtcgag caagcagggc ccaaaccact gcgagaccag ctcggtcggg 780
cccaaaccac cgcccactgc gggaccagct cggtcgggcc caaaccaccg cccactgcgg 840
gaccagctcg gtcgggccca aaccactgcc cactgcggga ccagctcggt cgtggagacc 900
ctaacccagc ggcgctagag gaattaaaga aacacacaca gaaatatagg gtgtggagtg 960
ggaaatcagg ggtctcacag ccttcgaagc tgaaagcctc g 1001

<210> 262
<211> 384
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 154
<223> 10-151-154 : polymorphic base A or G

<220>
<221> misc_binding
<222> 134..153
<223> 10-151-154.mis1, potential

<220>
<221> misc_binding
<222> 155..173
<223> 10-151-154.mis2, complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 367..384
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 142..166
<223> 10-151-154 potential probe

<220>
<221> misc_feature
<222> 346..347
<223> n=a, g, c or t

<400> 262
actcaamacc caaggagccc attctctccc ttggctttct ctcaggtcaa ggtgttgaaa 60
tgcatctcag aggtgcaggc caacaatgtg gtcctgggcc agtacgtggg gaaccccgat 120
ggagagggcg aggccaccaa agggtacctg gacraccca cggtgccccg cgggtccacc 180
accgccactt ttgcagccgt cgtcctctat gtggagaatg agaggtggga tggtaggtga 240
tgccttcgag gcccagcaag gcagaactgg gcatgccctg tgtgcgggca ctggagctcc 300
cactgagaca ctcacgcact ggtccacacc ctgagagagc tggtgnngag gctgcccttt 360
ccgccacgta ggggtgccct tcat 384

<210> 263
<211> 426
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 205
<223> 10-138-206 : polymorphic base C or T

<220>
<221> misc_binding
<222> 186..204
<223> 10-138-206.mis1

<220>
<221> misc_binding
<222> 206..225
<223> 10-138-206.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 406..425
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 193..217
<223> 10-138-206 potential probe

<220>
<221> misc_feature
<222> 243
<223> n=a, g, c or t

<400> 263
atgatgmcca agaagccggg catgttcttc aaccccgagg agtcggagct ggacctgact 60
acggcaacag atacaaggtg ccctacagag aaggagcagt gtggagggtg ggcggcctgg 120
gcccgggga ctccacatgg tggcaggcag tggcatcagc aagacactct ctccctcaca 180
gaacgtgaag ctccctgacg cctaygagcg cctcatcctg gacgtcttct gcgggagcca 240
gangcacttc gtgcgcaggt gaggcccagc tgccggcccc tgcatacctg tgggctatgg 300
ggtggccttt gccctccctc cctgtgtgcc accggcctcc caagccatac tatgtcccct 360
cagcgacgag ctccgtgagg cctggcgtat tttcacccca ctgctgcacc agattgagct 420
ggagag 426

<210> 264
<211> 426
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 351
<223> 10-138-352 : polymorphic base C or T

<220>
<221> misc_binding
<222> 332..350
<223> 10-138-352.mis1

<220>
<221> misc_binding
<222> 352..371
<223> 10-138-352.mis2, potential complement

<220>
<221> primer_bind
<222> 1..18
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 406..425
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 339..363
<223> 10-138-352 potential probe

<220>
<221> misc_feature
<222> 243
<223> n=a, g, c or t

<400> 264
atgatgmcca agaagccggg catgttcttc aaccccgagg agtcggagct ggacctgact 60
acggcaacag atacaaggtg ccctacagag aaggagcagt gtggagggtg ggcggcctgg 120
gcccgggga ctccacatgg tggcaggcag tggcatcagc aagacactct ctccctcaca 180
gaacgtgaag ctccctgacg cctacgagcg cctcatcctg gacgtcttct gcgggagcca 240
gangcacttc gtgcgcaggt gaggcccagc tgccggcccc tgcatacctg tgggctatgg 300
ggtggccttt gccctccctc cctgtgtgcc accggcctcc caagccatac yatgtcccct 360
cagcgacgag ctccgtgagg cctggcgtat tttcacccca ctgctgcacc agattgagct 420
ggagag 426

<210> 265
<211> 1001

<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-586-414 : polymorphic base A or G

<220>
<221> misc_binding
<222> 482..500
<223> 12-586-414.mis1

<220>
<221> misc_binding
<222> 502..521
<223> 12-586-414.mis2, potential complement

<220>
<221> primer_bind
<222> 88..107
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 552..572
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-586-414 potential probe

<400> 265
gtggtcagct atcccaaggc tcctggctgt tgacatttta tgttcagctt gcacttctct 60
ttctcttctt tagtgcctgc aacttctcac ccacactttc aacagagaat tcagccaggt 120
gcacggcagc gtcagtgact gtaaggtgag cacattgact gtaattttta gccagtatgt 180
tgataactga tttctccaca gcagcccaga ttacctattc ctggtttttg ctgcttttaa 240
gcaacttgtc atgggcatag cattgtattt gaaaatttat gacatactgc tctggtattc 300
attctaattt ttcagagtcc gaacactgac ttctgaagat aaaagtactc ctttgtgtct 360
cttagagtga ttatcagatg ggaaacattt tggctttttc atgactcctt tggaggagaa 420
tattctatgg ggaggtggta tgttattctt tgccagggta caaggaaacc ctgaggttcc 480
tggtggcata aagttttatt racttcaaca aagagtgaag taaacacttc agagaatttc 540
tgtgttattc actcaattct agtcagcttg accttaaacc ctccccggctc attcctgcct 600
tggggtcttt gcacacctac tatttctttg cctggaattg cctttctcca ggtattgcca 660
tggttggctc ccttacctct ttcatttttc tactccatta tcacctcctg tgagtcgact 720
ctgttaacac ctgataataa atctgacagc tgtctgaaac tttctaccta cccctctttc 780
ctgctttatt ttttgctata gcactaatta ctacctgatg ctttttaaag tgtttgttga 840
gtggtttatt gtctgtctta agctccaggg aggcagatcc tctgccatat tattagaaca 900
atgcctagta catggaaggt gcaccactgt aataccactt atattaattc aggggctggg 960
tgtggtggtg catacctgta atcccagcac tttgggaggc c 1001

<210> 266
<211> 999
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 499
<223> 12-587-379 : polymorphic base C or A

<220>

<221> misc_binding
<222> 479..498
<223> 12-587-379.mis1, potential

<220>
<221> misc_binding
<222> 500..519
<223> 12-587-379.mis2, potential complement

<220>
<221> primer_bind
<222> 857..877
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 478..498
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 487..511
<223> 12-587-379 potential probe

<400> 266
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cagcactttt ctagctctcc cgttccccat ctccattgct ctgtactctt ttcttttttc      60
ttgtgctgag aatctcgtta gtagcatgtg gcctaacaaa aggaaaaaat gtttttaaac     120
acacacacac acacacacac acacacacac atacacagac aaaaacacaa aaactctgag     180
gggatctggt gaatctccaa attattgtgg gtgtactttg gcttcctttt gtatgatagg     240
tccccatcat gaccacctct gatgtctgtg ctgctgtcac caggcacctt tgtttttcaa     300
gacaacatac tttttttttc ttttctctgt ttgtgatatc actttaattt ttcttgggtg     360
gcttagagac taagggagga gacatctggc ctttttagaa cctgagagga aaaaaagagt     420
cttttttttcc cctctgtctc tttttgccat ggctaatccc tgcatttcca ttcagggaaa     480
aggtggtagt gagcatagma ctgcaacagt tatattctga gtcaaagttg gggcttttta     540
cggcataatt atggaatttt tatttactgg tagagaggag acgagaggct ttttcagtgg     600
gcctgggaca gtggctgctc ttgactttgt gtgaagggaa atgccaagga tgcttctggt     660
ggacttcagg ggaccccagg gtttggccgt gggccgtgat ggcagcaggc ggtgggatgc     720
ttgtagctcc tcacagcagg attcctgccc actgtttttt ctctgttggg agggaagctc     780
ttttctagga gtgtctcagt tctgcttttg gcattagtga tggtggtggt acagttggaa     840
ttagtgccat gtcatacaca aatgttccac aaggcgggag tgtttcactt tctggtgata     900
aacttgatgg tcattgttat gattaagata atgccgggca ggccgggcac agtggctcac     960
gcctgtaatc caagcacttg gggaggccga ggcgggcag                            999
```

<210> 267
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-588-103 : polymorphic base G or A

<220>
<221> misc_binding
<222> 502..521
<223> 12-588-103.mis1, potential complement

<220>
<221> misc_binding
<222> 482..500
<223> 12-588-103.mis2

```
<220>
<221> primer_bind
<222> 585..603
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 60..77
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-588-103 potential probe

<400> 267
gcttaatgaa ttcatgtttt gttttcaaat gtgtccgtgc tctgtttttt ttatcctttc      60
ttttaggtcg tattcggaat aagcctgagg tggatgaagc tgcagttgat gccatcctct     120
ccctaaatat tatttctgcc aagtacctga agtcttccca caactctagc aggtgggaca     180
cccagagcag tgtgaagaag tccacacttg caggcgttaa ttggtacacc gttaggtgcc     240
ttattcatta atgactccca gttcggacaa agaaattaac tcccttctcc cttctagctt     300
caaaaatctc tttatttctt cacctgcctg ctgtactctc caaaaagaaa gaaagaaagt     360
attgcagata tttgtatgtg atcagttact cttagagaat ggaagtgatc ctgtcccatg     420
tgaagtttga atagatgtaa caagtgataa atgaaaattg gagaaagaaa acagtatatt     480
ccccaaggat ttaaaagtac raattaatta ttgccaagat taaatttttt cctgtgaaat     540
ggttgctgtg gagagaaagg tttctctcac tccccaagta tcatggaaat gtgccctctg     600
agataaaatg aagcctcttg tgttaagtct ttgctgctgc tgactatagg ctccattatc     660
cttagtattt gtttttcatt tatgcacaaa agcgataaat aatatgaact cttatgacca     720
agattggctg ccataaataa tagattttac tttgtttttt attttaaatg tttcacttaa     780
aattatcttt tataatcagg tgataacaga cagttcgtaa agtacatagc cattctgctt     840
tcctttgtaa gactagaact aaaccagctg ggatcctctt acctcaccca ggaagggagt     900
tctcattgtc tcagaggctc cgtctctata tcctaggggc tgggaaacag gagcggctgc     960
ctcttctaat gtgggctgag cacactgcct tcccaccaca g                        1001

<210> 268
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-589-152 : polymorphic base T or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-589-152.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-589-152.mis2, potential complement

<220>
<221> primer_bind
<222> 636..654
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 190..210
<223> downstream amplification primer
```

<220>
<221> misc_binding
<222> 489..513
<223> 12-589-152 potential probe

<220>
<221> misc_feature
<222> 393,614,617,695,819,849
<223> n=a, g, c or t

<400> 268
ggctgggtgt ggtagctcac gcctgtaatc ccagcacttt gggaggctga ggtgggtgaa 60
tcacctgaga tcaggagttt gagaccagcc tggccaacat ggtgaaaccc cacctcaaaa 120
aaaaaaaaaa agacatcaaa ggcatgaggt gtaggcatcg agtgcagaga ggactccagg 180
caggggacat gtgcgatggc tctttaatgg cccaggcctt gaaatgggca agtctagctg 240
gggtgcccat aatagaggag ggtgatctgt gtatgtgttg actttgaaag tgaaattatc 300
catttgatac cttacgccaa attctttgtc ttttaaattc tgttgcagta gttgttgttt 360
gagggtcttg tttagaactt tttagaactt ttncattctt acgttttttt acaccagagc 420
ttcaactctc tgtttcttag catttctctc tctcctgctt tggagcagac tgaaagggaa 480
gtggcattat ttcatctgat ktaatgttca tttgcagtta tttttgttat atgtttcatt 540
tgtatttcat ttatgctcta gttatgttaa catttgtttt tctgtgatgt attatgtctg 600
ttttcataat tttncantta ctttgagttg aaatcccaaa tacccagtct atcctcctcc 660
tctctttgtt ttaaaataga tttcagagca ggaanaagca tcagataaac atgtatgtca 720
cttggttttg tttgatttat tgatacaagt gtctgtcttt gtcttttgtc ttatgttcga 780
agatcagcat ataccaaatg ggaagactgg aatcatagnt aggaactaga ttctatttcc 840
ctttcactna attggaatga acactctagc tttgtgacca ccagttttta ttgctttttt 900
aaaaaagtag tagctacaca ataaagaaga aaatacaaat gtgataggac tttgctagtt 960
tgcttgaaat ataaagtgtt agagctataa tttagctttc a 1001

<210> 269
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-592-118 : polymorphic base A or T

<220>
<221> misc_binding
<222> 482..500
<223> 12-592-118.mis1

<220>
<221> misc_binding
<222> 502..521
<223> 12-592-118.mis2, potential complement

<220>
<221> primer_bind
<222> 384..402
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 830..849
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513

<223> 12-592-118 potential probe

<400> 269
ctcaaaacca gcctgggcaa cttagtgagc ccccatttct acaaaaaata aaaacaatta 60
actgggcatg gtggtacaca cctgtagcct cagctactca ggaagctgag atgggaggat 120
cccttgagcc caggagtttg agactgcagt gagctatgat ggtgccactg gcgcctgggt 180
aacaaagcaa gaccctgtct caaaaaaaaa aaaaaaaaaa aaaaggagct gggcatagtg 240
gcatgtgcct gtaaatgaaa ggcatcattt catgcaagct cctctgagcc caggagttcc 300
agcctagccc aggcaacagg gcaagaccac gtctcaaaaa aaaaaaaagt actctttcca 360
cctaaaatat attcaggtca tttgagttca gtttgagttc agctacgaga attatttagt 420
tgagtgagtg tcagagctgg gattttcaaa tctgccctta ctggtatgtt gctttacaca 480
ccctcttacg taaatcaaac waggattcca ccctgggagg tttgcataga gggctgttct 540
tgtagaactt gtgctcatgc tttgatttgg gatttgggga gttagggcaa gccagaaagt 600
ttttctggtg gataataatg tgggttgact ttcttaagca ttttaagcca agcacttgag 660
tttctaacaa ctaaaaagct aagtcagcct gacacagctc tagcgcgccc tggcttgatt 720
ctgttcatcc ccagggggag acttgccttt gttccagtcc tgctctccca agccagctta 780
ctgtagtttt ccagcaattc tgagaagcag tattttttac tgctgattag aaccttaaca 840
tggaaatgga aagtttgtgt agcatgtaac attattagaa gggaaaacat gactatatga 900
ttagatacat attgatttta tgcaatatgt ttgcataaaa tctcttcagt agtaacttgg 960
ttaaattatt cacattgact cagcataatt tctcccttgc t 1001

<210> 270
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-593-174 : polymorphic base T or C

<220>
<221> misc_binding
<222> 502..520
<223> 12-593-174.mis1, complement

<220>
<221> misc_binding
<222> 481..500
<223> 12-593-174.mis2, potential

<220>
<221> primer_bind
<222> 658..675
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 138..158
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-593-174 potential probe

<220>
<221> misc_feature
<222> 22,187,214,652,684
<223> n=a, g, c or t

<400> 270
aggtcaaagt ataaggattc tncaaaaatg cagagtaatt atgaaaattc tgtttaaaaa 60

gcttcagaat agaatgttta tatagcattg atttggagct aagggctata ttctggtaac 120
ataacaaggt gctatctagt gaatgtgtga ttgtgtagtc atggagctga tgtccctgcc 180
atagaantta cagaattatc taaaaaggga aatnctataa taatggcctt caatgctccc 240
acacttggac tagccattgc cataggcaga aaggcaatct catctttact gtgtgtgcaa 300
acagtacttt aatgtaatgt gtgcttaata taagcttttct ttaaaaaaaa aaaaggtggc 360
tcctgttttt gaatagctat ttttaagata gatatagtta ggaatctaaa tgtgttctat 420
atagttaata tccattatga ggtggctctg aaaaatcaac ctagtataag ttggatggct 480
ttgcttttct gcttctgtta yaacccattt ttctagaaaa gcttccactt ctacttaaag 540
ataagaggca aatcattttc ctgttccctt atgcacatag atgttcactt accaaatatt 600
tatagagtgg cccagccctc tgcagacagt ggtgagcaaa accagacatg gnttcctgcc 660
ctcatagact tatagtctga tggnatgaca cagacataaa ttaaataatt gcacaaataa 720
atgtaaatta tagcagtgat gaaatagttg tgtgtgttgt cggagatcac ataacgttgg 780
gggacctgtt atgagaaagt ggtgtttgaa ataagacctg aagatgtgaa atcaaaggcg 840
tgaggctggg tgtggtagct cacgcctgta atcccagcac tttgggaggc tgaggtgggt 900
gaatcacctg agatcaggag tttgagacca gcctggccaa catggtgaaa ccccacctca 960
aaaaaaaaaa aaaagacatc aaaggcatga ggtgtaggca t 1001

<210> 271
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-596-124 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-596-124.mis1, potential

<220>
<221> misc_binding
<222> 502..520
<223> 12-596-124.mis2, complement

<220>
<221> primer_bind
<222> 378..397
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 805..825
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-596-124 potential probe

<400> 271
gacagaccag gtcatctggc ttccgagatc atcagagaag ataagtctgt ctctttcagc 60
tgccagtaag ttttccagga tgagagggga aaaagaaagc ctccagtgac ttcagttgct 120
ttgccagttg tcttgggatt gttttacacc atcctttact tcccttgctc agacctctct 180
gtttcaccat tgctcaggca ttcaggaaag tatctgctca ctcccacttg gtgagtcctc 240
ggccttgagg ttgctgactc tcaggcgtta ggcagctgga tgacttcccg cttcacgcag 300
caaaggccag gggcttgcgc gcctctgcag agttgttgct agggagactt gtgtcatcat 360
ccacaacctt gtttctcact tcctggttgg gctcatctct gaagaacagg tctcccagct 420
tcgctcctta tcactgcatt gtgaagagga ggaaaagtga atcacggaga gagaaaggaa 480
aggatagaat cacaggctgc rtctgcacct gaaaagtgac ccgcggaaac tctatggcgg 540
atttttttt taactttctt cttcctgtta aaacataggt cactaactgt gatgttattt 600

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gttttctaag tggtatgtga gattttctaa tgtagttaga agtttcattg tctgatggac    660
acaatatgcc cttccggttc tattcaaacc agcaggatct gtcggtgctt agagatggct    720
gcctggactg gaatcaaatc taatttcagg gaaatgaaga tggaatttga aggtcacttt    780
taaaattaag tcattgatgc tgctgttaca gagtgtgaca gaggatccat gtctgtgaca    840
caggacggtg ggaagcctga gagagagtga aattatgtga tacactgaaa tgacttttgt    900
ttttcttcta actcatacaa aactggtttg gaaagtcttt gctttggaag cgtcagacat    960
tagaacaggc caaactggac tgtctgttca tagcgtgcct g                       1001
```

<210> 272
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-602-196 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-602-196.mis1, potential

<220>
<221> misc_binding
<222> 502..520
<223> 12-602-196.mis2, complement

<220>
<221> primer_bind
<222> 307..325
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 704..724
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-602-196 potential probe

<400> 272

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ggccagcctg ggtttctcca gttgggtctc ataatgcatc tgcaccctgg cgcagcatgt     60
tgccatggca cggtttcgct tttgccgtat tactttggca gataagattc taggccaaat    120
aggtcatttg cctgtttcat cgaatctaag gacttggcct aagtgtggcg tattttgatg    180
gtcctcagca cgattatttt ctttttgtga gaaactaact tttgtcatat tgtcgttttt    240
agctcagtgg tctctaagaa aggatacctt catttcaagg agcctcttta cagtaactgg    300
gctaaacatt ttgttgtcgt ccgtcggcct tatgtcttca tctataacag tgacaagac    360
cctgtggagc gtggaatcat taacctgtcc acagcacagg tggagtacag tgaggaccag    420
caggccatgg tgaaggtccg tcctgccctg ccttggtttc ttattgccac gtgtgccctt    480
ctcttttgat ttctgcactc yctgttacgt ggtgtgaaat ttccctattc tctctggttt    540
tgaacttcct ttgtgaagtg ctatatgcct tgggaatatg gcaaggcagt ccccattgct    600
gtctctgtag taactttctt gtctacctgc atttttcttt cagacaccaa acacctttgc    660
tgtctgcaca aagcaccgtg gggtcctttt gcaggccctc aatgacaaag acatgaacga    720
ctggttgtat gccttcaacc cacttctagc tggcacaata cggtaagaag ttttgttgtt    780
gttgttgttg tttttgagac ggagtctcac tttttctccc tgaagtgcag tggcttggtc    840
ttggctcact gcaacctccg ccccctggtt caagcgattc tcctgactca gcctccccag    900
tagctgagac tacaggcacg tgccaccatt gcctggctaa ttttcgtatt ttttgtagag    960
acggggtttt accacaatgg ccaggctggt ctcaaactcc t                       1001
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<210> 273

<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-602-350 : polymorphic base A or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-602-350.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-602-350.mis2, potential complement

<220>
<221> primer_bind
<222> 153..171
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 550..570
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-602-350 potential probe

<400> 273
tggcctaagt gtggcgtatt ttgatggtcc tcagcacgat tattttcttt ttgtgagaaa 60
ctaacttttg tcatattgtc gtttttagct cagtggtctc taagaaagga taccttcatt 120
tcaaggagcc tctttacagt aactgggcta aacattttgt tgtcgtccgt cggccttatg 180
tcttcatcta taacagtgac aaagaccctg tggagcgtgg aatcattaac ctgtccacag 240
cacaggtgga gtacagtgag gaccagcagg ccatggtgaa ggtccgtcct gccctgcctt 300
ggtttcttat tgccacgtgt gcccttctct tttgatttct gcactctctg ttacgtggtg 360
tgaaatttcc ctattctctc tggttttgaa cttcctttgt gaagtgctat atgccttggg 420
aatatggcaa ggcagtcccc attgctgtct ctgtagtaac tttcttgtct acctgcattt 480
ttctttcaga caccaaacac mtttgctgtc tgcacaaagc accgtggggt ccttttgcag 540
gccctcaatg acaaagacat gaacgactgg ttgtatgcct tcaacccact tctagctggc 600
acaatacggt aagaagtttt gttgttgttg ttgttgtttt tgagacggag tctcactttt 660
tctccctgaa gtgcagtggc ttggtcttgg ctcactgcaa cctccgcccc ctggttcaag 720
cgattctcct gactcagcct ccccagtagc tgagactaca ggcacgtgcc accattgcct 780
ggctaatttt cgtatttttt gtagagacgg ggttttacca caatggccag gctggtctca 840
aactcctgac ctcaagtaat ccacccacct cagcctccca aagtgctggg attacaggcc 900
tgagccactg cacccagcct agaagttgtt ctgtgttttc tttctctctt tggcttttgg 960
cttcaggaat atcaggataa ataggaaagg aagaattttt c 1001

<210> 274
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-603-191 : polymorphic base T or C

<220>
<221> misc_binding
<222> 502..520
<223> 12-603-191.mis1, complement

<220>
<221> misc_binding
<222> 481..500
<223> 12-603-191.mis2, potential

<220>
<221> primer_bind
<222> 668..688
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 240..260
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-603-191 potential probe

<220>
<221> misc_feature
<222> 339
<223> n=a, g, c or t

<400> 274
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tctatgtttt tgcaggctct ttcttgataa ggatattcct aggtattgtc tgtttgcttt     60
tttgcacgta ggattctagt ttatcagaat gctttctgtc ttatgttgct ttgccatttt    120
aattttgtag tcccctcccc atgtaaacct actgtaccta ggatagagta gaccctgttc    180
tgtaccctaa gaagcgtata gcttcttaaa tgatttttag agtttcaaat tattttttca    240
ttccatttgc taaacttgtc agttttattc ttagactctt tcaagttttc ctcttctaca    300
ttacaaagta gaatgtttct cccttcattt catacagana tctcaggttt tgttttctgt    360
tttcctcttt atctgtcttc tctccgtcaa aagcatgaag ggtttattgc tttataaaac    420
ctgagtccat tgcagtcttg caaaactgtt cactttcttc tctgttttgt cctgtgtggt    480
aatagagaca aatttggcta yttggatagc tgagtctatg agaaatattt tatatatatt    540
ttttaacatt tatctttctc ctgtcagggc tgcttgtttt atctgtttat tttcttcttt    600
tggaatagga aaaatcctgg tttggtatta aaggaagttt tttaaaaaat ctgtctcatt    660
tagggaagaa aattgaagga agtgatacat gacaatataa cctaaaatgt taaaaaaaat    720
acaacataaa cgggctgggc tcagtggctc acacctgtaa tcccagcact ttgggaggcc    780
aaggcgggtg gatcacgagg tcaggagttc aagaccagcc tggccaagat ggtgaaaccc    840
catctttact aaaaatacaa aaattagcct ggcatgatgg tgggcgcctg taatcccagc    900
tactcaggag gctgaggcag aggatcgctt gaacccggga ggcggaggtt gcagtgagcc    960
gagatcgcgc cactgcattc cagcctgggc gacagagcga g                       1001
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<210> 275
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-783-73 : polymorphic base G or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-783-73.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-783-73.mis2, potential complement

<220>
<221> primer_bind
<222> 429..446
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 858..878
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-783-73 potential probe

<220>
<221> misc_feature
<222> 202,209,236,281,447,461,627,992,995
<223> n=a, g, c or t

<400> 275
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acagactcta gcaaggcata cagtatagct ttccagattt tttgttgttt tcctcctagt 120
tttttattca tgtcatcctc acttactttg actattgttt gtttcactgg attgctgtta 180
attgttcttt ctaaaacatt anccttagnt tttctttcac agaaacagtg ctattncttt 240
ttgtgttcat tttttattgg tatatataat acttaacgtg nttcactcag caaacacacg 300
agtgctttac tatatgccaa gcatgattct aaatgctggg gatatactag tgaagaaagc 360
aaagtgcctg ccctcccgga gctgggaaga cagacagaaa taaatataca atatcaaact 420
agttagcgat gactgtgaga acgaagnagt aaactgggac naagatccgg tgattgcaga 480
aggcttctga ggaggcgaca stgcacagag acctaagtga agtgaggagc ccttgcctct 540
gaggagacaa cacttctggt ggccagaaat tcagtataac caggttcaga acaaacacaa 600
ctgactctgg gttagcataa aactcancca gcaggagcag aagtccccag gcagacgcga 660
gcagagcctg ctggcaaccg tgagcattgg tcagcgtgga cattggacaa ggggcttcct 720
tgctcagccc tcattcctct aacatggttc tctcctgtgt tctgcatgta ggcctttgag 780
gattggaata agacagagct agactcattc ctgattgaaa tcacagccaa tattctcaag 840
ttccaagaca ccgatggcaa acacctgctg ccaaagatca gggacagcgc ggggcagaag 900
ggcacaggga agtggaccgc catctccgcc ctggaatacg gcgtacccgt caccctcatt 960
ggtaatgtta tgcttttcac atgggccctt tngtncacta t 1001

<210> 276
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-783-421 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-783-421.mis1, potential

<220>
<221> misc_binding
<222> 502..521

<223> 12-783-421.mis2, potential complement

<220>
<221> primer_bind
<222> 81..98
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 510..530
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-783-421 potential probe

<220>
<221> misc_feature
<222> 99,113,279,644,647
<223> n=a, g, c or t

<400> 276
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agtgaagaaa gcaaagtgcc tgccctcccg gagctgggaa gacagacaga aataaatata     60
caatatcaaa ctagttagcg atgactgtga gaacgaagna gtaaactggg acnaagatcc    120
ggtgattgca gaaggcttct gaggaggcga cactgcacag agacctaagt gaagtgagga    180
gcccttgcct ctgaggagac aacacttctg gtggccagaa attcagtata accaggttca    240
gaacaaacac aactgactct gggttagcat aaaactcanc cagcaggagc agaagtcccc    300
aggcagacgc gagcagagcc tgctggcaac cgtgagcatt ggtcagcgtg gacattggac    360
aaggggcttc cttgctcagc cctcattcct ctaacatggt tctctcctgt gttctgcatg    420
taggcctttg aggattggaa taagacagag ctagactcat tcctgattga aatcacagcc    480
aatattctca agttccaaga yaccgatggc aaacacctgc tgccaaagat cagggacagc    540
gcggggcaga agggcacagg gaagtggacc gccatctccg ccctggaata cggcgtaccc    600
gtcaccctca ttggtaatgt tatgcttttc acatggcccc tttngtncac tattctgatc    660
ttgatgtctg gaggacagat acagactggt ctttagagaa tctcttcagc cctctttagc    720
tttcagagtg ccttttgctc tttcttgcgt tgaagaaact gacagtgtga gagaggctga    780
cgctgctttt gattctcttc cttgtagttc ttatctcatt cgtacaaact gtgaggtaaa    840
ttcagaagtg actgtccttc ctatccagtt ttatctttgg aatattttag cattagtgat    900
gtaattgtag tcagtgatct aagattttat ttatgaggca ggtaacttga gtaaaatttt    960
tcatagaaaa gttcatgaat aacagggccg ggcacagtgg t                       1001
```

<210> 277
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-785-200 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-785-200.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-785-200.mis2, potential complement

<220>
<221> primer_bind

<222> 302..322
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 791..811
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-785-200 potential probe

<400> 277
ggaatattac ccattgagca ttgatttcac ctatttaatg tgttttcact catacctca 60
aacttagggc aggatagtgt tcaccagatg aatctgtttt ttggaactgt tgctattatt 120
ctaatcaggc aactgatacg ttttatggaa aacatctatt tggttaactg atgtctgaag 180
tgacaataat agtgagttga cctttgtcct acaatctcct aaaaagagca gcatctctac 240
ctggtgttag ctctggggaa aagggcatgt tgcttctgtt gaaagcagcc tcaaaggcgt 300
cctgtgtttt tatagtcgct cctctggcct gtgccgggaa ggtatggctg cagagcactg 360
tgaatgagtt cacctgtcgt cagggaaccc caggaatgct gcggtgccag caatacagga 420
atcagggatt tggagcactt ggcaaaagca tgctagtgtt ctcagacggg tgaactaatt 480
tggaagacaa caagttcata ytaccagtct gtctgtcccc ccagttgaaa atagtttctt 540
tttctccatt ttttcttgat ggaaggggtg tccttctgat ggatttttct atctggcagt 600
aaatctttgt gttgggtcct ctttaactgt gcagttcttt ttatttcaga ctaataatag 660
ggagagagag agagagaacg ataacatctc actatctgtg aaaataacta aatatagccc 720
attgttttaa caaatctttc cagagtatct tctgtgtgtc gagacctgtg ggaaaacgct 780
tgctgtctgg gggagagagg catataaata cattattaca gtgaaatcat tgctattaag 840
gaaaaaaaca ttactagtaa tgtgggaaca caaagctgcc agggtaagtc aggaaagact 900
gcctggaaga ggtgacattt gaatccacaa cagactctta tgtaactatg ccatccacag 960
gctctcgcac taactgtgga agcttgagtc tgctaaattt t 1001

<210> 278
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-785-393 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-785-393.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-785-393.mis2, potential complement

<220>
<221> primer_bind
<222> 109..129
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 598..618
<223> downstream amplification primer, complement

<220>

<221> misc_binding
<222> 489..513
<223> 12-785-393 potential probe

<400> 278
gagttgacct ttgtcctaca atctcctaaa aagagcagca tctctacctg gtgttagctc 60
tggggaaaag ggcatgttgc ttctgttgaa agcagcctca aaggcgtcct gtgtttttat 120
agtcgctcct ctggcctgtg ccgggaaggt atggctgcag agcactgtga atgagttcac 180
ctgtcgtcag ggaaccccag gaatgctgcg gtgccagcaa tacaggaatc agggatttgg 240
agcacttggc aaaagcatgc tagtgttctc agacgggtga actaatttgg aagacaacaa 300
gttcatatta ccagtctgtc tgtcccccca gttgaaaata gtttcttttt ctccattttt 360
tcttgatgga aggggtgtcc ttctgatgga tttttctatc tggcagtaaa tctttgtgtt 420
gggtcctctt taactgtgca gttcttttta tttcagacta ataatággga gagagagaga 480
gagaacgata acatctcact rtctgtgaaa ataactaaat atagcccatt gttttaacaa 540
atctttccag agtatcttct gtgtgtcgag acctgtggga aaacgcttgc tgtctggggg 600
agagaggcat ataaatacat tattacagtg aaatcattgc tattaaggaa aaaaacatta 660
ctagtaatgt gggaacacaa agctgccagg gtaagtcagg aaagactgcc tggaagaggt 720
gacatttgaa tccacaacag actcttatgt aactatgcca tccacaggct ctcgcactaa 780
ctgtggaagc ttgagtctgc taaattttgt ctgtacaaaa tgacattgtt tttattttta 840
gtaaaaagct tttacaaagg aagaggagtt aattgaatgt acttcttcac tctctctaaa 900
gcattcttgc atatacctcc atatagctaa gtgatcaggg tcagttaatt tttcagtcat 960
ttttgaaata aaatctaaaa tgccctctgt gcaatatgga a 1001

<210> 279
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-787-103 : polymorphic base G or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-787-103.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-787-103.mis2, potential complement

<220>
<221> primer_bind
<222> 583..602
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 74..94
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-787-103 potential probe

<400> 279
atatattaaa aaaattattt cttaacccta tttttctgtt ttgtgctagg aaaccgtatc 60
atcatgggta aaaaccatgt tttccgcttt aaccacccgg aacaagcacg agctgagcga 120
gagaagactc cttctgctga gaccccctct gagcctgtgg actggacatt tgcccagagg 180
gagcttctgg aaaaacaagg aattgatatg aaacaagaga tggagaaaag gtaatgcaca 240

```
gttacgcagc ccatatgact gtttcttctt ttaaacatgt aatactaata gcattcttga    300
attttttttt tttttttac ttctaggcta caggaaatgg agatcttata caaaaaggag    360
aaggaagaag cagatcttct tttggagcag cagagactgg taggagtcct gaatctgcta    420
aactgttggg aaaagggcag cttgttccca tactttccct gttccacaga gcagtactca    480
cccaaattgc ttctgtctca rtgataccaa gcactattct ttaatttcct taatggagaa    540
tgaacttaaa tctcccggta gccttagcct gaaaaaatag tccacagagg tactcttttg    600
ggctttttat gtcttaaagc caaatcttaa cttctgttac aaccaaatac tttttaagga    660
aatagagctt ttctggtagc ctttgcctct tgatagtggt tttggaattt gcttcagtgg    720
tggttcttta aatgataatt actctgaata ttgaatttgg tgagagtttg ccttggtttt    780
gtttctgatc acttgatagt actaattctc tgctcttggg ctgactttgg gattgttctt    840
acgctgggca gacttttttt ttttaagtta aactgtgtct aaaagtgttg ctgcacagtt    900
gcatgtgtta ctcctttcct tatcccctgc atggagtctg aattctcaat caggttctca    960
gtggcatgtg tggtagcggt gggagcaaag gctgcatacc c                       1001
```

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<210> 280
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-790-396 : polymorphic base G or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-790-396.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-790-396.mis2, potential complement

<220>
<221> primer_bind
<222> 876..896
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 423..443
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-790-396 potential probe

<400> 280
gagactctgt ctcttaaaaa aaaaaaaaga aaaaaacaat taccaacaga atgttcataa     60
aaagtttttt ttgtttgtta gtttttgttt ttgagtcttg ctatgtggcc caagctggag    120
tgcagtggca agattgtagc tcgctgcagc ctcagacacc tgggctcgtg tgattctcct    180
acttcagcct ctcaagtagc taaaactata ggtgcatgcc actaggcctg gctaattttt    240
aaaaatttct tgtagagatg gggggtcttg ttaggttact caggctggtt tcaaattcct    300
ggcctcaagt gatcctcccc acttggcctc ctaaagtgtt gggattacag gtgtgagctg    360
cctcccgagg cctgtatttt tttatgtatg agtaggtttc attactttag tctggaactc    420
tctacccttc ttccatgaaa gacacttgat gtaatggaat aaacactata cagtctcata    480
agttgggttt aagtcctctc rctgttattt ccattgtgat cttgggcaaa tcacttaaat    540
tcatctgagc ctttttcttc atctttaata ggtactataa agctttatac aaatgtatta    600
ttatcaaggc tcataaaatg taaacactca ggatatttga tttagagata atagtatgtt    660
acttatgaga agtagaacat atgagaaatg acaagaacaa attttctttt tggatctaga    720
tatgcagatc gtgcaaaaca aattaaatgc aatgctgtta tcaatgagga ccccaatgcc    780
```

```
aaactggttc gtgaattaaa ggaggaggtg acacggctga aggaccttct tcgtgctcag    840
ggcctgggag atattattga tagtaagtga attaaggatc gttacaaaat ctaatccttt    900
cttcttcagg gttcttattc agcgttctta tatttaaaat aaacttcaag ttaaggagca    960
tgatgaagct aaatggtagt gaaaatgttt tgttttgttt t                       1001
```

<210> 281
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-791-211 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-791-211.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-791-211.mis2, potential complement

<220>
<221> primer_bind
<222> 291..311
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 671..690
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-791-211 potential probe

<400> 281

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tacattggaa tcttttagtt tgtaaatgca gaaatgattc tgaacctgta ggataccact      60
attaaagaca gacatgtttt agaactgcca tctagaacag ttgtaacctg tgtttgtatt     120
atagcgtgtc ttggtcttgg cgctttaatg ctgtcctttc ttacaacgat attccttcct     180
gtcttttttt cttcctctgc ttctttccct tttccctact tttcctgcct tctcttcttt     240
ctatctccca gatctgaaag attttcagaa caataagcat agatacttgc tagcctctga     300
gaatcaacgc cctggccatt tttccacagc atccatgggg tccctcactt catccccatc     360
ttcctgctca ctcagtagtc aggtgggctt gacgtctgtg accagtattc aagagaggat     420
catgtctaca cctggaggag aggaagctat tgaacgttta aaggtaagta atagttcaga     480
ctgaatacaa ggtattctat rtagctccac aaggaagaac taggagtaaa aatcactaag     540
atttcgactc agcatatgga gaactctttg actcttagaa gtgtcctgaa aattgaattt     600
tgtgctttgt aagttaattt cttttcatta gaatgcctga gtctgacatg gccaggcaga     660
gttgggagaa gtgcatgggc agttcatagg ctggcaaggc agagtaacag attaatagat     720
gtgtacgtta attctgggat agtacatcaa gttacagtgt aattgttttg ttagaaattt     780
atttggaaac gtggtttcat tgaaagatgg aattctgtgt agagccatgc ttctgttaat     840
aaagatgaag tttggccgg gtgcagtggc tcacgcctgt aatcccagca ctttgggagg     900
ccgaggcggg gtggatcacg aggtcaggag atcaagacca tcctggctaa cacggtgaga     960
ccctgtctct actaaaaata caaaaaatta gccgggcgtg g                        1001
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<210> 282
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-792-233 : polymorphic base G or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-792-233.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-792-233.mis2, potential complement

<220>
<221> primer_bind
<222> 712..732
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 284..304
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-792-233 potential probe

<220>
<221> misc_feature
<222> 204,218,454,485..486,512,566,576,579,614
<223> n=a, g, c or t

<400> 282
caggtgatcc acctgccttg gcctcccaaa gtgctgagat tacaggcgtg agccaccgcg 60
cctggcctgt ttgttttttt aacatgattt ttctctaagc ttaaatacca caaggccaaa 120
gagaaatggt cataatttaa accattatta tattgttgag gtatccctag ctattattat 180
agcaaagtgg gaaaaaagtg tttnattcta ttgaagtnta tgtaatgatc cgacattaat 240
gggaatatag aggagtccta attaattggt ataatttcac aaagcggaat ggtattcctt 300
ggagagttaa agacattctc tttagtaagt gtaaaccaaa gggcattttc tttattcctg 360
cttctaattc cttctagccc agtgaattat ttctcttttc actggtaatg tgatgaatgg 420
gaattgttta ttacattgaa gtgacttgaa gtgncctttt gtgctttagg tgcaggttga 480
cactnnaaaa aaaacaaaac rctgaatttt tnacacctat gtctgcatta aaggctgttt 540
tactaccgga agttacatag acttcntgca gtcagntgnt gtgccccagt gccttactgg 600
tcctttgtag attngcctta atgatttgta caaatgactg ggaggcgggg atgctgcctg 660
tgtcctggtg aaccttaatg aaggggccgt cttaggcaca gtgcaaaaca agcatttgtc 720
ctgtactgtt agagccaaaa ttgtgatgag caatactgat aattgtccag tttatgtcat 780
ctttcccaga ttttaaaatc tgttctagat attcttagct tgaaccactt ttgattgtga 840
aatgtattag gtgttgtccc attattactg taaaatgaag ttttgaatct tcttgttaat 900
aaactgtgga tttcccctct caatttctta aacaacaaca aaaaaatgct tgaagattgt 960
ctttgagtgt aagatctgcc ttttcagaaa gggagtgtta g 1001

<210> 283
<211> 989
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 505

<223> 12-793-383 : polymorphic base T or G

<220>
<221> misc_binding
<222> 485..504
<223> 12-793-383.mis1, potential

<220>
<221> misc_binding
<222> 506..525
<223> 12-793-383.mis2, potential complement

<220>
<221> primer_bind
<222> 866..884
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 365..385
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 493..517
<223> 12-793-383 potential probe

<220>
<221> misc_feature
<222> 505
<223> n=a, g, c or t

<400> 283
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agaaatacca acaaaaaact tgtgtagctt gtaaggaggt tatttggctt gagagggaag     60
aggtgggaca gacatggggg acaaagctac agcatatggc tctgtggtgc tgcttttttc    120
caatagttga tgaaatagtg aaataaaagt taactttggt tgggcttgga ataaaggaga    180
tgatacataa taaactattc tttggttagc attagtaatg cttgtagaca ctcaaacaag    240
gaaggcgaag tcctgatgat gatttattgt atcaatacct cattttattt ggttgtggtc    300
tcagtttgcc tcactggaga atccactaag aaagatggat tttaatggga agaaaagaat    360
tattttctac atcgttcctc atctcttgag tttgtcaaaa agttttctaa gaggcagtgt    420
gaagagccag agatgtccga aattgcctga cttcatgttt tggaagattc ctaagtcaca    480
tgaaatcatc tatcaaacac ttgtkcttcc aaacggtgtg aaaaactaca gccaagatag    540
cagttagcat tcaaggaagc cttaaagatt gtgattatgt tttttttcc tttgcgtgtg    600
ggcactatgc tttattagaa cacattattt ttaatcatag tattttttct ttgcctctaa    660
gaaaatactt tcttaatgct cagaaagttg cttccaatta atgttttttt ccccttaaaa    720
agagaagctt tgagagatat ttttgctttc atagctagaa cagttgaagt cttcaactga    780
ggttttatag cagattagac atgggtaaat gatgtctgta atgggttgag ttactgagat    840
gacaatctcc tgtgccattt ggtttgaatg tacttgatag gctgcttcaa atcagtcact    900
tcaatgcatt ttgtgtaaac ccagttgtcc ttttttattc ctctttagac ataaatgtgc    960
taactattcc tttctataca caatttatt                                        989
```

<210> 284
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-803-125 : polymorphic base T or A

<220>
<221> misc_binding

<222> 481..500
<223> 12-803-125.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-803-125.mis2, potential complement

<220>
<221> primer_bind
<222> 605..625
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 169..189
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-803-125 potential probe

<400> 284
caggagaatc ccttgaaccc aggaggcgga ggttacagtg agctaagatt gcgccaatgc 60
cctccagcct gggcaacaga gtgagactcc atctcaaaaa aaaaacaaaa acaaaaataa 120
tgtgcttgtt tcttccttca gaacatgtaa gtggaaagtg agtgaagttc tgcaacacct 180
agcaaaggga gaaggagtga gaaatctttc cattaaatgt tgtaggctgc agggtaactt 240
ttactgttgg taaaattgac tttgaaattt tactaaagac cttagtgaag aggagtggta 300
agactccatt cacacatttt ctcacaatag gcgtcagtga ccatgttgct ttgcagggct 360
cttttcagag ccagagtgag aaatagggag ctccttggga atgagaagta aaactcccac 420
ttactgagtc cttaatataa aatgttcttt ttctttgggg atcttaagtc ttaactattt 480
gcttattaaa gccttagctc wtacacttga gattaccctt tcctttgacc ttcctcttga 540
tgtaaaggag aaatttctcc ctaactgcca agtgggacca attgaaaata atgtcacatg 600
ttaggagtca agacattaac cagactcttc aagattcagg taacccagtg tcttccaaat 660
aatttctagg gaataacact gtcattattc agggaactct ccttccgact tccctatgtc 720
ccactaaagc aagacaaaac tgtattactt caatcagaaa acaaatttct ctgttttaat 780
tcttccttac gccaaaataa agaactcttc tgttttccct agttttattc tagaaagaaa 840
acagcttcct tagtgttttg tgttgtcttg agtttttaat gcagtgtggt agttcactga 900
agcataagca ccttagttct gctcttattt tgtgaatggt gagaatttct ttcgggcaga 960
cctgcatttt aatgctgcac gcagataaca tctttcatcc g 1001

<210> 285
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-805-115 : polymorphic base G or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-805-115.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-805-115.mis2, potential complement

<220>

<221> primer_bind
<222> 596..615
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 135..155
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-805-115 potential probe

<220>
<221> misc_feature
<222> 313,721
<223> n=a, g, c or t

<400> 285
gagccaccgc gcccggcttc tgtatgtgat ttctttttca ctctaattca ctttactaat 60
ttgttcatag gtgagctaca tggaaattta ctgtgaaaga gtacgagatt tgctgaatcc 120
aaaaaacaag ggtaatttgc gtgtgcgtga acacccactt cttggaccct atgtggagga 180
tctgtccaag ttggcagtta cttcctacac agacattgct gacctcatgg atgctgggaa 240
caaagccagg tatggtagga aatagagtaa tgactgaggt ctttggcacc ttttgaggtc 300
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aacttgatgg gctcacaaat aaggcagtat tgagagcaat tgtgtaagtg acaatcttgc 720
naatctgtga ataagtttaa gactattgct tgtgattgtt atgcttataa tgtggagcct 780
gctgtccatt tcaactctca tctaagaatt cccttgtcac gtggtcacct ttatgtttat 840
ttaggacagt ggcagctaca aacatgaatg aaacaagtag ccgttcccac gctgtgttta 900
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gagagtttca gtctctaggc ttgagttgtg aaggatggag a 1001

<210> 286
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-808-52 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-808-52.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-808-52.mis2, potential complement

<220>
<221> primer_bind
<222> 450..469
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 894..914
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-808-52 potential probe

<400> 286
ccttgtgatc cacccgcctc agcctcccaa agtgctagga ttacaggctt gagccaccgt 60
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caatggcacc atctcagctc actgcaacct ctgcctcccc agttcaaaca attctctttc 180
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cctcaggtga tccgcccacc tcggcctccc aaagtgctgg gattacaggc gtgagccacc 360
gtgcctggcc atgttgggtt tttttgggtg gggaagggta aatggggatt tgaaaagttg 420
aacatgtcaa tttaatttaa caagccctca tcacgagcag agcatgagca ggggccactg 480
tcctgggtgt ttggggagaa rcagaagaag ggagggagga gcagccctca ggttaaaagc 540
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agtaattcag cagccaacaa agcaagccca tgcacttgtg ccctcccatt ccagtgggga 660
agacaatgtt taaacaaatt tacaacatcg gtcctaagta ttttggagga aagcagctaa 720
ataaaaggat gaaagaggga tgggaacgag ggatgtttag atggcatagt cagggaaggc 780
ctctcttcgg agatcacatt tgagcagact ctagaatgaa aggatagggt aagccatgca 840
aacccctggg caaagaggtc tccaagtaga gaaatgaagc ccttgaggca gcagtgtcct 900
cagtaggttc cagaaatagc aaggtcgctg gtacagagtc agggactggg agcgcaatag 960
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<210> 287
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-808-75 : polymorphic base G or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-808-75.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-808-75.mis2, potential complement

<220>
<221> primer_bind
<222> 427..446
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 871..891
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-808-75 potential probe

<400> 287
ctcccaaagt gctaggatta caggcttgag ccaccgtgcc caacctataa ttattttttt 60
gagatggagt ttgactcttg tcacccatgc tggtgtgcaa tggcaccatc tcagctcact 120
gcaacctctg cctccccagt tcaaacaatt ctctttcctc agcctcccag gtagttgcaa 180
ttacaggtgc ccgccaccac acctggctaa tttttaaaaa tatttttagt agagacgggg 240
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gcctcccaaa gtgctgggat tacaggcgtg agccaccgtg cctggccatg ttgggttttt 360
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gccctcatca cgagcagagc atgagcaggg gccactgtcc tgggtgtttg gggagaaaca 480
gaagaaggga gggaggagca sccctcaggt taaaagcaat gatttgttcc aaccaatatt 540
tgagtaccca ccctgtgcct ggtgtgctgc tgggtgcagt aattcagcag ccaacaaagc 600
aagcccatgc acttgtgccc tcccattcca gtggggaaga caatgtttaa acaaatttac 660
aacatcggtc ctaagtattt tggaggaaag cagctaaata aaaggatgaa agagggatgg 720
gaacgaggga tgtttagatg gcatagtcag ggaaggcctc tcttcggaga tcacatttga 780
gcagactcta gaatgaaagg atagggtaag ccatgcaaac ccctgggcaa agaggtctcc 840
aagtagagaa atgaagccct tgaggcagca gtgtcctcag taggttccag aaatagcaag 900
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accaggatat ttagggctta ggtgaggact tggaatttca t 1001

<210> 288
<211> 987
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-809-119 : polymorphic base G or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-809-119.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-809-119.mis2, potential complement

<220>
<221> primer_bind
<222> 383..402
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 888..908
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-809-119 potential probe

<220>
<221> misc_feature
<222> 511
<223> n=a, g, c or t

<400> 288
gctggagtga gttcaaagaa gtatttttat atgtggactt gacctttggt cttttattct 60
cattttccac ttaagaaaat cttggctgtg tgaatgaaag agtgatactt ttaaggttat 120

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agaaagtgaa atgtaatcat gccagataat tttatataga tatttttatg tatggctgac    180
ctggatgact ctaacagtgc atgtgtttgt gagtgtgtgt gtgtgcatgt gcgtgtattt    240
aatgagaaaa gtaaacttgt gtataggagg cttaaaaaat gtgtagggaa ttttaggtga    300
ctgttctgat tccagacact tttattatgg aagcaatcaa gtaagtatag gaagaaatat    360
taataaaagg ttatttattt ctccttttac tctttacagc ccgaagatcc ctgttttgca    420
tctcaaaacc gtgtgtacaa tgacattggc aaggaaatgc tcttacacgc ctttgaggga    480
tataatgtct gtatttttgc statgggcag nactggtgct ggaaaatctt atacaatgat    540
gggtaaacaa gaagaaagcc aggctggcat cattccacag gtgaaaaaca aaacaaaaca    600
aaaatcttct cttcattatt agtgttagtc ttaaattgct ttaacagtta tttttatttg    660
gcgaacattt atgcggggat tgttttatgt caggcacaaa gatgaacaac ccattatttt    720
ccctcagagg agctcacaat tgaatgggaa ggattgacat gtacacatgt ctgtcattaa    780
aggtgggaaa gtcagtgttt tgtaatgatt ttgccatata tccaatgcca tattattttg    840
tcatttgaaa agtgttacca gcttgttaaa gctctgttct aagtcctgga gatgggggga    900
tattgttgat ctgatttttt ttcaaattcc atgcatagat tacctctgaa gaatgtgatt    960
atttttggtt tttttgatag ccttatt                                        987
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<210> 289
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-810-77 : polymorphic base G or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-810-77.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-810-77.mis2, potential complement

<220>
<221> primer_bind
<222> 558..577
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 126..146
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-810-77 potential probe

<400> 289

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gtagccacag ctctcgtgtt tattagtctg gcatcacagt cagtactgtg agtgccgttg    180
cttaggctta gcctataaat atccacaaat atccattaca gaagcaggca agggcaaatg    240
ctgtgctaag cagcccaagg gccacatttg gaacccactt aggaagcatg ctatgttcag    300
tacagtaaaa ccttggtgat tcaatggctt caacaaatgt tctgtgtagt aagtgttttt    360
catggaaata tttctgactt gtcctggtga tttctgtgtt tccttaactg aatcatcatc    420
aagaagagat taaattgttt agctatatga acataattta ttaaccagtg ctatacaaat    480
aactagagat gcagacagat rtgacgtgag accaaagagt gaatgacacc tgagcctggc    540
attcctcgga gcttaaagaa gagttcctgg tgtccctctg tttttggaa ttttttttt     600
ttcaaagaaa gggaggagga ttaaagattt atctcctcaa cccctcattt ctgaaccatg    660
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aatccacatt tcaagttcat cttacattag gcccctagag tggggtatgg gaagccctgg 720
acaccagcat gcctgcctgc cagcagaatg agttgatgct cctgagactg aatgctgttt 780
tgcacttggc ttccctattt atactaagtt tgctactcag gcttgaacag aatatccttc 840
acttttctt aacttagggt gaactgtttc atagaacatt tacttgaaag cctattgatc 900
ctgttttatt tgaagaaaga acagtgagtc agcaaatagc tctagacctg tctcagtgag 960
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<210> 290
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-265-178 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 10-265-178.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-265-178.mis2, potential complement

<220>
<221> primer_bind
<222> 324..341
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 662..681
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-265-178 potential probe

<400> 290
ctgggggtcg cctgagctca cttggggctc tgtgaccctg gccctacggc gtctcgggcc 60
cagagctcct tccctgcggg cccggccccc tgccctctcg gccgcgcagg catggggcgg 120
ggcgggtccc ttcgagggcc agggaggagg cgcggccagg cctcgccgag tctgcaggga 180
cacctgcggg acgcgtgcca gcgggagccg ggcgcgaggg cggggctggg ggccgcctgc 240
ccggccgagg ctctgcagcg tgcgcgcccg gcttctgggg gcccgcggga ggcgcggagg 300
aaagtgcaga ctcccagtca cggccaaatg tggaaggacc ggacccctgg gttgcagcgc 360
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ctgatcggat tggccgtcat gggccagaac ttaattctga acatgaatga ccacggcttt 480
gtggtaagcg gcgtgggcgc rttgtcttct ctctggttcc cgggcgcttt agccgaggcc 540
ggcgataggt ttgggagctt acgggtctcc tggccgtgct ttgctaatgt gctctgttgc 600
tgctcgtggc atttttgtat ggaaaggaga agcaccctgt aggcgtgggc gggccgatcc 660
cgaacttagt cctgcggagt gtgcctgtgg gtccgtgagg ttcacagccc gaatgaacga 720
attagtgtct taagtagaga agaagggtgc gggaggagaa cccttgctgg ctgtgtagag 780
ctctaacttg attgcctgat gagatctggg gagagtgaaa atgtttcttc taaatgttaa 840
agtggcttag acgccaggat gatcaataac aacagataga gcctgttgaa ccggccagtt 900
cctggatttg attttgagtc ctaacacgtt gggtgtggat tctacctgac acaccggggg 960
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<210> 291
<211> 1001

<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 10-266-203 : polymorphic base C or T

<220>
<221> misc_binding
<222> 483..502
<223> 10-266-203.mis1, potential

<220>
<221> misc_binding
<222> 504..523
<223> 10-266-203.mis2, potential complement

<220>
<221> primer_bind
<222> 301..320
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 701..720
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 10-266-203 potential probe

<400> 291
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cagcccgaat gaacgaatta gtgtcttaag tagagaagaa gggtgcggga ggagaaccct     60
tgctggctgt gtagagctct aacttgattg cctgatgaga tctggggaga gtgaaaatgt    120
ttcttctaaa tgttaaagtg gcttagacgc caggatgatc aataacaaca gatagagcct    180
gttgaaccgg ccagttcctg gatttgattt tgagtcctaa cacgttgggt gtggattcta    240
cctgacacac cgggggtagt tggccttcgc ctcggttgtc cgccgttttc atcctactga    300
ggtgacataa ctttacagtg agcctcccac agctggggga agaaaaggca aaggcaggtc    360
tgacctcccc agaacttggg ttgaatggaa aggtcattgt tactttggcc acagtctgaa    420
agtcttgtgt gtcctggatc tcctactcag gacttttgtc cttctaggtc tgtgctttta    480
ataggactgt ctccaaagtt gaygatttct tggccaatga ggcaaaggga accaaagtgg    540
tgggtgccca gtccctgaaa gagatggtct ccaagctgaa gaagccccgg cggatcatcc    600
tcctggtgaa ggctggcaa gctgtggatg atttcatcga gaaattggtg aggccagctg     660
tgctctcagc tgctaccacg atagcagctg tttttggttt cttcctttag ttctccttct    720
tttaactcta gagattttt tttttcaatt tctgctaagc tctgaccaaa tgattgctta     780
actgttgcag tgttggttaa cttgataagc gcttatgaag taactttgtc ctttggtggt    840
agtaattctg agaatactaa cagacatttc aataaacatt aaggcggggc acagtggctc    900
aggcctgtaa tcccagcact tttgggagg ctggttcaga tggatcgttt gagcccagga     960
gttcgagacc agcctgggca acatggcgaa accctgtctc t                       1001
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<210> 292
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-403-312 : polymorphic base C or T

<220>

<221> misc_binding
<222> 481..500
<223> 10-403-312.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-403-312.mis2, potential complement

<220>
<221> primer_bind
<222> 190..208
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 593..611
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-403-312 potential probe

<400> 292
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aacccttgcc tcagaattcc ttcagagaga ggtgactgtc caggacctat tgagctctgc    300
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tatggttttt gttggtggaa tcaactgcct tcaccaaaat ccactatccc aggtgtgtat    420
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agccccagat atatgctgag yaagcattct gagataattt aaaatgccct cttttgttaa    540
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ctgagatttc gggaaagcat tccttggaca ttttactctg tgtgctccag tggatagtaa    660
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ctgcagaaaa ctcagttgaa gcctgcacct tgccctggat tcagtcaggc aggcaatgtt    780
caggactgat gaaatcattc tttgatgatg atagatcctg gaaatgaaag ttgcctttgt    840
gaccctggtt aaagctccag tttctaaata ttctgataag aagctaaatc ctgcagtccg    900
ttctcttcta atgagtgaat caccagacag tcaggttctg acatgataca gaaaggttgt    960
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<210> 293
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-405-54 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 10-405-54.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-405-54.mis2, potential complement

<220>
<221> primer_bind
<222> 448..465
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 848..867
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-405-54 potential probe

<400> 293
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gaagtatcat tttctctaag agactcaaaa gtgtattagg gagaatttat ttaaaaataa    180
aataaatggg atattgtttc ttcatattaa atagaagtat ttctccaaaa agctgttggt    240
tagaacactg aatttatgtc ttacatttct gctcttatag ttctgcatcc acttgtttca    300
ttaagcaaac tttcccttaa agtgcaggaa agtgaaaaaa tcctaagtgc acagcttgat    360
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ggaacccgac catcgaatct tgcgaacaac acgatacttg ttaagtggct accccaaaac    660
gatctgcttg gtatgttggg cggattggat gtataggtca aaccagggtc aaattaagaa    720
aatggcttaa gcacagctat tctaaaggat tgttgagctt gaaaatatta tggccaacat    780
atcctacatt gctttttatc tagtggggta tctcaaccca cattttcttc tgcaaatttc    840
tgcaagggca tgtgagtaac actgagtctt tggagtgttt tcagaaccta gatgtgtcca    900
gctgtgaaac tcagagatgt aactgctgac atcctcccta ttttgcatct caggtcaccc    960
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<210> 294
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-408-356 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 10-408-356.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-408-356.mis2, potential complement

<220>
<221> primer_bind
<222> 146..165
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 546..565
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-408-356 potential probe

<400> 294
agaacatcat gcgcctctcc agccttcaca aggaccgccc ggtggagccg ctggacctgg 60
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cccacgacct cacctggtac cagtaccatt ccttggacgt gattggtttc ctcttggccg 180
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gtgttaaatt cattttattc ttattaagga aatactttgc ataaattaat cagccccaga 420
gtgctttaaa aaattctctt aaataaaaat aatagactcg ctagtcagta aagatatttg 480
aatatgtatc gtgccccctc yggtgtcttt gatcaggatg acatgtgcca tttttcagag 540
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ggagtgcggg attcaaaggt ggtcccaccg ctgcccctac tgcaaatggc agttttaatc 660
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ttagagtgta ggtgaaatga atgaatggct tggagtgcac tgagaacagc atatgatttc 840
ttgctttggg gaaaaagaat gatgctatga aattggtggg tggtgtattt gagaagataa 900
tcattgctta tgtcaaatgg agctgaattt gataaaaacc caaaatacag ctatgaagtg 960
ctgggcaagt ttacttttt tctgatgttt cctacaacta a 1001

<210> 295
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-409-148 : polymorphic base G or C

<220>
<221> misc_binding
<222> 481..500
<223> 10-409-148.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-409-148.mis2, potential complement

<220>
<221> primer_bind
<222> 354..372
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 779..798
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-409-148 potential probe

<400> 295
ctcacctggt accagtacca ttccttggac gtgattggtt tcctcttggc cgtcgtgctg 60
acagtggcct tcatcacctt taaatgttgt gcttatggct accggaaatg cttggggaaa 120

```
aaagggcgag ttaagaaagc ccacaaatcc aagacccatt gagaagtggg tgggaaataa    180
ggtaaaattt tgaaccattc cctagtcatt tccaaacttg aaaacagaat cagtgttaaa    240
ttcattttat tcttattaag gaaatacttt gcataaatta atcagcccca gagtgcttta    300
aaaaattctc ttaaataaaa ataatagact cgctagtcag taaagatatt tgaatatgta    360
tcgtgccccc tccggtgtct ttgatcagga tgacatgtgc catttttcag aggacgtgca    420
gacaggctgg cattctagat tacttttctt actctgaaac atggcctgtt tgggagtgcg    480
ggattcaaag gtggtcccac sgctgcccct actgcaaatg gcagttttaa tcttatcttt    540
tggcttctgc agatggttgc aattgatcct taaccaataa tggtcagtcc tcatctctgt    600
cctgcttcat aggtgccacc ttgtgtgttt aaagaaggga agctttgtac ctttagagtg    660
taggtgaaat gaatgaatgg cttggagtgc actgagaaca gcatatgatt tcttgctttg    720
gggaaaaaga atgatgctat gaaattggtg ggtggtgtat ttgagaagat aatcattgct    780
tatgtcaaat ggagctgaat ttgataaaaa cccaaaatac agctatgaag tgctgggcaa    840
gtttactttt tttctgatgt ttcctacaac taaaaataaa ttaataaatt tatataaatt    900
ctatttaagt gttttcactg gtgtcgcatt tatttcttgt taagttgcat tttctaatta    960
caaaagtaat gcatgattat gacagaaagt ttggaaaata t                       1001
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<210> 296
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-409-249 : polymorphic base G or C

<220>
<221> misc_binding
<222> 481..500
<223> 10-409-249.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-409-249.mis2, potential complement

<220>
<221> primer_bind
<222> 253..271
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 678..697
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-409-249 potential probe

<400> 296

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ccggaaatgc ttggggaaaa aagggcgagt taagaaagcc cacaaatcca agacccattg     60
agaagtgggt gggaaataag gtaaaatttt gaaccattcc ctagtcattt ccaaacttga    120
aaacagaatc agtgttaaat tcattttatt cttattaagg aaatactttg cataaattaa    180
tcagccccag agtgctttaa aaaattctct taaataaaaa taatagactc gctagtcagt    240
aaagatattt gaatatgtat cgtgcccccct ccggtgtctt tgatcaggat gacatgtgcc    300
atttttcaga ggacgtgcag acaggctggc attctagatt acttttctta ctctgaaaca    360
tggcctgttt gggagtgcgg gattcaaagg tggtcccacc gctgccccta ctgcaaatgg    420
cagttttaat cttatctttt ggcttctgca gatggttgca attgatcctt aaccaataat    480
ggtcagtcct catctctgtc stgcttcata ggtgccacct tgtgtgttta aagaagggaa    540
gctttgtacc tttagagtgt aggtgaaatg aatgaatggc ttggagtgca ctgagaacag    600
catatgattt cttgctttgg ggaaaaagaa tgatgctatg aaattggtgg gtggtgtatt    660
```

```
tgagaagata atcattgctt atgtcaaatg gagctgaatt tgataaaaac ccaaaataca     720
gctatgaagt gctgggcaag tttacttttt ttctgatgtt tcctacaact aaaaataaat     780
taataaattt atataaattc tatttaagtg ttttcactgg tgtcgcattt atttcttgtt     840
aagttgcatt ttctaattac aaaagtaatg catgattatg acagaaagtt tggaaaatat     900
agaggttcac acacacatgc cttcattgcg tgtgcatgca taaatgcatg agaaaagaaa     960
aataaccagt aatcgcatcg cccagaaata accccagtta c                       1001
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<210> 297
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-410-274 : polymorphic base A or C

<220>
<221> misc_binding
<222> 481..500
<223> 10-410-274.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-410-274.mis2, potential complement

<220>
<221> primer_bind
<222> 228..245
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 645..664
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-410-274 potential probe

<400> 297

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tgcaaatggc agttttaatc ttatcttttg gcttctgcag atggttgcaa ttgatcctta      60
accaataatg gtcagtcctc atctctgtcc tgcttcatag gtgccacctt gtgtgtttaa     120
agaagggaag ctttgtacct ttagagtgta ggtgaaatga atgaatggct tggagtgcac     180
tgagaacagc atatgatttc ttgctttggg gaaaaagaat gatgctatga aattggtggg     240
tggtgtattt gagaagataa tcattgctta tgtcaaatgg agctgaattt gataaaaacc     300
caaaatacag ctatgaagtg ctgggcaagt ttactttttt tctgatgttt cctacaacta     360
aaaataaatt aataaattta tataaattct atttaagtgt tttcactggt gtcgcattta     420
tttcttgtta agttgcattt tctaattaca aaagtaatgc atgattatga cagaaagttt     480
ggaaaatata gaggttcaca macacatgcc ttcattgcgt gtgcatgcat aaatgcatga     540
gaaaagaaaa ataaccagta atcgcatcgc ccagaaataa ccccagttac aattgtggca     600
aatacacata cttataaata ttgcagatat attaagtata cctagtattt gctaacactc     660
tttcttctac tctgtcatga agattctccc aaggtgtttt tgtataatat ttaattcatt     720
ttcagtggcc aagcagtatt ctacttcatg gatataccag gatttattta accataactt     780
ctggttggat tcactcttat tattttgttt aattaaaaaa aaaagacctc ggctgggcac     840
agtggctcat gcctgtaatc ccagcacttt gggaggccga ggtgggtgga tcacctaaga     900
tcgggagttt gagaccagcc tggccaacat ggcaaaaccc cgtctctact aaaaatacag     960
aaaattagcc gggtgtggtt gccagcacct gtaattccag c                       1001
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<210> 298
<211> 1001

<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-410-280 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 10-410-280.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-410-280.mis2, potential complement

<220>
<221> primer_bind
<222> 222..239
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 639..658
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-410-280 potential probe

<400> 298
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tggcagtttt aatcttatct tttggcttct gcagatggtt gcaattgatc cttaaccaat     60
aatggtcagt cctcatctct gtcctgcttc ataggtgcca ccttgtgtgt ttaaagaagg    120
gaagctttgt acctttagag tgtaggtgaa atgaatgaat ggcttggagt gcactgagaa    180
cagcatatga tttcttgctt tggggaaaaa gaatgatgct atgaaattgg tgggtggtgt    240
atttgagaag ataatcattg cttatgtcaa atggagctga atttgataaa aacccaaaat    300
acagctatga agtgctgggc aagtttactt tttttctgat gtttcctaca actaaaaata    360
aattaataaa tttatataaa ttctatttaa gtgttttcac tggtgtcgca tttatttctt    420
gttaagttgc attttctaat tacaaaagta atgcatgatt atgacagaaa gtttggaaaa    480
tatagaggtt cacacacaca ygccttcatt gcgtgtgcat gcataaatgc atgagaaaag    540
aaaaataacc agtaatcgca tcgcccagaa ataaccccag ttacaattgt ggcaaataca    600
catacttata aatattgcag atatattaag tatacctagt atttgctaac actctttctt    660
ctactctgtc atgaagattc tcccaaggtg tttttgtata atatttaatt cattttcagt    720
ggccaagcag tattctactt catggatata ccaggattta tttaaccata acttctggtt    780
ggattcactc ttattatttt gtttaattaa aaaaaaaaga cctcggctgg gcacagtggc    840
tcatgcctgt aatcccagca ctttgggagg ccgaggtggg tggatcacct aagatcggga    900
gtttgagacc agcctggcca acatggcaaa accccgtctc tactaaaaat acagaaaatt    960
agccgggtgt ggttgccagc acctgtaatt ccagctaatt g                       1001
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<210> 299
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-410-337 : polymorphic base A or G

<220>

<221> misc_binding
<222> 481..500
<223> 10-410-337.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-410-337.mis2, potential complement

<220>
<221> primer_bind
<222> 165..182
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 582..601
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-410-337 potential probe

<400> 299
aataatggtc agtcctcatc tctgtcctgc ttcataggtg ccaccttgtg tgtttaaaga 60
agggaagctt tgtaccttta gagtgtaggt gaaatgaatg aatggcttgg agtgcactga 120
gaacagcata tgatttcttg ctttggggaa aaagaatgat gctatgaaat tggtgggtgg 180
tgtatttgag aagataatca ttgcttatgt caaatggagc tgaatttgat aaaaacccaa 240
aatacagcta tgaagtgctg ggcaagttta cttttttttct gatgtttcct acaactaaaa 300
ataaattaat aaatttatat aaattctatt taagtgtttt cactggtgtc gcatttattt 360
cttgttaagt tgcattttct aattacaaaa gtaatgcatg attatgacag aaagtttgga 420
aaatatagag gttcacacac acatgccttc attgcgtgtg catgcataaa tgcatgagaa 480
aagaaaaata accagtaatc rcatcgccca gaaataaccc cagttacaat tgtggcaaat 540
acacatactt ataaatattg cagatatatt aagtatacct agtatttgct aacactcttt 600
cttctactct gtcatgaaga ttctcccaag gtgtttttgt ataatattta attcattttc 660
agtggccaag cagtattcta cttcatggat ataccaggat ttatttaacc ataacttctg 720
gttggattca ctcttattat tttgtttaat taaaaaaaaa agacctcggc tgggcacagt 780
ggctcatgcc tgtaatccca gcactttggg aggccgaggt gggtggatca cctaagatcg 840
ggagtttgag accagcctgg ccaacatggc aaaaccccgt ctctactaaa aatacagaaa 900
attagccggg tgtggttgcc agcacctgta attccagcta attgggaggc tgaggcagga 960
gaattgcttg aaccggggtc agggggttcg gaggtcggag g 1001

<210> 300
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-121-326 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-121-326.mis1, potential

<220>
<221> misc_binding
<222> 502..520
<223> 12-121-326.mis2, complement

<220>
<221> primer_bind
<222> 178..196
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 637..656
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-121-326 potential probe

<400> 300
ttcttgatac cctcggacga ggcctaccgg ggtactccca gcacctcgta gtagtccact 60
atgctggact gccaaagagc ctgcggggca ctggcacagc gagcggcaag gctgccagca 120
cccgcgcaca ggtcagaggc ttggcgacct gggccgcctg gagggccgcc ccttatgacg 180
cagccacatc tcattggccg aggcctgtga gcgcctcgca tcccaagatg cagtgctcct 240
gggactggcc ctgctctctg tgaggctctg tgaggccctg tgatgctcca agaccaggcc 300
ccgcccactc cggcctccaa ccagccatgg tctccaaaaa ggatgggaaa aagaggttgg 360
ggaaaagaga gggccttgac tttggctgcc tgaagaactg tttttcttaa agtaggcttt 420
atatcagtct ttttcctcgg ccacaggagg gaagagggtg gtgggagtga gtttagtctg 480
accggggctg aagacatcct rttgtttagg actgcggttc tccaacgttc cagccccggt 540
gcccatttgc ttttgttcat ctggattatg cctatcatat gtactgcatt agagattaaa 600
acagaattaa aaagacatat tcattgggca atttaagaag aataaaccca tgacacacta 660
acaaaccttt ttatgtaact ttttttgaga caaaatgtag tgagaagagt ggcatcgttt 720
tacagttttt gcatctctct ctttagtact tggctctata gagaggtgga ttctcatgtc 780
agcttctgca ttctatctat tgtgatatta cacatccccc atgtagcttc tggaaaactc 840
cactgtacac ttgtgggaga atgacaatga gaaaatcaag taacattatt acggaaatag 900
ttttgacttt gtaaaattct cctgaaaaat tactggggat ccctaggatt tcctggctca 960
tactttgaga atcgctagtc tagcagagta gtccctggta t 1001

<210> 301
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-122-341 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-122-341.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-122-341.mis2, potential complement

<220>
<221> primer_bind
<222> 162..180
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 595..612
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-122-341 potential probe

<400> 301
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gcttcggctt gccctcagtg ggatgcaccc actatccaac cagtcccaat gagatgaacc     60
aggtacctca gttggaaatg cagaaatcat ccatcttctg cgtcgatcat gctgggagct    120
gcagatcgga gctgttccta tttggccatt ggtgctgaag cttccgttct cctctccaac    180
acctcctttt tttttccttt tctcttccag tttttcaatg tgaacatatt ctctagagtt    240
aactacattg gctcaaatct tcactatcat ctcagtggag cagaacaaat tgggaactgt    300
ggcacaggtc actcttgcta tgccccttaa gaattccaca ttaacaaagc taattttcga    360
gtgtggtaaa gaacaggcta gtgtatttag tagtgagtcc attgactgtt tcccaacatg    420
aggtcacact agatttaata tggtttggct ctgtgtcccc caccaaatct catcttgaat    480
tgtaatcccc ataatcccca ygtgttgagg acaggacatg gtgggaggtc cccacctcct    540
aatctcatca tagtgagtga gttcttatga gatctgatgg ttttataagg ggcccttatc    600
ccttcacttg caagctattc ctctttctct ctttcatgta agacgtgtct ttgcctctct    660
ctcactttct gccaggatta taagtttcct gaggcccctc cagccacatg gaactggagt    720
caattaaagc tctttccttt ataaattacc cagtcttggg tatgtcttta tagcagtgtg    780
tgaatggact aatacagtaa attggtgtca tggagagtgg ggtactgcta taaaactact    840
tgaaaatgtg gaagtgactt ggaactgggt aacaggcaga ggctggaaca gtttggagag    900
ctcagaagac aggaagatgt gggaaagttt ggaacttcct ggagacttgt tgaacggttt    960
tgaccaaaat gctgataatg ttgtggacaa tgaagtccag g                       1001
```

<210> 302
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-122-381 : polymorphic base A or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-122-381.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-122-381.mis2, potential complement

<220>
<221> primer_bind
<222> 122..140
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 555..572
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-122-381 potential probe

<400> 302
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cagtcccaat gagatgaacc aggtacctca gttggaaatg cagaaatcat ccatcttctg     60
cgtcgatcat gctgggagct gcagatcgga gctgttccta tttggccatt ggtgctgaag    120
```

cttccgttct cctctccaac acctcctttt tttttccttt tctcttccag tttttcaatg 180
tgaacatatt ctctagagtt aactacattg gctcaaatct tcactatcat ctcagtggag 240
cagaacaaat tgggaactgt ggcacaggtc actcttgcta tgccccttaa gaattccaca 300
ttaacaaagc taattttcga gtgtggtaaa gaacaggcta gtgtatttag tagtgagtcc 360
attgactgtt tcccaacatg aggtcacact agatttaata tggtttggct ctgtgtcccc 420
caccaaatct catcttgaat tgtaatcccc ataatcccca cgtgttgagg acaggacatg 480
gtgggaggtc cccacctcct matctcatca tagtgagtga gttcttatga gatctgatgg 540
ttttataagg ggcccttatc ccttcacttg caagctattc ctctttctct ctttcatgta 600
agacgtgtct ttgcctctct ctcactttct gccaggatta taagtttcct gaggcccctc 660
cagccacatg gaactggagt caattaaagc tctttccttt ataaattacc cagtcttggg 720
tatgtcttta tagcagtgtg tgaatggact aatacagtaa attggtgtca tggagagtgg 780
ggtactgcta taaaactact tgaaaatgtg gaagtgactt ggaactgggt aacaggcaga 840
ggctggaaca gtttggagag ctcagaagac aggaagatgt gggaaagttt ggaacttcct 900
ggagacttgt tgaacggttt tgaccaaaat gctgataatg ttgtggacaa tgaagtccag 960
gctgagtctc agatagagat gaggaatctg ttgagaactg g 1001

<210> 303
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-124-169 : polymorphic base G or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-124-169.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-124-169.mis2, potential complement

<220>
<221> primer_bind
<222> 334..352
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 830..848
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-124-169 potential probe

<400> 303
caagctgatt caggtaaacg ggtaacaagt ttgctgaggc ctgggaggag gagaaagatg 60
ggagcagatg gaaaggcatt tggtgggctg ggcacatgag gagtttagaa gcccctaaag 120
gacatgttct ccttctgtca gagaagactt gggagttaca aagtctatag ctgtgtccat 180
ccccagggga gaactgagag aaccttccat cccgagagcc aggtggccag gagggcagca 240
gggagtgaca ccccttctgc tagccgccag agccacagcc attcctcaga cccacagaac 300
attattagca ctggatcagg gatctatgga cttagtgatc tggagatgtg ggcaagggaa 360
gcgagagagg gcaagtcagt actcaaggtc acgtagcatt cccagagccc aggcaagaac 420
aaggatgaag gcctttggcc cttctcacca acgtcttgtg cctccccagt ttctgcgaaa 480
ctccctcaag aagacccggg kgtctagctg gagcctgcgc ttgagcaaag agctgaacaa 540
ccagattgcg agctttgaca gcccctctct ggagaaggtt tgtcttcata gggacaggag 600
agtttggaca aggagtagac tccaggggtg atggagtgga gaggataaca ccgtgtgtgt 660

gagatcagct ggacctgtgg ctgtttacag ggtcctggga ggagaggagc gtggtctgga 720
ttggtggttt tagttttgtt ttggtttatt tttttgcttt gttttgttga tcctccagat 780
tctggctagc aatcacatgt gtgtatttct ttgtaaacac aaaactatac cgcattgcta 840
caaaattcta aaacattttt gaaagaaatc agtgagggtc tcaataaata gaaagcaccc 900
catgttcatg gattgaaaga tgctatagtt caaatggtga tactctccaa atttatcttc 960
agttttagca tgacacctat cacaatccaa gctagttctt t 1001

<210> 304
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-124-194 : polymorphic base C or T

<220>
<221> misc_binding
<222> 482..500
<223> 12-124-194.mis1

<220>
<221> misc_binding
<222> 502..521
<223> 12-124-194.mis2, potential complement

<220>
<221> primer_bind
<222> 309..327
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 805..823
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-124-194 potential probe

<400> 304
caagtttgct gaggcctggg aggaggagaa agatgggagc agatggaaag gcatttggtg 60
ggctgggcac atgaggagtt tagaagcccc taaaggacat gttctccttc tgtcagagaa 120
gacttgggag ttacaaagtc tatagctgtg tccatcccca ggggagaact gagagaacct 180
tccatcccga gagccaggtg gccaggaggg cagcagggag tgacacccct tctgctagcc 240
gccagagcca cagccattcc tcagacccac agaacattat tagcactgga tcagggatct 300
atggacttag tgatctggag atgtgggcaa gggaagcgag agagggcaag tcagtactca 360
aggtcacgta gcattcccag agcccaggca agaacaagga tgaaggcctt tggcccttct 420
caccaacgtc ttgtgcctcc ccagtttctg cgaaactccc tcaagaagac ccgggggtct 480
agctggagcc tgcgcttgag yaaagagctg aacaaccaga ttgcgagctt tgacagcccc 540
tctctggaga aggtttgtct tcatagggac aggagagttt ggacaaggag tagactccag 600
gggtgatgga gtggagagga taacaccgtg tgtgtgagat cagctggacc tgtggctgtt 660
tacagggtcc tgggaggaga ggagcgtggt ctggattggt ggttttagtt ttgttttggt 720
ttattttttt gctttgtttt gttgatcctc cagattctgg ctagcaatca catgtgtgta 780
tttctttgta aacacaaaac tataccgcat tgctacaaaa ttctaaaaca tttttgaaag 840
aaatcagtga gggtctcaat aaatagaaag caccccatgt tcatggattg aaagatgcta 900
tagttcaaat ggtgatactc tccaaattta tcttcagttt tagcatgaca cctatcacaa 960
tccaagctag ttcttttttt tgatcctaaa attgatccta a 1001

<210> 305
<211> 1001

<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-124-300 : polymorphic base G or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-124-300.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-124-300.mis2, potential complement

<220>
<221> primer_bind
<222> 203..221
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 699..717
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-124-300 potential probe

<400> 305
cttctgtcag agaagacttg ggagttacaa agtctatagc tgtgtccatc cccaggggag 60
aactgagaga accttccatc ccgagagcca ggtggccagg agggcagcag ggagtgacac 120
cccttctgct agccgccaga gccacagcca ttcctcagac ccacagaaca ttattagcac 180
tggatcaggg atctatggac ttagtgatct ggagatgtgg gcaagggaag cgagagaggg 240
caagtcagta ctcaaggtca cgtagcattc ccagagccca ggcaagaaca aggatgaagg 300
cctttggccc ttctcaccaa cgtcttgtgc ctccccagtt tctgcgaaac tccctcaaga 360
agacccgggg gtctagctgg agcctgcgct tgagcaaaga gctgaacaac cagattgcga 420
gctttgacag cccctctctg gagaaggttt gtcttcatag ggacaggaga gtttggacaa 480
ggagtagact ccaggggtga kggagtggag aggataacac cgtgtgtgtg agatcagctg 540
gacctgtggc tgtttacagg gtcctgggag gagaggagcg tggtctggat tggtggtttt 600
agttttgttt tggtttattt ttttgctttg ttttgttgat cctccagatt ctggctagca 660
atcacatgtg tgtatttctt tgtaaacaca aaactatacc gcattgctac aaaattctaa 720
aacatttttg aaagaaatca gtgagggtct caataaatag aaagcacccc atgttcatgg 780
attgaaagat gctatagttc aaatggtgat actctccaaa tttatcttca gttttagcat 840
gacacctatc acaatccaag ctagttcttt tttttgatcc taaaattgat cctaaaattt 900
atatggaaat accaggggct ctgaatagcc aacaaaatta tgagaagaag aataaagttg 960
gaggactcaa acttctcaat ttcaacttct tacacaactg c 1001

<210> 306
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-124-58 : polymorphic base A or C

<220>

<221> misc_binding
<222> 481..500
<223> 12-124-58.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-124-58.mis2, potential complement

<220>
<221> primer_bind
<222> 444..462
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 940..958
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-124-58 potential probe

<400> 306
gccttgaata ccaggcttag gggagcagtg gaagaaagtg gcatgtgtga ccatacatgt 60
gttcctgcag aacatactga gttcacttgg gatcagaaag cctgggaaga caagctgatt 120
caggtaaacg ggtaacaagt ttgctgaggc ctgggaggag gagaaagatg ggagcagatg 180
gaaaggcatt tggtgggctg ggcacatgag gagtttagaa gcccctaaag gacatgttct 240
ccttctgtca gagaagactt gggagttaca aagtctatag ctgtgtccat ccccagggga 300
gaactgagag aaccttccat cccgagagcc aggtggccag gagggcagca gggagtgaca 360
ccccttctgc tagccgccag agccacagcc attcctcaga cccacagaac attattagca 420
ctggatcagg gatctatgga cttagtgatc tggagatgtg ggcaagggaa gcgagagagg 480
gcaagtcagt actcaaggtc mcgtagcatt cccagagccc aggcaagaac aaggatgaag 540
gcctttggcc cttctcacca acgtcttgtg cctccccagt ttctgcgaaa ctccctcaag 600
aagacccggg ggtctagctg gagcctgcgc ttgagcaaag agctgaacaa ccagattgcg 660
agctttgaca gcccctctct ggagaaggtt tgtcttcata gggacaggag agtttggaca 720
aggagtagac tccaggggtg atggagtgga gaggataaca ccgtgtgtgt gagatcagct 780
ggacctgtgg ctgtttacag ggtcctggga ggagaggagc gtggtctgga ttggtggttt 840
tagttttgtt ttggtttatt tttttgcttt gttttgttga tcctccagat tctggctagc 900
aatcacatgt gtgtatttct ttgtaaacac aaaactatac cgcattgcta caaaattcta 960
aaacattttt gaaagaaatc agtgagggtc tcaataaata g 1001

<210> 307
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-126-222 : polymorphic base T or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-126-222.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-126-222.mis2, potential complement

<220>
<221> primer_bind
<222> 703..722
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 267..286
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-126-222 potential probe

<400> 307
agctatgtta ttaggtgcat aaacatttag gattgttatg tctggttgat gaactgaccc 60
ttattgtgat gacatgaccc tgtttatcta tggtaatgtc atttgctcta aaatgaactt 120
ttatatcaga acggcctctg gggccatctg gagtgcaggg tgggctgtgc tcctggccct 180
tcattacagg cagacatttg gagccaggcc aaatgcaaca gccaagcacc atcctggtga 240
gaatgctggg gatgctcttt ccctgcctac agcctcatct cccttcatga tggggcctgt 300
ctagaaccac aaggaagcat tgaaagtcga tctgagtagg agggtgaggt gggcaaaagc 360
tggccaggaa agggctggcc ccaggatttt aacacccact ttggtgttct gggctctacc 420
catagctcct ggaaaagtgg atcttgtcgg agaaagaatg ggagcgggaa aaggccgtga 480
gcctccatct ctatctcatg yggatttatg tccacagcac tgctgtctgt gtgagtccag 540
gagtccccag cccccagcct gctgctctga catgcacaga aaaattcctg tgtctatctg 600
gaagatgagg gaacacttat gaaatcaagt tctgtcccca gagggcccct tgggagaggc 660
tgcagtgacc tagtgccctg ggctgggtca gggagggaga gggtgggatt gtggttggca 720
gagctccagg ctttgtgggg cctgtggctt ctgtagcggt gagagccctt tttaagaaaa 780
aagatacata gttatgaacc ccacattggc taggaaaatg aatatttact ttgagaaaat 840
caagtgctgc aaaatcataa attttgcaaa gcttgacaag taccgcaacc cttaaaatgt 900
ctagaacgac gtagtgtttt tactgattga ccatctgaca cagcctgatg agacttaatt 960
gtctacactt tttggctcca tgctgtttga ctgtcttgtc c 1001

<210> 308
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-126-297 : polymorphic base T or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-126-297.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-126-297.mis2, potential complement

<220>
<221> primer_bind
<222> 778..797
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 342..361
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-126-297 potential probe

<400> 308
gaaatctctg actaatagtg tgaacttgtt tatttctcct tttggctctt tcattttttg 60
cttcatgtat tatttagcta tgttattagg tgcataaaca tttaggattg ttatgtctgg 120
ttgatgaact gacccttatt gtgatgacat gaccctgttt atctatggta atgtcatttg 180
ctctaaaatg aacttttata tcagaacggc ctctggggcc atctggagtg cagggtgggc 240
tgtgctcctg gcccttcatt acaggcagac atttggagcc aggccaaatg caacagccaa 300
gcaccatcct ggtgagaatg ctggggatgc tctttccctg cctacagcct catctcccctt 360
catgatgggg cctgtctaga accacaagga agcattgaaa gtcgatctga gtaggagggt 420
gaggtgggca aaagctggcc aggaaagggc tggccccagg attttaacac ccactttggt 480
gttctgggct ctacccatag ytcctggaaa agtggatctt gtcggagaaa gaatgggagc 540
gggaaaaggc cgtgagcctc catctctatc tcatgtggat ttatgtccac agcactgctg 600
tctgtgtgag tccaggagtc cccagccccc agcctgctgc tctgacatgc acagaaaaat 660
tcctgtgtct atctggaaga tgagggaaca cttatgaaat caagttctgt ccccagaggg 720
ccccttggga gaggctgcag tgacctagtg ccctgggctg ggtcagggag ggagagggtg 780
ggattgtggt tggcagagct ccaggctttg tggggcctgt ggcttctgta gcggtgagag 840
cccttttaa gaaaaaagat acatagttat gaaccccaca ttggctagga aaatgaatat 900
ttactttgag aaaatcaagt gctgcaaaat cataaatttt gcaaagcttg acaagtaccg 960
caacccttaa aatgtctaga acgacgtagt gtttttactg a 1001

<210> 309
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-128-225 : polymorphic base T or G

<220>
<221> misc_binding
<222> 502..520
<223> 12-128-225.mis1, complement

<220>
<221> misc_binding
<222> 481..500
<223> 12-128-225.mis2, potential

<220>
<221> primer_bind
<222> 706..725
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 276..295
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-128-225 potential probe

<400> 309
ccctgaaatg ggaccatgac agctgggtct gagagacagt ggtagaaaca tccagattca 60
gcacttactt gctggcttgg atgcagggtc tagaacgaaa agagaagaaa agtcacttct 120

atacagaaac atgtccagag cgcttactgt ctccaaaacc atggactggc acctgagtga 180
tagcatgatt ccaaagccaa aatcttgcct gtaaggaata tatatatata tatatatata 240
tatatatgta tatatgatat agctatagtc taatagcaag gacagatatg caaactgcta 300
aaagatacaa ggcagaacag aacaaaatgc tgtttttctg ggattttgga aattcaagga 360
attcaaggga ttcaaggaag gtggctttgc ttcccgggag ggtcctgtag atgatctaca 420
gggcactgga catgtttatg ttgctccttt agtaataagc ctgtcattct gatttgatga 480
aaggagatga aaggagctgg kagtgtgtct gatggtggcc tactaactta tgtcttcagc 540
ttaaaaagaa agtagcttca aaagggttcc agaaacactt tccatggacg tgtcactctt 600
tagcagcccc caaagcaaga ccatcatatt gctgccctgc tgtgtgattt ctcagcccct 660
agagcaccat cccctgtaat tgcctggtca tgagtttgtc tctgtctacc tgacccctcc 720
tttcaggcaa ggaccatttc taacttgact ttctgggcct agttcctagc atagtgactg 780
ccatccagta gggctcacac gttccataaa tatttggcag atgagggaat tagcaatggg 840
ttctgctttg gtttcagagc agatattaat tggattgctt agtagtggtt ctctgttgta 900
attcatgagc atgaatgtgg attgcccact attcagatta gtaagtattt cttggtcaag 960
ggcagagctg tggccacaaa ccatccaggt acacagcaga a 1001

<210> 310
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-129-176 : polymorphic base G or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-129-176.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-129-176.mis2, potential complement

<220>
<221> primer_bind
<222> 326..344
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 779..797
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-129-176 potential probe

<400> 310
ggttgtgcat gtccttcatt gggaaggagc agggacacta cattgagact tgacccatct 60
ggattttttg tttgcacaat tttcagggga aagatgatgc aacagcaaat tacaattgtt 120
aatgtgataa tttttagtgg tcctgtcttg cgaatgatag agaggtgacc acaggagacc 180
taagcactcg caggaagtag aagtgttaaa gaggttgact cagttcagtg gaagtagagc 240
aacgaacgtg ggatatatgt ctgtgattat agaattacac actgagttca gtttccagag 300
agggatctgt gctgacaaaa gatttttctg gtcaggattt ggggtctggt gcatgatgtg 360
gggacatctc agagttcgga aggcatagtt ttggttgcag gtcaattggg tcttctactt 420
ggaatgctga aattatcaag aaattgtgga agggtctagg gaggagataa aactgtgagc 480
gtataagccc agttaagctg kggacggtga tgaatggaca tgtgtccaag aagggaagtg 540
tttctcaggt gaagctgaac atatcaccaa acccacccta tcccactcca agtttctata 600
gtgggatcta cttctttacc aacaatttca aaggcagctt tctttaatcc agaatatttg 660

gggttcattg atgtggtact ctgggacctg aatattgttt cttattcctt ggtgtgccat 720
gtatttcatg agagaattca gccttttat gtcatattca ctgaatgcat atgaacttcc 780
atgacttgat cctttgtat ttttatttct gtacttcttt ttattaacat aggtattatt 840
gccaaacact ctaagcttca ttttttaaaa tcaaaccaca tgattttttt attggtgatt 900
ttctccctta tgcagtgtag ttattcaatt ataaaatatg tgtttattag atttgtaaca 960
atgttgaaaa gtgggatgga atttaaatag tgactcttgc c 1001

<210> 311
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-130-203 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-130-203.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-130-203.mis2, potential complement

<220>
<221> primer_bind
<222> 301..319
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 733..753
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-130-203 potential probe

<220>
<221> misc_feature
<222> 167
<223> n=a, g, c or t

<400> 311
aatcgttctt tgaaacagaa catcttctga tgaaattttc tagaagaatg gcaattatga 60
acaatatgtc tttgatcata cataggtctt gtgtggagct actgcataat gaggccctga 120
tcaggcacct gcatgctact tcctttgatg tggttctaac agacccnctt tcacctctgc 180
gcggcggtgc tggctaagta cctgtcgatt cctgctgtgt ttttcttgag gaacattcca 240
tgtgatttag actttaaggg cacacagtgt ccaaacccctt cctcctatat tcctagatta 300
ctaacgacca attcagacca catgacattc ctgcaaaggg tcaagaacat gctctaccct 360
ctggccctgt cctacctttg ccatgctgtt tctgctcctt atgcaagcct tgcctctgag 420
ctttttcaga gagaggtgtc agtggtggat cttgtcagcc atgcatctgt gtggctgttc 480
cgaggggact ttgtgatgga ytaccccagg ccgatcatgc ccaacatggt cttcattggg 540
ggcatcaact gtgccaacgg gaagccacta tctcaggtct gtattggtgc ctttatccaa 600
tcaatgttcc aggcaaaaca ctttttaaaa aatgtattta cttacaagtg cttccatatc 660
tacttatctt tccaaagatt tcatttctgc ttctcattgt tgtaatagtc ttcagtgaga 720
taaactttta aagggtcaat ggtagtgcag ttcagggttt caatggccac tgagaggaag 780
gagaggcagg gacgaggatc tgtcaaagga tgggcaagag tggtgtgact cacggagact 840
gttcgtttgt aaaagcacca tcttcatggc tgtggatgtg cttcagctgg gcaggagcag 900

ggacactaca ctgagaactg atccatccaa tcttgctggc aagattttca gtagaaagga 960
ggaaggaata gaaatttaca attgttgacg tgacaatttt t 1001

<210> 312
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-130-260 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-130-260.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-130-260.mis2, potential complement

<220>
<221> primer_bind
<222> 244..262
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 676..696
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-130-260 potential probe

<220>
<221> misc_feature
<222> 110
<223> n=a, g, c or t

<400> 312
tgaacaatat gtctttgatc atacataggt cttgtgtgga gctactgcat aatgaggccc 60
tgatcaggca cctgcatgct acttcctttg atgtggttct aacagacccn ctttcacctc 120
tgcgcggcgg tgctggctaa gtacctgtcg attcctgctg tgtttttctt gaggaacatt 180
ccatgtgatt tagactttaa gggcacacag tgtccaaacc cttcctccta tattcctaga 240
ttactaacga ccaattcaga ccacatgaca ttcctgcaaa gggtcaagaa catgctctac 300
cctctggccc tgtcctacct ttgccatgct gtttctgctc cttatgcaag ccttgcctct 360
gagctttttc agagagaggt gtcagtggtg gatcttgtca gccatgcatc tgtgtggctg 420
ttccgagggg actttgtgat ggattacccc aggccgatca tgcccaacat ggtcttcatt 480
gggggcatca actgtgccaa ygggaagcca ctatctcagg tctgtattgg tgcctttatc 540
caatcaatgt tccaggcaaa acacttttta aaaaatgtat ttacttacaa gtgcttccat 600
atctacttat ctttccaaag atttcatttc tgcttctcat tgttgtaata gtcttcagtg 660
agataaactt ttaaagggtc aatggtagtg cagttcaggg tttcaatggc cactgagagg 720
aaggagaggc agggacgagg atctgtcaaa ggatgggcaa gagtggtgtg actcacggag 780
actgttcgtt tgtaaaagca ccatcttcat ggctgtggat gtgcttcagc tgggcaggag 840
cagggacact acactgagaa ctgatccatc caatcttgct ggcaagattt tcagtagaaa 900
ggaggaagga atagaaattt acaattgttg acgtgacaat tttagtggt cccatcttgc 960
aaaagataga gaggtgacca caggagacct aagcactcag a 1001

<210> 313

<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-131-112 : polymorphic base T or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-131-112.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-131-112.mis2, potential complement

<220>
<221> primer_bind
<222> 594..612
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 104..124
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-131-112 potential probe

<400> 313
catcttgagc tcagcctccc tgcagctttt tttatattga cagccacttc agagagagtc 60
ctctttgagc tttacaagaa atatcctggt gtgaaaaacg accaaaacca gatagccagc 120
ctccccactc cctgtttaaa gaaagctggc ttagcaatgt tgtctgcatt ttggatgtgc 180
tgtgttaccc atatgtggga agaaagagta ttaagagtta gcaaataggg tcacatccag 240
cagagaccat atggttgggg actagggcaa tggtgactcc tcagacctca gctgcagcct 300
gataaacgtg gttaagagag aagtaggaga cagtgacatg aaatgggggt tcacagcctt 360
gtgttgggaa ttgaatgaga aacaagagct tgaacttgga tgttccccag agcgagcgca 420
aggtcagatg agtttttcaa gataggagtg atcggtcttt cccagggtgg ggcccataat 480
gcaagacaat tatagattaa ygggtaataa gtaactggag gagggcactc tgtcttcaat 540
tacatgttga tttgctaggt gtctcagtga caaggtaatt aagacgaagg aaacaattct 600
aggaggcaca acgtggggtg gacagtcagc tgtcggtggc ttctgctgag atggccacag 660
gactccaggt tcccctgccg cagctggcca caggactgct gcttctcctc agtgtccagc 720
cctgggctga gagtgggaag gtgctggtgg tgcccactga tggcagccac tggctcagca 780
tgcgggaggc cttgcgggac ctccatgcga gaggccacca ggtggtggtc ctcaccctgg 840
aggtgaatat gtacatcaaa gaagagaact ttttcaccct gacaacgtat gccatttcat 900
ggacccagga cgaatttgat cgccttttgc tgggtcacac tcaatcgttc tttgaaacag 960
aacatcttct gatgaaattt tctagaagaa tggcaattat g 1001

<210> 314
<211> 755
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 255
<223> 12-132-157 : polymorphic base C or T

<220>
<221> misc_binding
<222> 235..254
<223> 12-132-157.mis1, potential

<220>
<221> misc_binding
<222> 256..275
<223> 12-132-157.mis2, potential complement

<220>
<221> primer_bind
<222> 99..117
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 557..577
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 243..267
<223> 12-132-157 potential probe

<400> 314
cagctccatg gccaggatgt ggatgtcagc gtggctggca agagcaggca aggtgggcaa 60
agttcctgtc cagctgattg gattgggcag gtgggctgtc tccttgtctg ggaatgccca 120
cccctctcca cattcctccc accctcattc cccttctcc tggaaacatc caagtccaaa 180
ttaatactat taatgcctac ctggatatta atgcctacct gatcatatct aggtcatgtt 240
agaattgtgt aaacytcctt tggatagctc actcctcatg tcctgtcccc ccagcccaca 300
gccctggtcc agatcccatc cttgggagct cctggcccag cctttcccat gcatgacctt 360
actgggcctc tgctctgcct ggcttctctg agccagctag agtaactata ggcatcccat 420
cctctgtaga ctaccctcac tgtggtccac tcagagtggg cactgttaac accaggctct 480
caaaacaact atgcccacct accatgcttg ctcctgtccc cttccctcca actctggccc 540
caagggcatc gctggtgatg taggtgattg atggggtcct ttaggatcca gggctagcaa 600
agggcagagc ctgctctctg actttgatct aaacaagctg gccagtcaat cctctgaggt 660
cttcctcatg cccctctcac tcttgactct ggttgagtcc tctccaggtc ccctgcactg 720
gcatcttctc agcaggcctg gccgtgccct tgtcc 755

<210> 315
<211> 991
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-132-437 : polymorphic base A or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-132-437.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-132-437.mis2, potential complement

<220>
<221> primer_bind
<222> 68..86

<223> upstream amplification primer

<220>
<221> primer_bind
<222> 526..546
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-132-437 potential probe

<400> 315
tggctggcaa gagcaggcaa ggtgggcaaa gttcctgtcc agctgattgg attgggcagg 60
tgggctgtct ccttgtctgg gaatgcccac ccctctccac attcctccca ccctcattcc 120
cccttctcct ggaaacatcc aagtccaaat taatactatt aatgcctacc tggatattaa 180
tgcctacctg atcatatcta ggtcatgtta gaattgtgta aacctccttt ggatagctca 240
ctcctcatgt cctgtccccc cagcccacag ccctggtcca gatcccatcc ttgggagctc 300
ctggcccagc ctttcccatg catgacctta ctgggcctct gctctgcctg gcttctctga 360
gccagctaga gtaactatag gcatcccatc ctctgtagac taccctcact gtggtccact 420
cagagtgggc actgttaaca ccaggctctc aaaacaacta tgcccaccta ccatgcttgc 480
tcctgtcccc ttccctccaa mtctggcccc aagggcatcg ctggtgatgt aggtgattga 540
tggggtcctt taggatccag ggctagcaaa gggcagagcc tgctctctga ctttgatcta 600
aacaagctgg ccagtcaatc ctctgaggtc ttcctcatgc ccctctcact cttgactctg 660
gttgagtcct ctccaggtcc cctgcactgg catcttctca gcaggcctgg ccgtgccctt 720
gtccatttgt ttgtgcgctg ttggtttgct tttcctgggc tcattggctc ccaaagcctg 780
tggagagagt caggagtggg tagaatggca gtgtctaatt acttttggct caacagagga 840
tggggttcac agtaggagac aaaacactgt catggaaagt cttggtgtcc actacaaaat 900
gcgcatggcc tgaaaagagc atcttctaaa cctcaaccca ttagcacgat tctcccctct 960
tcccaggata agtgaaatgt aatgatgttc t 991

<210> 316
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 666
<223> 12-133-153 : polymorphic base T or C

<220>
<221> misc_binding
<222> 646..665
<223> 12-133-153.mis1, potential

<220>
<221> misc_binding
<222> 667..686
<223> 12-133-153.mis2, potential complement

<220>
<221> primer_bind
<222> 800..818
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 250..270
<223> downstream amplification primer

<220>
<221> misc_binding

<222> 654..678
<223> 12-133-153 potential probe

<400> 316
ggtctgggat ctaacggtga tagttctagt gaaaccctcc caccettcca ggagacccat 60
tcctataaga aatatgactg aagagcccag ctgtctcact ttgataacca attcttccat 120
ttgcatttcc attgatgtgt attgggccaa gagcagagct ttttcttgtg gttaatatct 180
gtttaatcca gaagaagacc ctaaggaaag gtcagtattt aggtcccaga gtagctcttt 240
aaaatccttt aaaggaaaag agagtatggg atagtaaagg gccatgggat ggatctttga 300
ggatcaagga acttgggaca ggaggagaaa ggatctgaga gcctttcttc caccatctcg 360
acatctatgt tggtgtttct caatttttaa gaagctgtgg atgttgagag aaccccttaa 420
aggagttatg agagatactg atatgaattt ctcattagcc attaattatc agtgtgtaga 480
agagagggcg agagggctct attaaactaa ggatattatc tattgctgtg taacaaatta 540
tcataaactc agtggcttaa aagaacatcc attgattatc tcacggttcc actggccagg 600
agtctaggca tggctttcct tggtcctttg tttagggtct cagagactgc agtcctttct 660
ggagtycagc ttcctcttcc aagctcatgt gcttattgga gaattcagtt tcttatggtt 720
gtaggactga ggccctcagt tccttgctac gtggccctca ccacaggcag tttgcatcat 780
ggctgtttac ttttcaaggc cagtagaatg tttctgttca atctgataag agggaatctc 840
atgtggcata gtgtgatcat gggaatgaca tcccaccatc tttgccatat gatgtaatcc 900
actcgagaga gggtcaccca tcacctttgc catattctgt tgattagaag gaagtcacag 960
gttccaccca cacaccctca aggggatggc tttatggaag g 1001

<210> 317
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-133-318 : polymorphic base T or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-133-318.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-133-318.mis2, potential complement

<220>
<221> primer_bind
<222> 800..818
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 250..270
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-133-318 potential probe

<400> 317
ggtctgggat ctaacggtga tagttctagt gaaaccctcc caccettcca ggagacccat 60
tcctataaga aatatgactg aagagcccag ctgtctcact ttgataacca attcttccat 120
ttgcatttcc attgatgtgt attgggccaa gagcagagct ttttcttgtg gttaatatct 180
gtttaatcca gaagaagacc ctaaggaaag gtcagtattt aggtcccaga gtagctcttt 240
aaaatccttt aaaggaaaag agagtatggg atagtaaagg gccatgggat ggatctttga 300

```
ggatcaagga acttgggaca ggaggagaaa ggatctgaga gcctttcttc caccatctcg    360
acatctatgt tggtgtttct caatttttaa gaagctgtgg atgttgagag aaccccttaa    420
aggagttatg agagatactg atatgaattt ctcattagcc attaattatc agtgtgtaga    480
agagagggcg agagggctct wttaaactaa ggatattatc tattgctgtg taacaaatta    540
tcataaactc agtggcttaa aagaacatcc attgattatc tcacggttcc actggccagg    600
agtctaggca tggctttcct tggtcctttg tttagggtct cagagactgc agtcctttct    660
ggagttcagc ttcctcttcc aagctcatgt gcttattgga gaattcagtt tcttatggtt    720
gtaggactga ggccctcagt tccttgctac gtggccctca ccacaggcag tttgcatcat    780
ggctgtttac ttttcaaggc cagtagaatg tttctgttca atctgataag agggaatctc    840
atgtggcata gtgtgatcat gggaatgaca tcccaccatc tttgccatat gatgtaatcc    900
actcgagaga gggtcaccca tcacctttgc catattctgt tgattagaag gaagtcacag    960
gttccaccca cacaccctca aggggatggc tttatggaag g                       1001
```

<210> 318
<211> 643
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 249
<223> 12-136-238 : polymorphic base A or G

<220>
<221> misc_binding
<222> 229..248
<223> 12-136-238.mis1, potential

<220>
<221> misc_binding
<222> 250..269
<223> 12-136-238.mis2, potential complement

<220>
<221> primer_bind
<222> 12..32
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 442..461
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 237..261
<223> 12-136-238 potential probe

<400> 318

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acacagggtg agcaaaaggg agacttttta tccttttttg agaaagcaac cacaaaattt     60
tgaccttatg aagtatcttt gaaactttcc aaagctgatt agaatagcgt tgatgtattt    120
taatcagata cagaaagact ttacaaagta tgagctgcac acttgctgtc gtaatgctta    180
taagcactaa tttttttgta tacattcatg tacttgtaat tgcacaaaat gcgaaggaca    240
catttggcrg tgaggatgct gtgcacaatc aactcctaat cattttcagg aaaggataaa    300
cattccgcta aaaatgagga aagacaagaa atgttcaaaa gcatgtcaaa agtgtccagc    360
tgttttcata gaatataggt gatttcctgg tgctagcaaa atccagaaga aacgttataa    420
taactagaaa tgtctataat tgtgaggaag cccaagtatg aagattcaca aaaatagaat    480
aagtggatga aattagttaa aacaaccttc ttagtaatga ggtactctga ttataaaagt    540
actttgactc tttagaatgt gtcactgaac accaagctga aaaaacaaat taacagtctg    600
tcactagagc atgatctccc acagacaata tgctcataaa tga                      643
```

<210> 319
<211> 1001

<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-138-141 : polymorphic base G or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-138-141.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-138-141.mis2, potential complement

<220>
<221> primer_bind
<222> 623..641
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 186..204
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-138-141 potential probe

<400> 319
tgatgtgtgg tactgggata cagagatggg caagactgtg aggtgcttac tccctgagga 60
ccaattggga cctgagatgt tcataatttt taaaagttcc cttgtcttct gacacagtgg 120
gtttgggagc cattgtccta cagcacatga gctgagttgc aaagatgttg agccagtggg 180
catgggagag taaagataca ccagacacag tgtgcaggga tgtttggcta gtggggagat 240
gcctagctgg gttaaggggc tggggtagag gatgttggag ggagtgatac aaagtgcaac 300
caggggacct ggtgggcttg tacagacaag gtttgcatca cgtggtacca gacaaggttt 360
tggactagac aagggtttgg aacagagctg atccaaacct tgctgggcac cacccccaga 420
gtttctgatt cagtaagtct ggggtggagc ctgagaatca gcatttctaa caagttccca 480
ggtgatgcca aggctgatct rgagagccta ctttgagaac tgttggattt tagactaccc 540
ttttgtcttg gagtgggtag caaaggggtg ctatgagcag aggagcttat ttataaaaag 600
ttttattatt tttgttggat ttggatttgc atttgcgttt tccccctttt atttttagtt 660
gacacataac aattgtacat atttatagaa tacaaagtga tatttcaaaa catatataca 720
atgtgtaatg accgaatcag ggtaattagt atatccaaca ctgcaaacat ttatcatttc 780
tttgtgttgc aagcattcaa aactgtttct tctagttttt tgaaaatata caatcaatca 840
ttgttgacta tattcacaac ctacagtgct atagaacaca agagcttatt ccttctctcc 900
agctgtaatt ttgtatcttt taatcaactt ctccctatcc tcccctgccc ttagctttcc 960
tataccctaa taccgaaatt ctactcttga cttctatgag c 1001

<210> 320
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-138-42 : polymorphic base T or G

<220>

<221> misc_binding
<222> 481..500
<223> 12-138-42.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-138-42.mis2, potential complement

<220>
<221> primer_bind
<222> 524..542
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 87..105
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-138-42 potential probe

<400> 320
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ccttgtcttc tgacacagtg ggtttgggag ccattgtcct acagcacatg agctgagttg     60
caaagatgtt gagccagtgg gcatgggaga gtaaagatac accagacaca gtgtgcaggg    120
atgtttggct agtggggaga tgcctagctg ggttaagggg ctggggtaga ggatgttgga    180
gggagtgata caaagtgcaa ccaggggacc tggtgggctt gtacagacaa ggtttgcatc    240
acgtggtacc agacaaggtt ttggactaga caagggtttg gaacagagct gatccaaacc    300
ttgctgggca ccaccccag agtttctgat tcagtaagtc tggggtggag cctgagaatc    360
agcatttcta acaagttccc aggtgatgcc aaggctgatc tggagagcct actttgagaa    420
ctgttggatt ttagactacc cttttgtctt ggagtgggta gcaaaggggt gctatgagca    480
gaggagctta tttataaaaa kttttattat ttttgttgga tttggatttg catttgcgtt    540
ttccccccttt tatttttagt tgacacataa caattgtaca tatttataga atacaaagtg    600
atatttcaaa acatatatac aatgtgtaat gaccgaatca gggtaattag tatatccaac    660
actgcaaaca tttatcattt ctttgtgttg caagcattca aaactgtttc ttctagtttt    720
ttgaaaatat acaatcaatc attgttgact atattcacaa cctacagtgc tatagaacac    780
aagagcttat tccttctctc cagctgtaat tttgtatctt ttaatcaact tctccctatc    840
ctcccctgcc cttagctttc ctataccсta ataccgaaat tctactcttg acttctatga    900
gctcaccatt tttatagctc ccatatatga gtgagaacat gtggtattta tctatctgtg    960
cctgactcat ttcacttgac ataatgtcct ccagttttat t                       1001
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<210> 321
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-138-67 : polymorphic base G or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-138-67.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-138-67.mis2, potential complement

<220>
<221> primer_bind
<222> 549..567
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 112..130
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-138-67 potential probe

<400> 321
agatgttcat aatttttaaa agttcccttg tcttctgaca cagtgggttt gggagccatt 60
gtcctacagc acatgagctg agttgcaaag atgttgagcc agtgggcatg ggagagtaaa 120
gatacaccag acacagtgtg cagggatgtt tggctagtgg ggagatgcct agctgggtta 180
aggggctggg gtagaggatg ttggagggag tgatacaaag tgcaaccagg ggacctggtg 240
ggcttgtaca gacaaggttt gcatcacgtg gtaccagaca aggttttgga ctagacaagg 300
gtttggaaca gagctgatcc aaaccttgct gggcaccacc cccagagttt ctgattcagt 360
aagtctgggg tggagcctga gaatcagcat ttctaacaag ttcccaggtg atgccaaggc 420
tgatctggag agcctacttt gagaactgtt ggattttaga ctaccctttt gtcttggagt 480
gggtagcaaa ggggtgctat ragcagagga gcttatttat aaaaagtttt attattttttg 540
ttggatttgg atttgcattt gcgttttccc ccttttattt ttagttgaca cataacaatt 600
gtacatattt atagaataca aagtgatatt tcaaaacata tatacaatgt gtaatgaccg 660
aatcagggta attagtatat ccaacactgc aaacatttat catttctttg tgttgcaagc 720
attcaaaact gtttcttcta gttttttgaa aatatacaat caatcattgt tgactatatt 780
cacaacctac agtgctatag aacacaagag cttattcctt ctctccagct gtaattttgt 840
atcttttaat caacttctcc ctatcctccc ctgcccttag ctttcctata ccctaatacc 900
gaaattctac tcttgacttc tatgagctca ccatttttat agctcccata tatgagtgag 960
aacatgtggt atttatctat ctgtgcctga ctcatttcac t 1001

<210> 322
<211> 663
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-139-380 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-139-380.mis1, potential

<220>
<221> misc_binding
<222> 502..520
<223> 12-139-380.mis2, complement

<220>
<221> primer_bind
<222> 122..139
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 602..620
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-139-380 potential probe

<220>
<221> misc_feature
<222> 655,658
<223> n=a, g, c or t

<400> 322
caagtctgac acctgtgtgg caggccagca ggctggagac tagcaggggc ggatgctgca 60
gccttgtggc tgaatatctt cttcctcaga gaaatcccag cgtttcactc ttaaggcgtt 120
tcacccacct atgttattga ggataatctc ttttatggat tatgcacttt cgtcacacct 180
acaagctacc ttcacaacaa cacctagatt ggtgtttgac tgaatgacta ggtacagtcg 240
cctagccaag ttgacacaca aaactgaccg tcataccagg catgcacaac tggatcatct 300
gcccggggtg cccctctaga ggacttggga tcagagggag ggccctggat gagaagggtt 360
tgatgagtgt gggtttgtat gaggctggca gtgataggag ttgggcaaca gggatgctgg 420
ccccagcagg gactagcaga ctctcttgcc acatcagggt gggtgacact taaatgcccc 480
tgacaaagac tggatttggc rgtggagcca gttcagggct gagactgtca ggggacatct 540
ctggggaagc agggatggga tggcaccatg gcagagcctg actgttctcc ttagaagccc 600
agggcttggg ctaattctga gccccttct ctcccacccc taccccagca gtttngcntg 660
agg 663

<210> 323
<211> 951
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-140-134 : polymorphic base G or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-140-134.mis1, potential

<220>
<221> misc_binding
<222> 502..520
<223> 12-140-134.mis2, complement

<220>
<221> primer_bind
<222> 368..386
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 868..888
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-140-134 potential probe

<220>
<221> misc_feature
<222> 923

<223> n=a, g, c or t

<400> 323
ctgtagatca ttctggctaa ataatgggat tcacttttaa gtgaaggagg ccttgaatgc 60
cacactcagg ggcctagcgc agcacttccc aagccttgct gtggttagga acaacctggg 120
ggctgggtga aatgcaggct tggattcagc aggaccgggg tagggcctga gagtctgcat 180
ttctaatcag ctcccaggga atgctggtgc tcagtgggtc agtgggcccc tgagtagcga 240
gggtctagag tttgaccttg agttggtaga aggtcacctg ccaccatttg ccaatccact 300
gcaggtcttg aggcagatcc tggaactgtc agtcaccacc aacacccctg tcccccaaat 360
gcagctacac accattttca cagaactgca cgtccaggtg aggccagcaa gctcagctgg 420
acaagggcat tctctgggtg gatcagcagg aagctggcgg cgggaggtgg cctggcccac 480
aactcactcg cgtgcttcct ktatcctgat ggggtatgag gctgtggtgc ccatgcagcc 540
ccaggtatgg tcagctgggc tgcccctgca cctgtgtccc tgtgatctcc tccagcctca 600
ctgcacgtcc cttaccaggt gtgcaacaag gccccggccc agcatcagta cagcagccag 660
aatctgatgg agatggtgca ctgcttcgta gccctcggtg aggctctgcg gcagggtgct 720
ccctgcctgc cccgaggcct gcaggaggcc tctaggagtc ccggcccctc tgagcgctgg 780
gcctgggact gccttgctgg gcctgctctg gacccggtga gcatgactaa agctgtcctt 840
ccaccctgca gctcgctcct accccaagga gctgatgaag ttcttcttca gccagatgga 900
gacaaacaag gaggccgtcc gcntggggac tctgaatctg attagggcta t 951

<210> 324
<211> 756
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-140-329 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-140-329.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-140-329.mis2, potential complement

<220>
<221> primer_bind
<222> 173..191
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 673..693
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-140-329 potential probe

<220>
<221> misc_feature
<222> 728
<223> n=a, g, c or t

<400> 324
agggaatgct ggtgctcagt gggtcagtgg gcccctgagt agcgagggtc tagagtttga 60
ccttgagttg gtagaaggtc acctgccacc atttgccaat ccactgcagg tcttgaggca 120

gatcctggaa ctgtcagtca ccaccaacac ccctgtcccc caaatgcagc tacacaccat 180
tttcacagaa ctgcacgtcc aggtgaggcc agcaagctca gctggacaag ggcattctct 240
gggtggatca gcaggaagct ggcggcggga ggtggcctgg cccacaactc actcgcgtgc 300
ttcctttatc ctgatggggt atgaggctgt ggtgcccatg cagccccagg tatggtcagc 360
tgggctgccc ctgcacctgt gtccctgtga tctcctccag cctcactgca cgtcccttac 420
caggtgtgca acaaggcccc ggcccagcat cagtacagca gccagaatct gatggagatg 480
gtgcactgct tcgtagccct yggtgaggct ctgcggcagg gtgctccctg cctgccccga 540
ggcctgcagg aggcctctag gagtcccggc ccctctgagc gctgggcctg ggactgcctt 600
gctgggcctg ctctggaccc ggtgagcatg actaaagctg tccttccacc ctgcagctcg 660
ctcctacccc aaggagctga tgaagttctt cttcagccag atggagacaa acaaggaggc 720
cgtccgcntg gggactctga atctgattag ggctat 756

<210> 325
<211> 700
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-140-385 : polymorphic base G or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-140-385.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-140-385.mis2, potential complement

<220>
<221> primer_bind
<222> 117..135
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 617..637
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-140-385 potential probe

<220>
<221> misc_feature
<222> 672
<223> n=a, g, c or t

<400> 325
ttgaccttga gttggtagaa ggtcacctgc caccatttgc caatccactg caggtcttga 60
ggcagatcct ggaactgtca gtcaccacca acacccctgt cccccaaatg cagctacaca 120
ccattttcac agaactgcac gtccaggtga ggccagcaag ctcagctgga caagggcatt 180
ctctgggtgg atcagcagga agctggcggc gggaggtggc ctggcccaca actcactcgc 240
gtgcttcctt tatcctgatg gggtatgagg ctgtggtgcc catgcagccc caggtatggt 300
cagctgggct gcccctgcac ctgtgtccct gtgatctcct ccagcctcac tgcacgtccc 360
ttaccaggtg tgcaacaagg ccccggccca gcatcagtac agcagccaga atctgatgga 420
gatggtgcac tgcttcgtag ccctcggtga ggctctgcgg cagggtgctc cctgcctgcc 480
ccgaggcctg caggaggcct staggagtcc cggcccctct gagcgctggg cctgggactg 540
ccttgctggg cctgctctgg acccggtgag catgactaaa gctgtccttc caccctgcag 600

ctcgctccta ccccaaggag ctgatgaagt tcttcttcag ccagatggag acaaacaagg 660
aggccgtccg cntggggact ctgaatctga ttagggctat 700

<210> 326
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-141-159 : polymorphic base T or C

<220>
<221> misc_binding
<222> 502..521
<223> 12-141-159.mis1, potential complement

<220>
<221> misc_binding
<222> 482..500
<223> 12-141-159.mis2

<220>
<221> primer_bind
<222> 640..658
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 181..200
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-141-159 potential probe

<400> 326
gggagtgctg ccgccatcat ggtcaccaaa agccaccacc ccctgcttgt gttggacagg 60
cggtcatcaa ggcagaaccg actgacaacc tggtttctcc agtgcgagcc ttggcgatgg 120
aggccctctc gcacctgagg tgagctgggt tcccaccctc accccatccc aaggggtagg 180
gaaaagttca agaccattcc tcggtgctcc ttcaggggtt gtgcctcctt tttcctctcc 240
tccctctgta gcaggggtct cacttggcgg ctccccaggg caatgggcca gcctagatga 300
tgggggtcgg cctcagccac tcttttctat aattctcagc cagatttcaa gttgggtgct 360
tctccttgga tttatggcac atgggtgggc tgctcttcca ttgattgggg atattttgag 420
caaaataaca gtgataacac tgaagagcat tgcaagcatc cttcaagatg agtcaggctc 480
agtgagtgag ttgaagggct yagtcaacta tttgttgata ccactggtac aaaatgatct 540
aaagcccaag acttaccttc ctggagatgc caatccattg gtggggaggg ggaaagggga 600
agaagttatg gatttataaa attagtattt aaagagtttg ggtcatctct aagaatacct 660
cccctatagg ggaagattca ttacttaggc gcatagcaga actatctgtt actttaagct 720
gcatcaaaca ggcagatttt aaaataaatg tcatgaacat caactaagca caatgatatg 780
ctgagtactg aagggacaca gagatacata agacctagtc ccagcctttt aaggacttag 840
agataagaca gacacataca aacaggatta taggtcaaag ctgactaaca ggactgtgtt 900
tacaggtaaa cccacacaca catcagcaaa aaaatatctg agaacaaaaa aaaaggggct 960
actaacaaaa gcaactcagt ttatacaaaa ggagctatca a 1001

<210> 327
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>

<221> allele
<222> 501
<223> 12-141-392 : polymorphic base C or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-141-392.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-141-392.mis2, potential complement

<220>
<221> primer_bind
<222> 873..891
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 414..433
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-141-392 potential probe

<400> 327
ggtcttgttt tacagagaag gggacttggg ctcaggcaga ggaagtgctg gcccaggggc 60
acacagcaag tagatgagca gcgcgagctg ggagcccagg cccactttgg gccctgctcc 120
cactctgctg cctcccctaa gatgccaaaa gccaaatggc cctaaaaaga atgaaagaga 180
tgtggggtgt tagacacttt gggaagtgcc aggtcttcct catgctaaca ctggggagtg 240
ctgccgccat catggtcacc aaaagccacc accccctgct tgtgttggac aggcggtcat 300
caaggcagaa ccgactgaca acctggtttc tccagtgcga gccttggcga tggaggccct 360
ctcgcacctg aggtgagctg ggttcccacc ctcaccccat cccaaggggt agggaaaagt 420
tcaagaccat tcctcggtgc tccttcaggg gttgtgcctc ctttttcctc tcctccctct 480
gtagcagggg tctcacttgg mggctcccca gggcaatggg ccagcctaga tgatggggt 540
cggcctcagc cactcttttc tataattctc agccagattt caagttgggt gcttctcctt 600
ggatttatgg cacatgggtg ggctgctctt ccattgattg gggatatttt gagcaaaata 660
acagtgataa cactgaagag cattgcaagc atccttcaag atgagtcagg ctcagtgagt 720
gagttgaagg gctcagtcaa ctatttgttg ataccactgg tacaaaatga tctaaagccc 780
aagacttacc ttcctggaga tgccaatcca ttggtgggga gggggaaagg ggaagaagtt 840
atggatttat aaaattagta tttaaagagt ttgggtcatc tctaagaata cctcccctat 900
aggggaagat tcattactta ggcgcatagc agaactatct gttactttaa gctgcatcaa 960
acaggcagat tttaaaataa atgtcatgaa catcaactaa g 1001

<210> 328
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-142-315 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-142-315.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-142-315.mis2, potential complement

<220>
<221> primer_bind
<222> 187..205
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 637..657
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-142-315 potential probe

<400> 328
tggcagtggt gtgcaagaga atgagaacct tttattcgaa cccttcctgc tcagagcaga 60
tatgagggca gagagaggag gggctcgccc ccagggccac acagggtcta gagtaggcca 120
gggatgggag ttacttctgg ggtcctagtc actccggagc cgccctcact ctagtcccct 180
ttgtaaaaag gagatagaca ttgactgatt cactgacaac ctcaaccaag tccccaggaa 240
gaggagggag aaacccagag atgttacgac atctttccgg ggttatcttg ccaccagggt 300
ccaggcaccg atgtggccct gcccagctct tggcaaacgt caggcagggg tggggccgcc 360
tccacgacct ggcactgtct ctcctctgca ggctgtgcat gcagcacgtg gagggccaca 420
ggcagaggct ggccgagctg gtgctcaggg gcatggactc agaagtcctg agctgccgca 480
tcagcagcac agcggtctgc rtggaagtga ggcaccgggt gtgggcgggg tgcaagcgga 540
ggggatgggg tccctggatt cttctgggga tggcttgtct ccaaggcatg ggagtcgggg 600
ggacaggcga gcgcccctcc tctgagtgct cattctctca tctgctcctt cattcattca 660
tcacatgagt agtgcagggc aggccctgct ggaaagacag gctgagccct gcagcattgc 720
agttaactga tgtgtgaccc aggcaagtac agtgacccag gggacccagg gagggcacct 780
gggttctcgc tggggcaggc ttcctgcagg aggactcaga gaggccgagg ggctttgcta 840
ggtgggaagg cagggcccag cgaccctatc tcagagtgag tgttggagcg tcctgagggc 900
aatgatgccc aatgcaccct aggaaccaac cacagcccag gccagaggcc ggccagtgtt 960
ttctgtaaag gactgcagag taaatttttg gctttgtggc c 1001

<210> 329
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-142-321 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-142-321.mis1, potential

<220>
<221> misc_binding
<222> 502..520
<223> 12-142-321.mis2, complement

<220>
<221> primer_bind
<222> 181..199
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 631..651
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-142-321 potential probe

<400> 329
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tggtgtgcaa gagaatgaga accttttatt cgaacccttc ctgctcagag cagatatgag      60
ggcagagaga ggaggggctc gcccccaggg ccacacaggg tctagagtag gccagggatg     120
ggagttactt ctggggtcct agtcactccg gagccgccct cactctagtc ccctttgtaa     180
aaaggagata gacattgact gattcactga caacctcaac caagtcccca ggaagaggag     240
ggagaaaccc agagatgtta cgacatcttt ccggggttat cttgccacca gggtccaggc     300
accgatgtgg ccctgcccag ctcttggcaa acgtcaggca ggggtggggc cgcctccacg     360
acctggcact gtctctcctc tgcaggctgt gcatgcagca cgtggagggc cacaggcaga     420
ggctggccga gctggtgctc aggggcatgg actcagaagt cctgagctgc cgcatcagca     480
gcacagcggt ctgcatggaa rtgaggcacc gggtgtgggc ggggtgcaag cggaggggat     540
ggggtccctg gattcttctg gggatggctt gtctccaagg catgggagtc gggggacag      600
gcgagcgccc ctcctctgag tgctcattct ctcatctgct ccttcattca ttcatcacat     660
gagtagtgca gggcaggccc tgctggaaag acaggctgag ccctgcagca ttgcagttaa     720
ctgatgtgtg acccaggcaa gtacagtgac ccaggggacc cagggagggc acctgggttc     780
tcgctggggc aggcttcctg caggaggact cagagaggcc gaggggcttt gctaggtggg     840
aaggcagggc ccagcgaccc tatctcagag tgagtgttgg agcgtcctga gggcaatgat     900
gcccaatgca ccctaggaac caaccacagc ccaggccaga ggccggccag tgttttctgt     960
aaaggactgc agagtaaatt tttggctttg tggccaactc a                        1001
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<210> 330
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-143-453 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-143-453.mis1, potential

<220>
<221> misc_binding
<222> 502..520
<223> 12-143-453.mis2, complement

<220>
<221> primer_bind
<222> 50..68
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 533..552
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513

<223> 12-143-453 potential probe

<400> 330
gcccaggatg agtatcaggg ccatctacct ggctatccgg gtagtcaaga acaccatctc 60
tgatacccgg tccaaggtaa cagggcagag acctggaaat ggggggcact caggggaccc 120
tgccagggag gcaaagggaa gtctgggctc tgggaggcag aggcttttga tggaaaaccc 180
ggctttccat cggtctcga ctggggctgc agaatggtga ggccagtgaa agctgaggtt 240
ccactctcga gacctcattc tctccatgga tctagagttt ttgagtggtg tgtctcaggc 300
accaccttgg acccaacaga ggccgagtaa atccagctgc agctagagtc acttggctgt 360
caagggtttt gtgaggtctt tatcgcatgt gaaaaaagca actaaggggt actcctctac 420
ccatcctcaa aaggctgaaa accacagtcc caggctccat ggcagccaca tccaccttgg 480
agtggagctt ggttctggcc rtgggctggg gaagggaggt ccggcatagt gaggggtctg 540
cacagcagtt ttgaggaaca tcagagaggg aatggaggag aatgggggct agagatttag 600
gcagagctgt cttcagtccc tggaggctgt ggagggaagc gagaagaggc tcgttctgca 660
tctccttcac atagtgattc tcatcaatgg agcaagcccc agggggtcca ggataacaga 720
tgggctcccc atggcaaggg ctgctagaat ggagcagccg aggttggaag ggagggaggg 780
agctttgtgt ctctccaagg ctcaattagg ctcccaggtg ggcatgctgc agagtgggac 840
ccctggatga ggcagggggа ggtggacaga gtgggcagta atcaggtagt ccctgaggcc 900
ccttctagcc cagagcaccc ccaattccta gctctctatg tcacaggatt gggtgccttg 960
gagcccaccc caaccccag catgtccacg gtcctgtccc c 1001

<210> 331
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-144-169 : polymorphic base G or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-144-169.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-144-169.mis2, potential complement

<220>
<221> primer_bind
<222> 651..669
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 148..167
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-144-169 potential probe

<400> 331
cctgacctcg tgatccgccc accttggcct cccaaagtgc tgggattaca ggcgtgagac 60
accgtgccct tctagctcac tttttaatgc ttttctgact cctggactat ttcctggcc 120
ccagccagga cagagggcta agccagctct ggactgttag gggttggagg tggagggcag 180
cagggttgtc ctctctgcct tctctctgct cacccccagc cccaacttcc tgtaatcatc 240
cctcacaacc tcacagtgtt tgagttcatg ccatacatgg gcatcacccct ggctaccata 300
ttcaccatgc tgagacttgc caatgaagcc aagatacgcc aggcgatctg cagtggtgag 360

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tgtcccactt gagcctgcag gtctggctcg atcagggcgc cggagggaga ctgctgggta     420
aggagcagat ggaggggttg ttgaaaaaga ggtgcactgt tcacttgttc tccaaaggcg     480
tttgcttaat cttttacttc rtgtggcctc tgattggctg cctggggcac aagaggctga     540
gacatggtgg gggcctttta gaagatcccg gcttagaggg aagaagctgc aacggtgact     600
ccatttagct tgctttgtaa ttaagcactt cagttcatga gaccacagaa cagcaatgag     660
cattcacagg agagggagac cggggaaaac ggctccatgt ggagcttgac ggggactggt     720
cttagatgct atttcaatct gatcaccttg ccccagattt tgattactta atgttcttgt     780
gggcttataa aaagccctag tgcctgagaa aaagagggcc acatgtgttc actgttcact     840
gccctctgac ctggaatccc caggatgtgg gcagggtcat actccaggcc tcgcccttga     900
ccccgtctct gtccttgaag gagagggacc cagacacccc cgagtgctca gttctcacac     960
acacaggcac gcagagtaaa aatgaaggtg ctgtgggggg t                        1001
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<210> 332
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-144-33 : polymorphic base G or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-144-33.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-144-33.mis2, potential complement

<220>
<221> primer_bind
<222> 515..533
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 12..31
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-144-33 potential probe

<400> 332

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tgtttgagtt catgccatac atgggcatca ccctggctac catattcacc atgctgagac     180
ttgccaatga agccaagata cgccaggcga tctgcagtgg tgagtgtccc acttgagcct     240
gcaggtctgg ctcgatcagg gcgccggagg gagactgctg ggtaaggagc agatggaggg     300
gttgttgaaa aagaggtgca ctgttcactt gttctccaaa ggcgtttgct taatctttta     360
cttcgtgtgg cctctgattg gctgcctggg gcacaagagg ctgagacatg gtgggggcct     420
tttagaagat cccggcttag agggaagaag ctgcaacggt gactccattt agcttgcttt     480
gtaattaagc acttcagttc rtgagaccac agaacagcaa tgagcattca caggagaggg     540
agaccgggga aaacggctcc atgtggagct tgacggggac tggtcttaga tgctatttca     600
atctgatcac cttgccccag attttgatta cttaatgttc ttgtgggctt ataaaaagcc     660
ctagtgcctg agaaaaagag ggccacatgt gttcactgtt cactgccctc tgacctggaa     720
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gaaggagagg gacccagaca cccccgagtg ctcagttctc acacacacag gcacgcagag     840
taaaaatgaa ggtgctgtgg ggggttggaa gggcagggtg cagcctgctc gctacggcaa     900
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ggcatgagca cttccactcg ggaagctggg ctgggaaggc ttggttctgc ttccagcccc 960
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<210> 333
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-146-174 : polymorphic base T or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-146-174.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-146-174.mis2, potential complement

<220>
<221> primer_bind
<222> 655..674
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 271..291
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-146-174 potential probe

<400> 333
tttcttgact gctaaaacaa ccagggagat cctctcagac aaaaggaaat acagcactat 60
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ggatgcagtg attatttcca ctagaactgc tatatcatga ccatgaattt tgggggaatt 180
tttttgagat ctgagttctc ttcacctcct tattctcttt ttgacactgg attcttttct 240
ttgataaatt gtgaggcaat acactagtaa aggtcactca gttctaaggg gaaaatgatt 300
aaccaaagaa cattctaaga tttcctatag ggtattaggt ctaatgggga tgtgttatgt 360
caccagaaca aacttctaag tttatatagc ctctagtgac ataacctgag acccggactt 420
ggcacttggt aagcacacaa tgaacagtca tagaaagctg gccgagggta gagttcagtg 480
tgaacaaagc aatttgggaa yatcaaagca agtttggaga acaacaagtg atccagaatg 540
gctggagggt aagaggcaga gggagggggc aagcagaagg ggtggagagg aggaatgagc 600
ttagacaggg gggctggggt ctatcccaga gttttgagag caaggcagag gactctgaat 660
tttcttctgt gcccaggaag ctgctgacca aggttccaga agtgttggtg gggtggcgtt 720
tttcagggag cagctgaggc agtgattcag aagggacagc tgggggttgg gcaactgggg 780
gacaggggcc ctgaaatggg accatgacag ctgggtctga gagacagtgg tagaaacatc 840
cagattcagc acttacttgc tggcttggat gcagggtcta gaacgaaaag agaagaggag 900
tcacttctat acagaaacat gtccagagtg cttactgtct gcaaaactgt ggactggcac 960
ctgagtgata gcatgattcc aaagccaaaa tcttgcctgt a 1001

<210> 334
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>

<221> allele
<222> 501
<223> 12-146-47 : polymorphic base G or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-146-47.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-146-47.mis2, potential complement

<220>
<221> primer_bind
<222> 528..547
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 144..164
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-146-47 potential probe

<400> 334
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gatctgagtt ctcttcacct ccttattctc tttttgacac tggattcttt tctttgataa 120
attgtgaggc aatacactag taaaggtcac tcagttctaa ggggaaaatg attaaccaaa 180
gaacattcta agatttccta tagggtatta ggtctaatgg ggatgtgtta tgtcaccaga 240
acaaacttct aagtttatat agcctctagt gacataacct gagacccgga cttggcactt 300
ggtaagcaca caatgaacag tcatagaaag ctggccgagg gtagagttca gtgtgaacaa 360
agcaatttgg gaacatcaaa gcaagtttgg agaacaacaa gtgatccaga atggctggag 420
ggtaagaggc agagggaggg ggcaagcaga aggggtggag aggaggaatg agcttagaca 480
ggggggctgg ggtctatccc rgagttttga gagcaaggca gaggactctg aatttcttc 540
tgtgcccagg aagctgctga ccaaggttcc agaagtgttg gtggggtggc gtttttcagg 600
gagcagctga ggcagtgatt cagaagggac agctgggggt tgggcaactg ggggacaggg 660
gccctgaaat gggaccatga cagctgggtc tgagagacag tggtagaaac atccagattc 720
agcacttact tgctggcttg gatgcagggt ctagaacgaa aagagaagag gagtcacttc 780
tatacagaaa catgtccaga gtgcttactg tctgcaaaac tgtggactgg cacctgagtg 840
atagcatgat tccaaagcca aaatcttgcc tgtaaggaat atatgtatag gatatagcta 900
tactctaata gcaaggacag atatgcaaac tgctaaaaga tacaaggcag aacagaacaa 960
aacgctgtgg ggattcaagg aaggtggctt tgtttccctt g 1001

<210> 335
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-148-283 : polymorphic base G or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-148-283.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-148-283.mis2, potential complement

<220>
<221> primer_bind
<222> 765..783
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 375..395
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-148-283 potential probe

<400> 335
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ggattgactt ggagaagagc ctgaccataa tcttcaggat gaaataaagg cctggatgac    180
tgaaataaag actggagcct tcggcattca gaagaggaat tcagactgtg caagatctga    240
ggccaggctc cagctccccc agtcccttgg tgagcaggag ctccctgaac ccaccatggg    300
tctttgctag ggttgtcttg cccatgtgtg ctttagatag cagcacctct tcttccatgg    360
tgtatatgga gaatcctcaa caaagtcttc ccaagaatct gatcatcaca tcttgagctc    420
agcctccctg cagctttttc tatattgaca gccacttcag agagagtcct ctctgatcct    480
tacaagaaat atcctggtgc raaaaacgac caaaaccaca tagccagcct ccacgctgtt    540
cagagaaagc tggcttagca atgttgtatg gtttttggat gcgctgcgtt actcatacat    600
gagaagaaag tttcaagggt tagcaaatag ggtcacatcc agcagagagc atatgactgg    660
gggctagggc aatggtgact cctcagacct cagctgctgc ctgataaaca tggttaacag    720
agaagtagga gacagtgaca tgaaatgggt gttcacagcc ttgtgttggg aattggatga    780
gaaacaagag cttgaacttg gatgttcccc agagtgagca cagggtcaga cgtgtttttc    840
aagatagtca tgatcggtct tttccagggt ggggcccaca gtgaaaaaca gtgatagatt    900
aatggttaat aattaactag aggagggcac tctgtcttcc aattacacgt tgatttgcta    960
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<210> 336
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-148-311 : polymorphic base T or C

<220>
<221> misc_binding
<222> 502..520
<223> 12-148-311.mis1, complement

<220>
<221> misc_binding
<222> 481..500
<223> 12-148-311.mis2, potential

<220>
<221> primer_bind
<222> 793..811
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 403..423
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-148-311 potential probe

<400> 336
ttgggcttga ggcccttgtg agtgctcagg gtctctcctt tagaaaggca catatttaat 60
tctccatctt gaaatttgga ctagggcccc cacaaattgt gcagcccatt ctgttctgga 120
ggaaccattc ttatcagaac ttggtgctgg attgacttgg agaagagcct gaccataatc 180
ttcaggatga aataaaggcc tggatgactg aaataaagac tggagccttc ggcattcaga 240
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agcaggagct ccctgaaccc accatgggtc tttgctaggg ttgtcttgcc catgtgtgct 360
ttagatagca gcacctcttc ttccatggtg tatatggaga atcctcaaca aagtcttccc 420
aagaatctga tcatcacatc ttgagctcag cctccctgca gctttttcta tattgacagc 480
cacttcagag agagtcctct ytgatcctta caagaaatat cctggtgcga aaaacgacca 540
aaaccacata gccagcctcc acgctgttca gagaaagctg gcttagcaat gttgtatggt 600
ttttggatgc gctgcgttac tcatacatga gaagaaagtt tcaagggtta gcaaataggg 660
tcacatccag cagagagcat atgactgggg gctagggcaa tggtgactcc tcagacctca 720
gctgctgcct gataaacatg gttaacagag aagtaggaga cagtgacatg aaatgggtgt 780
tcacagcctt gtgttgggaa ttggatgaga aacaagagct tgaacttgga tgttccccag 840
agtgagcaca gggtcagacg tgtttttcaa gatagtcatg atcggtcttt tccagggtgg 900
ggcccacagt gaaaaacagt gatagattaa tggttaataa ttaactagag gagggcactc 960
tgtcttccaa ttacacgttg atttgctaag tggctcagtg a 1001

<210> 337
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-149-320 : polymorphic base T or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-149-320.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-149-320.mis2, potential complement

<220>
<221> primer_bind
<222> 800..820
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 368..387
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513

<223> 12-149-320 potential probe

<400> 337
cagcacctgt aattccagct aattgggagg ctgaggcagg agaattgctt gaaccggggt 60
caggggggttc ggaggtcgga ggttgcagtg agtccggatc atgccactgc attccagcct 120
gggtgacaca gccagactct gtctcaaaaa caacaacaac aacaaaacaa caacaacaac 180
aacaacaaaa atctcactgg acatcctagt agctaaggct ttccacatat tcatgattac 240
ttctgttgga aagtgcttta caacaaattg ctagttgtct cagtctgggt tcccctgaga 300
tgaggattca agggccagga gtttatttag gaagtaaagg aaacactgat agaggagtgg 360
cagagtgaga aggggtgatg gtcatccaca gctggctctc ttgtggtcaa tcggagctta 420
atcctgctgg gtgactctgg gagccagtgg agaaaagaca ccccagactt atcccaatga 480
ggaacacggc tgttgggtgc ytgagtactt gcctcgtcag ggattgaaac gtactcccag 540
gtagtagtaa tttctctgcc cttccattag gccacaaagg gggctctgac agagagagct 600
gacgagaaaa aacacacgcc cttgtcactg aagaggtaca caggggatct gtgtggggca 660
ccacctgcac tgctaccctg gacaaatagc ttaagaaatc cccacactgc atccccaaac 720
ttactatcag cgtgtgaggg agacaggttc ccacaccctc attagcacaa agtactatct 780
tgaaaaagaa agcctgtcag tttgatagga gaaaagcagg atcttgttta caatgtgctt 840
ttattattgt tattattaga gattgtattt cttttcaagc tgatgagccg tctgtgttta 900
ttttttggag gataccсttt gcccactttc ctattggagt gtattaccct gaggatttgg 960
taagagtgct tattgcattc accagaatgt cctttttgtc a 1001

<210> 338
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-151-174 : polymorphic base G or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-151-174.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-151-174.mis2, potential complement

<220>
<221> primer_bind
<222> 328..345
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 827..845
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-151-174 potential probe

<400> 338
gcctgctgct ctgacatgca cagaaaaatt cctgtgtcta tctggaagat gagggaacac 60
ttatgaaatc aagttctgtc cccagagggc cccttgggag aggctgcagt gacctagtgc 120
cctgggctgg gtcagggagg gagagggtgg gattgtggtt ggcagagctc caggctttgt 180
ggggcctgtg gcttctgtag cggtgagagc cctttttaag aaaaaagata catagttatg 240
aaccccacat tggctaggaa aatgaatatt tactttgaga aaatcaagtg ctgcaaaatc 300
ataaattttg caaagcttga caagtaccgc aacccttaaa atgtctagaa cgacgtagtg 360

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tttttactga ttgaccatct gacacagcct gatgagactt aattgtctac actttttggc    420
tccatgctgt ttgactgtct tgtcctcagg atggctgtgg caggaggatg atggagtcag    480
ggtctggggc gcagggatgg kcgtctggtg cagggagaga agtgggctgg gcaggaggac    540
cctggtcctg ggcacctgga tggaggtggg gatgaaggct cagcaaaatg aggcaggggc    600
caagtccaac actcagtaac atgtgaggcc agaggctgtg tggaaggctt cacctgggct    660
ctcatgacat tccctgcaag aggaggtgcc atcatcatct ccactgtgca gacaggaaac    720
atgagactga gaggcagagt accctgcctg gactgctcag ctagtgagca ggaagctctg    780
atttgatccc cagggttcgt tacaggaaca actgggccca agttcagagc tgtgaactga    840
gcagagctga gtcagaggga gtcctgatcc agggcccaca gatccaggct gctcagcctc    900
caggggccca gctgtgggca ggggaggctg atgcttggac aggggacaga cagtggcacc    960
ctccccttcc ccaaatgggt gtttcagagc agggtttgcc c                       1001
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<210> 339
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-151-196 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-151-196.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-151-196.mis2, potential complement

<220>
<221> primer_bind
<222> 306..323
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 805..823
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-151-196 potential probe

<400> 339

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cagagggccc cttgggagag gctgcagtga cctagtgccc tgggctgggt cagggaggga    120
gagggtggga ttgtggttgg cagagctcca ggctttgtgg ggcctgtggc ttctgtagcg    180
gtgagagccc tttttaagaa aaaagataca tagttatgaa ccccacattg gctaggaaaa    240
tgaatattta ctttgagaaa atcaagtgct gcaaaatcat aaatttttgca aagcttgaca    300
agtaccgcaa cccttaaaat gtctagaacg acgtagtgtt tttactgatt gaccatctga    360
cacagcctga tgagacttaa ttgtctacac tttttggctc catgctgttt gactgtcttg    420
tcctcaggat ggctgtggca ggaggatgat ggagtcaggg tctggggcgc agggatgggc    480
gtctggtgca gggagagaag ygggctgggc aggaggaccc tggtcctggg cacctggatg    540
gaggtgggga tgaaggctca gcaaaatgag gcaggggcca agtccaacac tcagtaacat    600
gtgaggccag aggctgtgtg gaaggcttca cctgggctct catgacattc cctgcaagag    660
gaggtgccat catcatctcc actgtgcaga caggaaacat gagactgaga ggcagagtac    720
cctgcctgga ctgctcagct agtgagcagg aagctctgat ttgatcccca gggttcgtta    780
caggaacaac tgggcccaag ttcagagctg tgaactgagc agagctgagt cagagggagt    840
cctgatccag ggcccacaga tccaggctgc tcagcctcca ggggcccagc tgtgggcagg    900
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ggaggctgat gcttggacag gggacagaca gtggcaccct ccccttcccc aaatgggtgt 960
ttcagagcag ggtttgccct atcaagttgt cctttacact g 1001

<210> 340
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-151-270 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-151-270.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-151-270.mis2, potential complement

<220>
<221> primer_bind
<222> 232..249
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 731..749
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-151-270 potential probe

<400> 340
ggagaggctg cagtgaccta gtgccctggg ctgggtcagg gagggagagg gtgggattgt 60
ggttggcaga gctccaggct ttgtggggcc tgtggcttct gtagcggtga gagccctttt 120
taagaaaaaa gatacatagt tatgaacccc acattggcta ggaaaatgaa tatttacttt 180
gagaaaatca agtgctgcaa aatcataaat tttgcaaagc ttgacaagta ccgcaacccct 240
taaaatgtct agaacgacgt agtgttttta ctgattgacc atctgacaca gcctgatgag 300
acttaattgt ctacactttt tggctccatg ctgtttgact gtcttgtcct caggatggct 360
gtggcaggag gatgatggag tcagggtctg gggcgcaggg atgggcgtct ggtgcaggga 420
gagaagtggg ctgggcagga ggaccctggt cctgggcacc tggatggagg tggggatgaa 480
ggctcagcaa aatgaggcag rggccaagtc caacactcag taacatgtga ggccagaggc 540
tgtgtggaag gcttcacctg ggctctcatg acattccctg caagaggagg tgccatcatc 600
atctccactg tgcagacagg aaacatgaga ctgagaggca gagtaccctg cctggactgc 660
tcagctagtg agcaggaagc tctgatttga tcccccagggt tcgttacagg aacaactggg 720
cccaagttca gagctgtgaa ctgagcagag ctgagtcaga gggagtcctg atccagggcc 780
cacagatcca ggctgctcag cctccagggg cccagctgtg ggcaggggag gctgatgctt 840
ggacagggga cagacagtgg caccctcccc ttccccaaat gggtgtttca gagcagggtt 900
tgccctatca agttgtcctt tacactgccc ctgggcagcc ccaggtgtgc atgagagcac 960
agaggtgtga gccccacggt ctcctgtccc tcagatccac c 1001

<210> 341
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>

<221> allele
<222> 501
<223> 12-152-453 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-152-453.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-152-453.mis2, potential complement

<220>
<221> primer_bind
<222> 50..68
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 553..572
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-152-453 potential probe

<220>
<221> misc_feature
<222> 260
<223> n=a, g, c or t

<400> 341
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gccacggctc tgggcaggag gcttagggaa ttgggggctc ccaagtgttt aaaggggatg     60
agtgggagcc ggggggatgt cagatatttt gacactgtgt caggaacccg acatctgtgc    120
cctgcgaggg aggggcgtgg agcctggcac ccgtgggact catgggaatg aacactgccc    180
ttccgggtgg aagggaccag gtgctggtcc ctcggaggct gcagtgaggc tgtggccttt    240
gcattagttt gttagggttn gctgtaacaa agaaccacac atgcgtagct tgaagcaaca    300
gagatgtatt ctctgtacgt cctggaggtc aggagtccaa actcagggtg tcggcagggc    360
tgtgctcctt ctgaaggctc taaggaagca agctctcttg cctcttccag cttctggtgg    420
ccccacatgt tctgtgactg tggcagcatc actccaattt ctcccttcct cattgcgtgg    480
cctttccctg tgtgtccctc ygtgtcctct tcttacaagg acacctaccc aaaatccagg    540
atgatctcac ttcgaaatcc tgaactaatt ccatcacaaa gaccctattt ccaaataagg    600
tcacattatc agattctggg cgagcctgaa ttttggaagg acaccggtca actcaaggca    660
gccttggtag aggggtgaga tgtgtgagat ggagccgttg cagtgttccg cgtggagctg    720
tggatggggc tggtgcccat gtaaagggat cactcatcta taaggagggt gtgggtctca    780
gctcttaaag caaggagtgg aaagggatgt gactgattta ggagccatct gtagatcatt    840
ctggctaaat aatgggattc acttttaagt gaaggaggcc ttgaatgcca cactcagggg    900
cctagcgcag cacttcccaa gccttgctgt ggttaggaac aacctggggg ctgggtgaaa    960
tgcaggcttg gattcagcag gaccggggta gggcctgaga g                       1001
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<210> 342
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-153-116 : polymorphic base C or T

<220>
<221> misc_binding
<222> 482..500
<223> 12-153-116.mis1

<220>
<221> misc_binding
<222> 502..520
<223> 12-153-116.mis2, complement

<220>
<221> primer_bind
<222> 386..405
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 867..887
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-153-116 potential probe

<400> 342
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cccttgaccc cgtctctgtc cttgaaggag agggacccag acaccccega gtgctcagtt 180
ctcacacaca caggcacgca gagtaaaaat gaaggtgctg tggggggttg gaagggcagg 240
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ggcttggttc tgcttccagc ccctctggcg ccaagtgcat tcccctgttg ctgttggtag 360
ccatggagac cttctgtgag acggtgcagt tttatctgaa gcacctggag gagagcgtgt 420
accccgtgat gactgaggag gagtttgccc tgaaggtgtt ccccatgtat cgctacttcg 480
tgacagtgtg gctgaggcac yacaaccccg aggtgagatg cacccctctt aggagggcct 540
ggtggtcccc aggccacagc tccccagcct gtggggccgg gaggtgctga gggaccgtcg 600
ggtccacact tactcccagg accctagagg gcagtgacct gactcatggc agagccgggg 660
aactcatgga tgctgaacag ctgggaccta ggagcctcat ccacgaggcc aggcttgatg 720
aaggttggtg ataatcctga gagcacttgt tacatgctgg gcactctacc agcgtcttac 780
ccatgggagc tattttcaca cccactctgt gatataggac tagttgacaa atgaggaaac 840
tcaggcacag aggggttaag tacctgctca aggtcatgtg gctgctaagt gggagggact 900
caaacccggc cgcctgtgca ggaaagacct tgctctgctt ctgaggcgcc ttctgtcctg 960
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<210> 343
<211> 1000
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-154-480 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-154-480.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-154-480.mis2, potential complement

<220>
<221> primer_bind
<222> 23..43
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 522..540
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-154-480 potential probe

<400> 343
ccatggagat gcagtgcagc atcttcaagt ctctaattct tacatctgtc tctttcactt 60
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aaacccttaa tataatcaca tctataaagt ctcttccacc tgtaatggaa tatattccca 180
ggtttgcgca actacaatgt agatactttg tggggctgtg attctgccta ccacagacac 240
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acaatacttt caaagagcaa aaattttaga atttgatgag gtttattcta gtgaagtttt 480
tatcgtttgt actttttgta ycctaaggaa gctttgttta ccccaagata tagtttctac 540
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ggggagctag atcactcagg tcaggctttc gggatgcctt tttctgtctc tggacgttgc 660
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tatctgtgca gcccagaccc ctcctcatct ccagaccctg gaagctgatg ccttgggcag 780
ctcctcctat ttcccaggca ccaggaatgt gagcttctcc ctcccccacag tcctgctgtc 840
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<210> 344
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-155-403 : polymorphic base A or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-155-403.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-155-403.mis2, potential complement

<220>
<221> primer_bind
<222> 99..116
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 628..647

<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-155-403 potential probe

<220>
<221> misc_feature
<222> 49,58,62,639
<223> n=a, g, c or t

<400> 344
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tcttggtcct aaaaaatgaa gagtgtttgg gtgtggggag gagcttcagt gtgcatgtgc     180
atgcaaagta cctactctaa ggagaagaat gagagggtac cctaattacc tgttaatatg     240
tcccatagga caccaaaact ctagttagct gtttctctat gatcctctaa gcacatcccc     300
aagtatggct ggccagtgat gtgtatggtt caaatgttgg gatctgtgca gttatcttgg     360
aattgtatag tacagcagta tatccccccc aaaaagagtg taatacttcc aattctggct     420
gcacaatact tgccccatag tccatggtca ataaatacaa atttgagttg tttttgctca     480
tctttccctt ttgacttcaa mtcagtcatc agaatttccc caaatgcctt tcccctggat     540
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ctgttgtgaa caaaagttct ctgaaaagga atttggaana aagagacttt gttctagtga     660
acagtttgca aaccagggag ttacagcctc tggtacgcaa tgaaggtgag ttccacagaa     720
cacaaggcag gcaggtttca cggcaaaaag ttccttccca ggttcccaat caggtccatt     780
tatgcaaatg aaggatggaa acttgcttag ttcttattgg tcactgcagc tgcattctga     840
ttggttgatg aagctgagcc ctgagtggct gaggtgggtg agctttaatt ggttggttca     900
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<210> 345
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-156-91 : polymorphic base A or G

<220>
<221> misc_binding
<222> 482..500
<223> 12-156-91.mis1

<220>
<221> misc_binding
<222> 502..520
<223> 12-156-91.mis2, complement

<220>
<221> primer_bind
<222> 412..429
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 844..862
<223> downstream amplification primer, complement

<220>
<221> misc_binding

<222> 489..513
<223> 12-156-91 potential probe

<400> 345
cagctgtccg tgtcttctgc tgagatggcc acaggactcc aggttcccct gccgtggctg 60
gccacaggac tgctgcttct cctcagtgtc cagccctggg ctgagagtgg aaaggtgttg 120
gtggtgccca ttgatggcag ccactggctc agcatgcggg aggtcttgcg ggagctccat 180
gccagaggcc accaggcagt ggtcctcacc ccagaggtga atatgcacat caaagaagag 240
aactttttca ccctgacaac ctatgccatt tcgtggaccc aggatgaatt tgatcgccat 300
gtgctgggcc acactcaact gtactttgaa acagaacatt ttctgaagaa atttttcaga 360
agtatggcaa tgttgaacaa tatgtctttg gtctatcata ggtcttgtgt ggagctacta 420
cataatgagg ccctgatcag gcacctgaat gctacttcct ttgatgtggt tttaacagac 480
cccgttaacc tctgcgcggc rgtgctggct aagtacctgt cgattcctac tgtgtttttt 540
ttgaggaaca ttccatgtga tttagacttt aagggcacac agtgtccaaa cccttcctcc 600
tatattccta gattactaac aaccaattca gaccacatga cattcatgca aagggtcaag 660
aacatgctct accctctggc cctgtcctac atttgccatg ctttttctgc tccttatgca 720
agccttgcct ctgagctttt tcagagagag gtgtcagtgg tggatattct cagtcatgca 780
tctgtgtggc tgttccgagg ggactttgtg atggactacc ccaggccaat catgcccaac 840
atggtcttca ttgggggcat caactgtgcc aacaggaagc cactatctca ggtctgtatt 900
ggtgccttca tccaatcaat gttccaggca aaacactttt taaaaaaatg tatttattta 960
aaattgcttc catatttact tatctttcca aatatttcat t 1001

<210> 346
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-157-437 : polymorphic base A or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-157-437.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-157-437.mis2, potential complement

<220>
<221> primer_bind
<222> 67..87
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 513..533
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-157-437 potential probe

<400> 346
tcttttctat aattctcagc cagatttcaa gttgggtgct tctccttgga tttatggcac 60
atgggtgggc tgctcttcca ttgattgggg atattttgag caaaataaca gtgataacac 120
tgaagagcat tgcaagcatc cttcaagatg agtcaggctc agtgagtgag ttgaaggggct 180
cagtcaacta tttgttgata ccactggtac aaaatgatct aaagcccaag acttaccttc 240
ctggagatgc caatccattg gtggggaggg ggaaagggga agaagttatg gatttataaa 300

attagtattt aaagagtttg ggtcatctct aagaatacct cccctatagg ggaagattca 360
ttacttaggc gcatagcaga actatctgtt actttaagct gcatcaaaca ggcagatttt 420
aaaataaatg tcatgaacat caactaagca caatgatatg ctgagtactg aagggacaca 480
gagatacata agacctagtc mcagcctttt aaggacttag agataagaca gacacataca 540
aacaggatta taggtcaaag ctgactaaca ggactgtgtt tacaggtaaa cccacacaca 600
catcagcaaa aaaatatctg agaacaaaaa aaaagggct actaacaaaa gcaactcagt 660
ttatacaaaa ggagctatca agaggcttgg tgcaaagttg gcatttggct tttgacctgg 720
gcttaggcag aacgactgga cttggcgctt cctaggagag tgtaatacaa gacactttgg 780
gggagcagga gtttaaagca ggatggtggc tctcaactct aggggcacaa tagaactcat 840
ggggaacttt taacagtatg gatatccagg tcccacccca gatcctgggg cttggacgtg 900
gtccctgggg gtccttaaaa aatcctcgag gtatctttaa tatgcatcaa gcttgagaat 960
tgttgatgaa ggagctagaa gaagaatgag ctagcatgca c 1001

<210> 347
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-158-213 : polymorphic base T or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-158-213.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-158-213.mis2, potential complement

<220>
<221> primer_bind
<222> 691..710
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 230..247
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-158-213 potential probe

<400> 347
ttttctgtct ctggacgttg ctggggtgac ctcactgaca cccatggctt cagctaccac 60
atatgctgat ggctccaagt ctatctgtgc agcccagacc cctcctcatc tccagaccct 120
ggaagctgat gccttgggca gctcctccta tttcccaggc accaggaatg tgagcttctc 180
cctccccaca gtcctgctgt cctcagggcc cctatgtctc tgaaggcacc accatcttcc 240
aagatacatg ggcctccgca gggtctagga gtgccagaca cgtaaccaga aatcagatga 300
catcactatc taaataaaac accactacat ggaaatagaa caccactaca tggaaataga 360
acatgggagc cccttgaatg tggcaagagc accctcccag gcatgttcca ccctcacccc 420
gggctcatca ggagggttct taagatgcag acagttttaa gggggttgga ggaatagttg 480
agaagctgag atgttgcacc yacagctgag aatccctttc tagcactctg tgtcctcaca 540
aatccccaga aatcgtcctc ccctggggag ttctcaagcc cttacagacc tgccctctct 600
gtgccatcct gcatatgcct ccccttgagct gggtgtccct ctgatggacg catccattca 660
ctgcctgtcc catgggttgt gtccaaaggt ggaatctgtt atcaatgtgg atttctaatg 720
ggagtaactt cctccataag ggaagcctca gcctcaccag caatggcaga catggccagg 780
catgtagaca cagaggtagt gagatggaaa gtgggcacag cccagagagc ctgcccacct 840

catcctgggg cgaccaggac aaggaagcat cagcaatctt gcgagcacat gtaggagtga 900
ctttctggag caggacgagc ctcatgggca tgagaccatt gtgagtgctc agggtctccc 960
cctagaaagg cacacattta attctccatt ttgaaatttg a 1001

<210> 348
<211> 980
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 480
<223> 12-158-450 : polymorphic base T or G

<220>
<221> misc_binding
<222> 460..479
<223> 12-158-450.mis1, potential

<220>
<221> misc_binding
<222> 481..500
<223> 12-158-450.mis2, potential complement

<220>
<221> primer_bind
<222> 907..926
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 446..463
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 468..492
<223> 12-158-450 potential probe

<400> 348
atactttcaa agagcaaaaa ttttagaatt tgatgaggtt tattctagtg aagtttttat 60
cgtttgtact ttttgtaccc taaggaagct ttgtttaccc caagatatag tttctacatt 120
ctcttaaaaa cactaaagag ttccagttta tatgtttagc tctgtgagat tgggagaggg 180
gagctagatc actcaggtca ggctttcggg atgccttttt ctgtctctgg acgttgctgg 240
ggtgacctca ctgacaccca tggcttcagc taccacatat gctgatggct ccaagtctat 300
ctgtgcagcc cagacccctc ctcatctcca gaccctggaa gctgatgcct tgggcagctc 360
ctcctatttc ccaggcacca ggaatgtgag cttctccctc cccacagtcc tgctgtcctc 420
agggccccta tgtctctgaa ggcaccacca tcttccaaga tacatgggcc tccgcagggk 480
ctaggagtgc cagacacgta accagaaatc agatgacatc actatctaaa taaaacacca 540
ctacatggaa atagaacacc actacatgga aatagaacat gggagcccct tgaatgtggc 600
aagagcaccc tcccaggcat gttccaccct caccccgggc tcatcaggag ggttcttaag 660
atgcagacag ttttaagggg gttggaggaa tagttgagaa gctgagatgt tgcacccaca 720
gctgagaatc cctttctagc actctgtgtc ctcacaaatc cccagaaatc gtcctcccct 780
ggggagttct caagccctta cagacctgcc ctctctgtgc catcctgcat atgcctccct 840
tgagctgggt gtccctctga tggacgcatc cattcactgc ctgtcccatg ggttgtgtcc 900
aaaggtggaa tctgttatca atgtggattt ctaatgggag taacttcctc cataagggaa 960
gcctcagcct caccagcaat 980

<210> 349
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-161-157 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-161-157.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-161-157.mis2, potential complement

<220>
<221> primer_bind
<222> 345..363
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 729..749
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-161-157 potential probe

<400> 349
cagtcatgtg gaactgtgag tcaattaaac ctctttcttt tataaattac ccagtctcag 60
ctgcgtcttt atagcaggct gagaatagac taatacaaga ttggtggtga ttgaagttat 120
actgaaaggg tttaaaggag agtctgagaa aaggaaatga atctgcattt attgagaaag 180
ttgatgagaa agtggaatta gaaattccta gaaaggtaag ttgttgtgtg aattatttcc 240
caaaatgggg aagtctctct acctgtttgg agacagaaag tggaatcaga ggagaagaag 300
atgatggaca gaaaggatca ttccctcttc cagatgcttt ccagtgtgtg atgtaagctg 360
aactaaaatc agctgtgttg aactccagcc agaaaaaatg tccggcattt tgttttttgg 420
gaccctaatg aaatggttac aggtctccag gtctcttggg gctcacaggg tcatgccttt 480
ccttgcccag tgtacttggt ragaaggtac aggtgtttcc atggagggtg ttcattttag 540
ggatttcaag agggtcatct ttgcaccaca ggaaatgccc ccttttacac tctgaaaacc 600
ttatcaaacc gttgtataaa agatgaatac ccacataaca ggctctagca ctgttctgtt 660
tttgagctga gacattttaa aaggagattt ttcaattcta aaaattcttt aaataaaatg 720
ctcttgcagg gacaacatag taggtcaaca ttgttcccat ctccacaaaa agttttttttt 780
ttaattagct aggtgtggta gcatttctgt agtcctagct actgggaatg ctgaggagga 840
aggatcactt gagcccagga attcgtggtt acagtaagct atgatcttgc ctaggtaaca 900
gctacagagc gagaccctgt ctttaaaaca aacaagcaaa cagacaatca agctttacac 960
ttctataaaa gcaacacttt ccatttatga cagcactaat c 1001

<210> 350
<211> 998
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 498
<223> 12-162-21 : polymorphic base A or G

<220>
<221> misc_binding
<222> 478..497
<223> 12-162-21.mis1, potential

<220>
<221> misc_binding
<222> 499..518
<223> 12-162-21.mis2, potential complement

<220>
<221> primer_bind
<222> 478..497
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 909..927
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 486..510
<223> 12-162-21 potential probe

<400> 350
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agctgatgcc ttgggctgct cctcctattt cctgggcacc aggaatatga gctactccct     60
ccccacagtc ctgctctccc cagtgctccc atgtcgctga aggcaccacc atcttccaag    120
atacatgggc ctccccaggg tctaggagtc ctagacgtgg gagtagaaat tagatgacat    180
tggtgtctaa acaaaacacc actgcatgga gatagaacag gggagccccc tgaatgtggt    240
gagagcaccc tcccaggtgt gttccaccct caccccgggc tcatcaggag ggtgcttagg    300
atgcatacag ttttaagggg gttggaggaa tagttcagag gctgagatgt tgcacccaca    360
gctgagaatc cctttctagc gctctgtgtc ctcacaactc cccgggaatc atcctcccct    420
ggagagttcc caaagccctt gcaggcctgc cttctctgtg ccttcctgcc tgcgccctct    480
ggtggacagc tccattcrct gcctgtccca tgggttctgt ccaaaggtgg aatctattat    540
caatgtggat ttctaatggg ggtaacttcc tccctaaggg aagcctcagc ttcaccagca    600
atggcagaca cggccaggca tgtagacaca gaggaagtga gatagaaagt gtgcacagcc    660
cagagagcct gcccacatca tcctggggcg accaggacaa ggaggcgtca gcaatcttgc    720
caagcacaag tatgagtgac tttctggagc aggacgagtc tcatggcgt gagaccattg     780
tgagtgctca gggtctctcc attagaaagg cacacgttta attctccatt ttgaaatttg    840
aactagagcc cccacaaatt attctgttct ggaggaacca ttcttatcag aacttggtgc    900
tggattgact tggaaaaaag cctgaccata atcttcagga tgaaataaag gcctggatga    960
atggacactt cagtctctaa gcagacttgc agaagact                            998
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<210> 351
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 10-470-25 : polymorphic base A or T

<220>
<221> misc_binding
<222> 484..502
<223> 10-470-25.mis1

<220>
<221> misc_binding
<222> 504..523
<223> 10-470-25.mis2, potential complement

<220>
<221> primer_bind
<222> 479..498

<223> upstream amplification primer

<220>
<221> primer_bind
<222> 880..899
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 10-470-25 potential probe

<220>
<221> misc_feature
<222> 271,364,831,842
<223> n=a, g, c or t

<400> 351
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ccttttacag ctacttttt ttctcttttg aaaaaagact ggaaaactct gacaaacttt       60
aagtgaagtg taaaggatta tagaataaga taaatgtagg tttacgtaat cccagctgtg     120
agtaactttt cctcagtgct cagagtcagg gaagtcaacc actaatgact tcaaactaaa     180
ataattctgt agaaaacctg cctaaaataa gcatatgtga tttagcgagc aacaatatag     240
cattaaagcc aactggtgcc actttaaaga ncctatatta gtacttataa tatgataagt     300
gaagagtttg ggtatctcct caaatactgt gtaataactc tatttcattt ctccctttca     360
caancgcaca cacatacaca cacacatatt tacacaaaga cccttaacag aggcaaccta     420
tctcatatta tacatattgc aaaaaaaaac tgagtaattg agtcagttaa aaaacatcct     480
ttactccaat aattcctgat aawacttgat tttctctctt tttataacaa ttctttcaca     540
gtgcttgctg tgctgataat ctattatgat agaacaaatt ctttttttc acaggaaatg      600
gaagagtttg tccagagctc tggagaaaat ggtgttgtgg tgttttctct ggggtcgatg     660
gtcagtaaca cgtcagaaga aagggccaat gtaattgcat cagcccttgc caagatccca     720
caaaaaggta agataaaatg ttttaatggt gtaaaaaact actgaaagag gctgttaaag     780
tttgtaaaga acccaaattg tagaaacttc ctgcctatat atttcagctg ntgggaaaag     840
cnctaattat ctcagatatt aattcaaaat caaaaatatg tatggaagat gataaactca     900
tacagaaggt gtttttcatt ggtaattaat ttggcattaa tattgtgatc aggaataaat     960
acaattaaga gttgcaggta aagttttggt attatcatga t                        1001
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<210> 352
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 10-471-84 : polymorphic base A or T

<220>
<221> misc_binding
<222> 484..502
<223> 10-471-84.mis1

<220>
<221> misc_binding
<222> 504..523
<223> 10-471-84.mis2, potential complement

<220>
<221> primer_bind
<222> 420..439
<223> upstream amplification primer

<220>
<221> primer_bind

<222> 788..807
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 10-471-84 potential probe

<400> 352
atttactttg aatgatctgg cactttaaaa acctttcgtg gacttgatgt gctcaggcaa 60
attaacttac cttctctttt tttgagaggg aagtctcact ctgtcaccag gctggagtgc 120
agtggtgtga ttgtggctca ctgcaacttc cgcctcttgg gttcaagcga ttctcctgcc 180
tcagcctctc aagtagctgg gactacaggc acatgccacc acgcctgggt aatctttttt 240
tttttttttt tttttttca tatttttact ggagacgggg tgacggggtt tcaccgtgtt 300
agccaggatg gtcttgatct cctgacctcg tgatccgccc gcctcgacct cggaaagtgc 360
tgggattgca ggtgtgagcc tccgtgcttg gccaaattaa cttactttca atgttgatac 420
ttttctgctt atcgtttaga tataaagaga atgctatgaa attatcaaga attcatcatg 480
atcaaccagt gaagcccctt gawagagcag tcttctggat tgaatttgtc atgcgccata 540
aaggagccaa gcaccttcgg gttgcagccc acgacctcac ctggttccag taccactctt 600
tggatgtgac tgggttcctg ctggcctgtg tggcaactgt gatattcatc atcacaaaat 660
gtctgttttg tgtctggaag tttgttagaa caggaaagaa ggggaaaaga gattaattac 720
gtctgaggct ggaagctggg aaacccaata aatgaactcc tttagtttat tacaacaaga 780
agacgttgtg atacaagaga ttcctttctt cttgtgacaa aacatctttc aaaacttacc 840
ttgtcaagtc aaaatttgtt ttagtacctg tttaaccatt agaaatattt catgtcaagg 900
aggaaaacat tagggaaaac aaaaatgata taaagccata tgaggttata ttgaaatgta 960
ttgagcttat attgaaattt attgttccaa ttcacaggtt a 1001

<210> 353
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 10-471-85 : polymorphic base A or C

<220>
<221> misc_binding
<222> 483..502
<223> 10-471-85.mis1, potential

<220>
<221> misc_binding
<222> 505..523
<223> 10-471-85.mis2, complement

<220>
<221> primer_bind
<222> 420..439
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 788..807
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 10-471-85 potential probe

<400> 353

atttactttg aatgatctgg cactttaaaa acctttcgtg gacttgatgt gctcaggcaa 60
attaacttac cttctctttt tttgagaggg aagtctcact ctgtcaccag gctggagtgc 120
agtggtgtga ttgtggctca ctgcaacttc cgcctcttgg gttcaagcga ttctcctgcc 180
tcagcctctc aagtagctgg gactacaggc acatgccacc acgcctgggt aatctttttt 240
tttttttttt ttttttttca tatttttact ggagacgggg tgacggggtt tcaccgtgtt 300
agccaggatg gtcttgatct cctgacctcg tgatccgccc gcctcgacct cggaaagtgc 360
tgggattgca ggtgtgagcc tccgtgcttg gccaaattaa cttactttca atgttgatac 420
ttttctgctt atcgtttaga tataaagaga atgctatgaa attatcaaga attcatcatg 480
atcaaccagt gaagcccctt gamagagcag tcttctggat tgaatttgtc atgcgccata 540
aaggagccaa gcaccttcgg gttgcagccc acgacctcac ctggttccag taccactctt 600
tggatgtgac tgggttcctg ctggcctgtg tggcaactgt gatattcatc atcacaaaat 660
gtctgttttg tgtctggaag tttgttagaa caggaaagaa ggggaaaaga gattaattac 720
gtctgaggct ggaagctggg aaacccaata aatgaactcc tttagtttat tacaacaaga 780
agacgttgtg atacaagaga ttcctttctt cttgtgacaa aacatctttc aaaacttacc 840
ttgtcaagtc aaaatttgtt ttagtacctg tttaaccatt agaaatattt catgtcaagg 900
aggaaaacat tagggaaaac aaaaatgata taaagccata tgaggttata ttgaaatgta 960
ttgagcttat attgaaattt attgttccaa ttcacaggtt a 1001

<210> 354
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 10-472-202 : polymorphic base C or T

<220>
<221> misc_binding
<222> 484..502
<223> 10-472-202.mis1

<220>
<221> misc_binding
<222> 525..543
<223> 10-472-202.mis2, complement

<220>
<221> primer_bind
<222> 304..322
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 714..732
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 10-472-202 potential probe

<400> 354
gatataaaga gaatgctatg aaattatcaa gaattcatca tgatcaacca gtgaagcccc 60
ttgaaagagc agtcttctgg attgaatttg tcatgcgcca taaaggagcc aagcaccttc 120
gggttgcagc ccacgacctc acctggttcc agtaccactc tttggatgtg actgggttcc 180
tgctggcctg tgtggcaact gtgatattca tcatcacaaa atgtctgttt tgtgtctgga 240
agtttgttag aacaggaaag aaggggaaaa gagattaatt acgtctgagg ctggaagctg 300
ggaaacccaa taaatgaact cctttagttt attacaacaa gaagacgttg tgatacaaga 360
gattcctttc ttcttgtgac aaaacatctt tcaaaactta ccttgtcaag tcaaaatttg 420
ttttagtacc tgtttaacca ttagaaatat ttcatgtcaa ggaggaaaac attagggaaa 480
acaaaaatga tataaagcca taygaggtta tattgaaatg tattgagctt atattgaaat 540

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ttattgttcc aattcacagg ttacatgaaa aaaaatttac taagcttaac tacatgtcac    600
acattgtaca tggaaacaag aacattaaga agtccactga cagtatcagt actgttttgc    660
aaatactcag catactttgg atccatttca tgcaggattg tgttgtttta actgttgttg    720
aggaagctaa taaataatta aattgtatag aaagtctctt cctcttgata ttttgagatg    780
attagtgctg cttggctttt attgtgcatc gtgcttcaac gtcatttttt ttcctaaaag    840
gtatgataaa aatgcttacc attttagagc ttaagtcatt tcccagtgaa aagtatgtgg    900
aattagaaat atagcaactc ctacctggtt tctactacaa aatgaactaa ttttacaatg    960
cgtttggttt tttgagccaa ttctattttt ctgttcattt g                       1001
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<210> 355
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 10-473-333 : polymorphic base C or T

<220>
<221> misc_binding
<222> 483..502
<223> 10-473-333.mis1, potential

<220>
<221> misc_binding
<222> 504..523
<223> 10-473-333.mis2, potential complement

<220>
<221> primer_bind
<222> 171..189
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 582..600
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 10-473-333 potential probe

<220>
<221> misc_feature
<222> 887
<223> n=a, g, c or t

<400> 355

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gaagctggga aacccaataa atgaactcct ttagtttatt acaacaagaa gacgttgtga     60
tacaagagat tcctttcttc ttgtgacaaa acatctttca aaacttacct tgtcaagtca    120
aaatttgttt tagtacctgt ttaaccatta gaaatatttc atgtcaagga ggaaaacatt    180
agggaaaaca aaaatgatat aaagccatat gaggttatat tgaaatgtat tgagcttata    240
ttgaaattta ttgttccaat tcacaggtta catgaaaaaa aatttactaa gcttaactac    300
atgtcacaca ttgtacatgg aaacaagaac attaagaagt ccactgacag tatcagtact    360
gttttgcaaa tactcagcat actttggatc catttcatgc aggattgtgt tgttttaact    420
gttgttgagg aagctaataa ataattaaat tgtatagaaa gtctcttcct cttgatattt    480
tgagatgatt agtgctgctt ggytttttatt gtgcatcgtg cttcaacgtc atttttttc    540
ctaaaaggta tgataaaaat gcttaccatt ttagagctta agtcatttcc cagtgaaaag    600
tatgtggaat tagaaatata gcaactccta cctggtttct actacaaaat gaactaattt    660
tacaatgcgt ttggtttttt gagccaattc tatttttctg ttcatttgaa aatattcatc    720
ttttttatt ctttgttttt taggtatttc aatagctttt gggtgacaac tggtttttgg    780
```

ttacatggat aagctcttta gtggtgattt ttcagatttt ggtgcactca ttactcaaga 840
agtatacact gtacccagtg tgtactgttt tatccctcac atccctncct acccttccct 900
ctgagttcca agagtccatt atatcattct tatgcctcta tgtcctaata gcttaggtcc 960
cccttataag tgagaacata cattgtttgg ttttatattt c 1001

<210> 356
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 10-494-284 : polymorphic base C or T

<220>
<221> misc_binding
<222> 483..502
<223> 10-494-284.mis1, potential

<220>
<221> misc_binding
<222> 504..523
<223> 10-494-284.mis2, potential complement

<220>
<221> primer_bind
<222> 220..238
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 624..641
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 10-494-284 potential probe

<400> 356
ctggtgtgag atggtatctc tttgtggatt tgaccagtga tgtaaacctt tttttcatat 60
agtggtttgc cacatatagt tttcttttga aaagtgtaac aactttttaa atacttgaac 120
ttttcattga ttatcttatt tgtctaagct actattttga aaaatcatga tttccttata 180
tacctaatta tgaaattaag gaaatgaaat atgagtattc tatttacatc agtctgagta 240
gttcttgtta cttaacatcc cttgttcttc tcattgttaa tctctttaga tttctaacat 300
tctatgactt ttgagttcca ctcatggaat aagatatttt cttcactgta acaggttctg 360
tggagatttg atgggaataa accagatact ttaggactca atactcggct gtacaagtgg 420
ataccccaga atgatcttct tggtaagtct ctgaagaaca aatactgaat atattagtaa 480
cagattatta aagtgttaat agytatcatg aaacaagctt actgaacatt tgttatggaa 540
aaacttaaaa tgaaacttct ttatatttat tttccagtcc cgggggaaaa gaataaatga 600
taattgttgg cattttatga tatgcaccca cattctttac aatcagagtc agagtatctt 660
tatttcaggt gttattacct cccacagaat ttttctggca cttcctgggt tgtcttcctt 720
tctcatattt ctacaacttt acacctgttc tttcctcctc tgtagggtta tttcaaatgt 780
cactaaaagt aacagctctt ctgctatcac cagggatgct gcattttctg taggattaaa 840
tccctaatct taatcaaaaa gtgatgacac atttcataat gaaatgtgac ctgtctttcc 900
tcaattctag caccaccacc acctcactgc ctgctgcctt gcacacccta catatcacac 960
tccgtgactg tacttaagag aacacattct ggctgggcac g 1001

<210> 357
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 499
<223> 12-637-219 : polymorphic base G or A

<220>
<221> misc_binding
<222> 500..519
<223> 12-637-219.mis1, potential complement

<220>
<221> misc_binding
<222> 480..498
<223> 12-637-219.mis2

<220>
<221> primer_bind
<222> 698..717
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 230..250
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 487..511
<223> 12-637-219 potential probe

<220>
<221> misc_feature
<222> 953
<223> n=a, g, c or t

<400> 357
ttttgtgtct ggaagtttgt tagaacagga aagaagggga aaagagatta attacgtctg 60
aggctggaag ctgggaaacc caataaatga actcctttag tttattacaa caagaagacg 120
ttgtgataca agagattcct ttcttcttgt gacaaaacat ctttcaaaac ttaccttgtc 180
aagtcaaaat ttgttttagt acctgtttaa ccattagaaa tatttcatgt caaggaggaa 240
aacattaggg aaaacaaaaa tgatataaag ccatatgagg ttatattgaa atgtattgag 300
cttatattga aatttattgt tccaattcac aggttacatg aaaaaaaatt tactaagctt 360
aactacatgt cacacattgt acatggaaac aagaacatta agaagtccac tgacagtatc 420
agtactgttt tgcaaatact cagcatactt tggatccatt tcatgcagga ttgtgttgtt 480
ttaactgttg ttgaggaarc taataaataa ttaaattgta tagaaagtct cttcctcttg 540
atattttgag atgattagtg ctgcttggct tttattgtgc atcgtgcttc aacgtcattt 600
tttttcctaa aaggtatgat aaaaatgctt accattttag agcttaagtc atttcccagt 660
gaaaagtatg tggaattaga aatatagcaa ctcctacctg gtttctacta caaaatgaac 720
taattttaca atgcgtttgg ttttttgagc caattctatt tttctgttca tttgaaaata 780
ttcatctttt tttattcttt gttttttagg tatttcaata gcttttgggt gacaactggt 840
ttttggttac atggataagc tctttagtgg tgatttttca gattttggtg cactcattac 900
tcaagaagta tacactgtac ccagtgtgta ctgttttatc cctcacatcc ctncctaccc 960
ttccctctga gttccaagag tccattatat cattcttatg c 1001

<210> 358
<211> 668
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 499

<223> 12-639-95 : polymorphic base G or A

<220>
<221> misc_binding
<222> 500..519
<223> 12-639-95.mis1, potential complement

<220>
<221> misc_binding
<222> 480..498
<223> 12-639-95.mis2

<220>
<221> primer_bind
<222> 573..593
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 144..164
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 487..511
<223> 12-639-95 potential probe

<220>
<221> misc_feature
<222> 57,198,240,552,616,630
<223> n=a, g, c or t

<400> 358
aataaacaag ggacctttgt gtatttgtga attacttttt aatttcctat ctgatanaag 60
ctttcttgta atgacctcta actttttgct gaaacctgag ttactttaac actgatgtag 120
caaataaaag ttaaacactg taaattattg ttcagtttgt gaggattgct tcggagtttc 180
aaaattagta acttaaanat aaaaatgtct tggctatagc agaacatatt attcactgtn 240
tgtcaaatct ttgtagcacg ttgtctaagt gttaataatc agttgaccaa attccgcaaa 300
atacaatttt gagtttattc aatagctttt tttgtattca tgataccaac aggttcctca 360
tttctaggcc aaaaaaaaat ccaaaattaa caatactggt aatattctga atttgtgtca 420
aaaattgtca cttgaaattt ttcttggaag tagtgcttga taatttgtaa ttctaatgaa 480
gttatacata aaaccctarc agcatttatt tatttcttat aagtagctta ttttatagac 540
ttgctatttt gncaatcaaa ggacaacagg ctctaatata ataacctacc gacaaagtag 600
atacatttga acttcntctc ttattattcn aaaacaaatg aatacactgc aattaaattt 660
ggagatga 668

<210> 359
<211> 814
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 499
<223> 12-639-241 : polymorphic base T or G

<220>
<221> misc_binding
<222> 479..498
<223> 12-639-241.mis1, potential

<220>
<221> misc_binding

<222> 500..519
<223> 12-639-241.mis2, potential complement

<220>
<221> primer_bind
<222> 719..739
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 290..310
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 487..511
<223> 12-639-241 potential probe

<220>
<221> misc_feature
<222> 38,95,116,203,344,386,698,762,776
<223> n=a, g, c or t

<400> 359
taactaccag attaacaact cctcccaatg gaggcagnca gaaggaagta tagaaaggag 60
tcaaacagaa ggaagccaag tgggggaaca ggttncagat gtcccctcca tagaancata 120
gtaggaatat attttcttct atataaaata aacaagggac ctttgtgtat ttgtgaatta 180
ctttttaatt tcctatctga tanaagcttt cttgtaatga cctctaactt tttgctgaaa 240
cctgagttac tttaacactg atgtagcaaa taaaagttaa acactgtaaa ttattgttca 300
gtttgtgagg attgcttcgg agtttcaaaa ttagtaactt aaanataaaa atgtcttggc 360
tatagcagaa catattattc actgtntgtc aaatctttgt agcacgttgt ctaagtgtta 420
ataatcagtt gaccaaattc cgcaaaatac aattttgagt ttattcaata gctttttttg 480
tattcatgat accaacagkt tcctcatttc taggccaaaa aaaaatccaa aattaacaat 540
actggtaata ttctgaattt gtgtcaaaaa ttgtcacttg aaatttttct tggaagtagt 600
gcttgataat ttgtaattct aatgaagtta tacataaaac cctagcagca tttatttatt 660
tcttataagt agcttatttt atagacttgc tattttgnca atcaaaggac aacaggctct 720
aatataataa cctaccgaca aagtagatac atttgaactt cntctcttat tattcnaaaa 780
caaatgaata cactgcaatt aaatttggag atga 814

<210> 360
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 499
<223> 12-640-151 : polymorphic base G or A

<220>
<221> misc_binding
<222> 479..498
<223> 12-640-151.mis1, potential

<220>
<221> misc_binding
<222> 500..519
<223> 12-640-151.mis2, potential complement

<220>
<221> primer_bind
<222> 629..649
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 156..176
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 487..511
<223> 12-640-151 potential probe

<220>
<221> misc_feature
<222> 62
<223> n=a, g, c or t

<400> 360
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agaaatagca catcaattta acagtgtgat ttcagggcaa taggtgttcc acctaaacaa     60
tnaacctgaa aggtacaatt attcaacaac taactataaa ctctacaatt ccatgtgata    120
aatgagactc ccaagactga ttcataaaaa ttccaaatca caatactaga ctcaggaatg    180
tcagtgattc ttaaccacca gcttttattt tcattttttg aaaaactact ggaaaactct    240
gacaaacttt aagtgaagca taaagcattg tagaggaaca taaatgtaga tataaaatta    300
tcccaactgt gaatagcttt tcctcagtgc tcatatttag ggaagtagac cactaatggc    360
ttcaaactaa aagaattcta cagaaaacct gcctgaaata aacacaagtg atttagtaga    420
acaaaaatat aggattaaag cctagtggtg ccacttttcc aagaacttat attagtaatt    480
atagtattat aagtgaagrg tctgggtata ttttttcaca ttatctccct gactacaatg    540
taatagctcc atttcttttc tccattacac acatgcagac acatacatac atatacacac    600
atatttacac aaatatcctt aacagaggcc aactatctca aatatcttct tgcaaagaaa    660
ctgagtgatt gagtcagtta aaaaatatta tttactccaa taattcctca aaatacttga    720
ttttctctct ttaatatttg gtaccagttc tttagtagtg cctgctgtgg tgatactctt    780
ttgtgattaa acaatttttt tttcacagga aatggaggag tttgtacaga gctctggaga    840
aaatggtgtt gtggtgtttt ctctgcggtc aatcataagt aacatgacag cagaaagggc    900
caatgtaatt gcaacagccc tggccaagat cccacaaaag gtaagataaa gtaccttact    960
ggtgtggaaa actactgaaa gaggcttgag atccatatag a                       1001
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<210> 361
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 499
<223> 12-640-296 : polymorphic base T or G

<220>
<221> misc_binding
<222> 479..498
<223> 12-640-296.mis1, potential

<220>
<221> misc_binding
<222> 500..519
<223> 12-640-296.mis2, potential complement

<220>
<221> primer_bind
<222> 769..789
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 296..316

<223> downstream amplification primer

<220>
<221> misc_binding
<222> 487..511
<223> 12-640-296 potential probe

<220>
<221> misc_feature
<222> 1..4,6..8,12..22,25..28,30,32..37,39,41..44,47..50,202
<223> n=a, g, c or t

<400> 361
nnnntnnngt gnnnnnnnnn nnctnnnnan annnnnnana nnnnccnnnn gaagaaaggc 60
ctggtggcct cttctattct ggtgccagtg ctgcctctga gacacaacaa agtgatgatg 120
agagttcctc acatgcagtt agaaatagca catcaattta acagtgtgat ttcagggcaa 180
taggtgttcc acctaaacaa tnaacctgaa aggtacaatt attcaacaac taactataaa 240
ctctacaatt ccatgtgata aatgagactc ccaagactga ttcataaaaa ttccaaatca 300
caatactaga ctcaggaatg tcagtgattc ttaaccacca gcttttattt tcattttttg 360
aaaaactact ggaaaactct gacaaacttt aagtgaagca taaagcattg tagaggaaca 420
taaatgtaga tataaaatta tcccaactgt gaatagcttt tcctcagtgc tcatatttag 480
ggaagtagac cactaatgkc ttcaaactaa aagaattcta cagaaaacct gcctgaaata 540
aacacaagtg atttagtaga acaaaaatat aggattaaag cctagtggtg ccacttttcc 600
aagaacttat attagtaatt atagtattat aagtgaagag tctgggtata ttttttcaca 660
ttatctccct gactacaatg taatagctcc atttcttttc tccattacac acatgcagac 720
acatacatac atatacacac atatttacac aaatatcctt aacagaggcc aactatctca 780
aatatcttct tgcaaagaaa ctgagtgatt gagtcagtta aaaaatatta tttactccaa 840
taattcctca aaatacttga ttttctctct ttaatatttg gtaccagttc tttagtagtg 900
cctgctgtgg tgatactctt ttgtgattaa acaatttttt tttcacagga aatggaggag 960
tttgtacaga gctctggaga aaatggtgtt gtggtgtttt c 1001

<210> 362
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 499
<223> 12-640-325 : polymorphic base T or C

<220>
<221> misc_binding
<222> 500..518
<223> 12-640-325.mis1, complement

<220>
<221> misc_binding
<222> 479..498
<223> 12-640-325.mis2, potential

<220>
<221> primer_bind
<222> 797..817
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 324..344
<223> downstream amplification primer

<220>
<221> misc_binding

<222> 487..511
<223> 12-640-325 potential probe

<220>
<221> misc_feature
<222> 6,24..25,28..32,34..36,40..50,53..56,58,60..65,67,69..72,75..78
230
<223> n=a, g, c or t

<400> 362
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tgcagncaag cacatcttca ccannagnnn nntnnngtgn nnnnnnnnnn ctnnnnanan     60
nnnnnanann nnccnnnnga agaaaggcct ggtggcctct tctattctgg tgccagtgct    120
gcctctgaga cacaacaaag tgatgatgag agttcctcac atgcagttag aaatagcaca    180
tcaatttaac agtgtgattt cagggcaata ggtgttccac ctaaacaatn aacctgaaag    240
gtacaattat tcaacaacta actataaact ctacaattcc atgtgataaa tgagactccc    300
aagactgatt cataaaaatt ccaaatcaca atactagact caggaatgtc agtgattctt    360
aaccaccagc ttttattttc attttttgaa aaactactgg aaaactctga caaactttaa    420
gtgaagcata aagcattgta gaggaacata aatgtagata taaaattatc ccaactgtga    480
atagcttttc ctcagtgcyc atatttaggg aagtagacca ctaatggctt caaactaaaa    540
gaattctaca gaaaacctgc ctgaaataaa cacaagtgat ttagtagaac aaaaatatag    600
gattaaagcc tagtggtgcc acttttccaa gaacttatat tagtaattat agtattataa    660
gtgaagagtc tgggtatatt ttttcacatt atctccctga ctacaatgta atagctccat    720
ttcttttctc cattacacac atgcagacac atacatacat atacacacat atttacacaa    780
atatccttaa cagaggccaa ctatctcaaa tatcttcttg caaagaaact gagtgattga    840
gtcagttaaa aaatattatt tactccaata attcctcaaa atacttgatt ttctctcttt    900
aatatttggt accagttctt tagtagtgcc tgctgtggtg atactctttt gtgattaaac    960
aatttttttt tcacaggaaa tggaggagtt tgtacagagc t                       1001
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<210> 363
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 499
<223> 12-640-413 : polymorphic base C or G

<220>
<221> misc_binding
<222> 479..498
<223> 12-640-413.mis1, potential

<220>
<221> misc_binding
<222> 500..519
<223> 12-640-413.mis2, potential complement

<220>
<221> primer_bind
<222> 885..905
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 412..432
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 487..511
<223> 12-640-413 potential probe

<220>
<221> misc_feature
<222> 94,112..113,116..120,122..124,128..138,141..144,146,148..153,155
157..160,163..166,318
<223> n=a, g, c or t

<400> 363
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ttttacccca atgattaaat ctgaaaatat ttaaatttaa atattggtat acattgggga     60
actcaagtca gaataattct caatcaattg cagncaagca catcttcacc annagnnnnn    120
tnnngtgnnn nnnnnnnnct nnnnanannn nnnanannnn ccnnnngaag aaaggcctgg    180
tggcctcttc tattctggtg ccagtgctgc ctctgagaca caacaaagtg atgatgagag    240
ttcctcacat gcagttagaa atagcacatc aatttaacag tgtgatttca gggcaatagg    300
tgttccacct aaacaatnaa cctgaaaggt acaattattc aacaactaac tataaactct    360
acaattccat gtgataaatg agactcccaa gactgattca taaaaattcc aaatcacaat    420
actagactca ggaatgtcag tgattcttaa ccaccagctt ttattttcat tttttgaaaa    480
actactggaa aactctgasa aactttaagt gaagcataaa gcattgtaga ggaacataaa    540
tgtagatata aaattatccc aactgtgaat agcttttcct cagtgctcat atttagggaa    600
gtagaccact aatggcttca aactaaaaga attctacaga aaacctgcct gaaataaaca    660
caagtgattt agtagaacaa aaatatagga ttaaagccta gtggtgccac ttttccaaga    720
acttatatta gtaattatag tattataagt gaagagtctg ggtatatttt ttcacattat    780
ctccctgact acaatgtaat agctccattt cttttctcca ttacacacat gcagacacat    840
acatacatat acacacatat ttacacaaat atccttaaca gaggccaact atctcaaata    900
tcttcttgca aagaaactga gtgattgagt cagttaaaaa atattattta ctccaataat    960
tcctcaaaat acttgatttt ctctctttaa tatttggtac c                       1001
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<210> 364
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 499
<223> 12-641-120 : polymorphic base G or A

<220>
<221> misc_binding
<222> 479..498
<223> 12-641-120.mis1, potential

<220>
<221> misc_binding
<222> 500..519
<223> 12-641-120.mis2, potential complement

<220>
<221> primer_bind
<222> 600..618
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 127..147
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 487..511
<223> 12-641-120 potential probe

<220>
<221> misc_feature
<222> 5,519,564,828,846..847,850..854,856..858,862..872,875..878,880

882..887,889,891..894,897..900
<223> n=a, g, c or t

<400> 364
tgganaatat tcacaaaatt aacattagaa gtaatccaac atctttatac gaaagaatga 60
ttaaaactta tgtgcatata gtagcattaa aataatttta tcaatgaaat gttcagttac 120
actttcagcc ataatacaaa caaagtgaat tagaaaatga taaatatagc aagatggcaa 180
gtttttgcag gaggaaatgt atatacaata agattaaaat tttctaaata agtgtcacat 240
gtatacattg acctatataa atttgacaaa atccataata aaaaatacat attttctaaa 300
aattatacct ctagatagaa attttagaaa aattatcttt taaaaaggtt ttcatacttt 360
tataaaattt cttacattaa ttttgtatta tttttataat attatcacaa aaggagaaac 420
aagcagtcca tatcagtgat gaatctctaa acagaggtta gattccttca acacctggta 480
gaaaaacaag gctctggtrt caagccagtg agatgaaanc actgaaaacg agttacatta 540
aatgtggcta caggtaactg caantcacat acaacaccta gaagccccag gtattacgtg 600
gaatagtagt acaaggactc tcacgttaac gtaagattaa aaatcatatt ttaagaaaac 660
actctgccat atgtgatgca ctgtttacat ttagactttt ttttctttgt tttgttaaaa 720
accatttgga aaagttttac cccaatgatt aaatctgaaa atatttaaat ttaaatattg 780
gtatacattg gggaactcaa gtcagaataa ttctcaatca attgcagnca agcacatctt 840
caccannagn nnnntnnngt gnnnnnnnnn nnctnnnnan annnnnnana nnnnccnnnn 900
gaagaaaggc ctggtggcct cttctattct ggtgccagtg ctgcctctga gacacaacaa 960
agtgatgatg agagttcctc acatgcagtt agaaatagca c 1001

<210> 365
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 499
<223> 12-641-122 : polymorphic base T or G

<220>
<221> misc_binding
<222> 479..498
<223> 12-641-122.mis1, potential

<220>
<221> misc_binding
<222> 500..519
<223> 12-641-122.mis2, potential complement

<220>
<221> primer_bind
<222> 602..620
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 129..149
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 487..511
<223> 12-641-122 potential probe

<220>
<221> misc_feature
<222> 7,521,566,830,848..849,852..856,858..860,864..874,877..880,882
884..889,891,893..896,899..902
<223> n=a, g, c or t

<400> 365
tatgganaat attcacaaaa ttaacattag aagtaatcca acatctttat acgaaagaat 60
gattaaaact tatgtgcata tagtagcatt aaaataattt tatcaatgaa atgttcagtt 120
acactttcag ccataataca aacaaagtga attagaaaat gataaatata gcaagatggc 180
aagtttttgc aggaggaaat gtatatacaa taagattaaa attttctaaa taagtgtcac 240
atgtatacat tgacctatat aaatttgaca aaatccataa taaaaaatac atattttcta 300
aaaattatac ctctagatag aaattttaga aaaattatct tttaaaaagg ttttcatact 360
tttataaaat ttcttacatt aattttgtat tatttttata atattatcac aaaaggagaa 420
acaagcagtc catatcagtg atgaatctct aaacagaggt tagattcctt caacacctgg 480
tagaaaaaca aggctctgkt gtcaagccag tgagatgaaa ncactgaaaa cgagttacat 540
taaatgtggc tacaggtaac tgcaantcac atacaacacc tagaagcccc aggtattacg 600
tggaatagta gtacaaggac tctcacgtta acgtaagatt aaaaatcata ttttaagaaa 660
acactctgcc atatgtgatg cactgtttac atttagactt tttttctttt gttttgttaa 720
aaaccatttg gaaaagtttt accccaatga ttaaatctga aaatatttaa atttaaatat 780
tggtatacat tggggaactc aagtcagaat aattctcaat caattgcagn caagcacatc 840
ttcaccanna gnnnnntnnn gtgnnnnnnn nnnnctnnnn anannnnnna nannnnccnn 900
nngaagaaag gcctggtggc ctcttctatt ctggtgccag tgctgcctct gagacacaac 960
aaagtgatga tgagagttcc tcacatgcag ttagaaatag c 1001

<210> 366
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 432
<223> 12-641-223 : polymorphic base G or A

<220>
<221> misc_binding
<222> 412..431
<223> 12-641-223.mis1, potential

<220>
<221> misc_binding
<222> 433..452
<223> 12-641-223.mis2, potential complement

<220>
<221> primer_bind
<222> 636..654
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 163..183
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 420..444
<223> 12-641-223 potential probe

<220>
<221> misc_feature
<222> 24,41,555,600,864,882..883,886..890,892..894,898..908,911..914
916,918..923,925,927..930,933..936
<223> n=a, g, c or t

<400> 366
atcataaaaa aatcaaggtg tatntattaa accttatgga naatattcac aaaattaaca 60
ttagaagtaa tccaacatct ttatacgaaa gaatgattaa aacttatgtg catatagtag 120

```
cattaaaata attttatcaa tgaaatgttc agttacactt tcagccataa tacaaacaaa    180
gtgaattaga aaatgataaa tatagcaaga tggcaagttt ttgcaggagg aaatgtatat    240
acaataagat taaaattttc taaataagtg tcacatgtat acattgacct atataaattt    300
gacaaaatcc ataataaaaa atacatattt tctaaaaatt atacctctag atagaaattt    360
tagaaaaatt atcttttaaa aaggttttca tacttttata aaatttctta cattaatttt    420
gtattatttt trtaatatta tcacaaaagg agaaacaagc agtccatatc agtgatgaat    480
ctctaaacag aggttagatt ccttcaacac ctggtagaaa aacaaggctc tggtgtcaag    540
ccagtgagat gaaancactg aaaacgagtt acattaaatg tggctacagg taactgcaan    600
tcacatacaa cacctagaag ccccaggtat tacgtggaat agtagtacaa ggactctcac    660
gttaacgtaa gattaaaaat catattttaa gaaaacactc tgccatatgt gatgcactgt    720
ttacatttag actttttttt ctttgttttg ttaaaaacca tttggaaaag ttttacccca    780
atgattaaat ctgaaaatat ttaaatttaa atattggtat acattgggga actcaagtca    840
gaataattct caatcaattg cagncaagca catcttcacc annagnnnnn tnnngtgnnn    900
nnnnnnnnct nnnnanannn nnnanannnn ccnnnngaag aaaggcctgg tggcctcttc    960
tattctggtg ccagtgctgc ctctgagaca caacaaagtg a                       1001
```

```
<210> 367
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 388
<223> 12-641-267 : polymorphic base T or C

<220>
<221> misc_binding
<222> 368..387
<223> 12-641-267.mis1, potential

<220>
<221> misc_binding
<222> 389..408
<223> 12-641-267.mis2, potential complement

<220>
<221> primer_bind
<222> 636..654
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 163..183
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 376..400
<223> 12-641-267 potential probe

<220>
<221> misc_feature
<222> 24,41,555,600,864,882..883,886..890,892..894,898..908,911..914
      916,918..923,925,927..930,933..936
<223> n=a, g, c or t

<400> 367
atcataaaaa aatcaaggtg tatntattaa accttatgga naatattcac aaaattaaca     60
ttagaagtaa tccaacatct ttatacgaaa gaatgattaa aacttatgtg catatagtag    120
cattaaaata attttatcaa tgaaatgttc agttacactt tcagccataa tacaaacaaa    180
gtgaattaga aaatgataaa tatagcaaga tggcaagttt ttgcaggagg aaatgtatat    240
acaataagat taaaattttc taaataagtg tcacatgtat acattgacct atataaattt    300
```

gacaaaatcc ataataaaaa atacatattt tctaaaaatt atacctctag atagaaattt 360
tagaaaaatt atcttttaaa aaggtttyca tacttttata aaatttctta cattaatttt 420
gtattatttt tataatatta tcacaaaagg agaaacaagc agtccatatc agtgatgaat 480
ctctaaacag aggttagatt ccttcaacac ctggtagaaa aacaaggctc tggtgtcaag 540
ccagtgagat gaaancactg aaaacgagtt acattaaatg tggctacagg taactgcaan 600
tcacatacaa cacctagaag ccccaggtat tacgtggaat agtagtacaa ggactctcac 660
gttaacgtaa gattaaaaat catattttaa gaaaacactc tgccatatgt gatgcactgt 720
ttacatttag actttttttt ctttgttttg ttaaaaacca tttggaaaag ttttacccca 780
atgattaaat ctgaaaatat ttaaatttaa atattggtat acattgggga actcaagtca 840
gaataattct caatcaattg cagncaagca catcttcacc annagnnnnn tnnngtgnnn 900
nnnnnnnnct nnnnanannn nnnanannnn ccnnnngaag aaaggcctgg tggcctcttc 960
tattctggtg ccagtgctgc ctctgagaca caacaaagtg a 1001

<210> 368
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 12-642-387 : polymorphic base A or G

<220>
<221> misc_binding
<222> 483..502
<223> 12-642-387.mis1, potential

<220>
<221> misc_binding
<222> 504..523
<223> 12-642-387.mis2, potential complement

<220>
<221> primer_bind
<222> 117..135
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 592..612
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 12-642-387 potential probe

<220>
<221> misc_feature
<222> 537,804,808,881,899,903,920,936,958,962..963,967,985,995
<223> n=a, g, c or t

<400> 368
tttattcgaa tattttactc tcattaaaca ttaagtaata tataattata attttagaaa 60
acctaaaata actcaatatt aatgcttatt tatgtatatt tctaaactga aaaaaaaacg 120
agattcactg aaaactcagg ctgtttattt gagaaggtca gaaatagtgt gtttctactg 180
tgcattttta gaaaaccctt ttttattttt attttatttt ttatttccaa catttattgt 240
aaattcagag gtacatgtgc aagaggtata ggtttgttac ataggtaaaa aaacactctt 300
gtataaacaa atacaatgat atggactata tgtgtccctg tcaagaaaaa cagagcaaaa 360
cccttcttaa aaatggcaag acacatttta ttctgactgg tgaattaggg gatagagact 420
acagtataaa ttgagctcaa ctctaattaa gacaaaggta actggggctt ttaaagagaa 480
aaccgatatg actaaaaatg acraaaacat aaaggagcta ggaggttata tgaaaantgg 540

```
aatattacat aaaaattcag tgtgaaataa ttgaaaatta ttaggtaagg tgggttaggc    600
agtgtatatt ttgcagtttg gcaggatcat attcctttga gccaagacct accatggaag    660
ctagggtggc ctttaaagac aaattcatga cctagtgccc atataagcta agctaaactt    720
ggcccagtct cttaacatgg tgtttatgca agtcttttgt gttacgtggg agtgtaaaat    780
tcaagtcctt catgaaatac aaanatantt tcttaatggg aatattctgt gtttcaaaat    840
tattaacggt cgtaactgac ttcctatcca aaactgtgca ncctggtaaa aatccttgnt    900
tanaaagaca aaagatgttn tccacatgag gcctgnaata tgcttgagtt actatttnca    960
cnntagnaac aaccctttgt aatgngataa taatncacag a                        1001
```

<210> 369
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 12-642-417 : polymorphic base A or G

<220>
<221> misc_binding
<222> 484..502
<223> 12-642-417.mis1

<220>
<221> misc_binding
<222> 504..523
<223> 12-642-417.mis2, potential complement

<220>
<221> primer_bind
<222> 87..105
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 562..582
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 12-642-417 potential probe

<220>
<221> misc_feature
<222> 507,774,778,851,869,873,890,906,928,932..933,937,955,965,976,981
983,988..989,998,1001
<223> n=a, g, c or t

<400> 369

```
ttaagtaata tataattata attttagaaa acctaaaata actcaatatt aatgcttatt     60
tatgtatatt tctaaactga aaaaaaaacg agattcactg aaaactcagg ctgtttattt    120
gagaaggtca gaaatagtgt gtttctactg tgcattttta gaaaaccctt ttttattttt    180
attttatttt ttatttccaa catttattgt aaattcagag gtacatgtgc aagaggtata    240
ggtttgttac ataggtaaaa aaacactctt gtataaacaa atacaatgat atggactata    300
tgtgtccctg tcaagaaaaa cagagcaaaa cccttcttaa aaatggcaag acacatttta    360
ttctgactgg tgaattaggg gatagagact acagtataaa ttgagctcaa ctctaattaa    420
gacaaaggta actggggctt ttaaagagaa aaccgatatg actaaaaatg acgaaaacat    480
aaaggagcta ggaggttata tgraaantgg aatattacat aaaaattcag tgtgaaataa    540
ttgaaaatta ttaggtaagg tgggttaggc agtgtatatt ttgcagtttg gcaggatcat    600
attcctttga gccaagacct accatggaag ctagggtggc ctttaaagac aaattcatga    660
cctagtgccc atataagcta agctaaactt ggcccagtct cttaacatgg tgtttatgca    720
```

```
agtcttttgt gttacgtggg agtgtaaaat tcaagtcctt catgaaatac aaanatantt     780
tcttaatggg aatattctgt gtttcaaaat tattaacggt cgtaactgac ttcctatcca     840
aaactgtgca ncctggtaaa aatccttgnt tanaaagaca aaagatgttn tccacatgag     900
gcctgnaata tgcttgagtt actatttnca cnntagnaac aaccctttgt aatgngataa     960
taatncacag aataanagaa nangatannt ccctttantt n                        1001
```

<210> 370
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 434
<223> 12-646-429 : polymorphic base C or T

<220>
<221> misc_binding
<222> 414..433
<223> 12-646-429.mis1, potential

<220>
<221> misc_binding
<222> 435..454
<223> 12-646-429.mis2, potential complement

<220>
<221> primer_bind
<222> 6..26
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 474..494
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 422..446
<223> 12-646-429 potential probe

<220>
<221> misc_feature
<222> 31..32,35,59,514
<223> n=a, g, c or t

<400> 370

```
ctacacttgg aaaatatctg taccccaaat nnganagtca atataacctg gtggttaana      60
gctggcactc tggatccaga tggccttgat tcaagtctta gaaaccactg tataatgatg     120
tgggactgga caagttactt gaacttcatt tgactcagct tcctcaccaa tgaaatggca     180
atagttgtca tcacattatc aatatcatgg gttgctgaaa gaacgaattc attaatattg     240
caaagcacta acaattgtgt gtacagcaaa ataaaattgt actattatca ttaaacaagt     300
caaaaaattt ccacaataat aattttagtg ttcatataat tgcataatat attatagttt     360
caaaacatgc tatgtttcta atgcaaatga taaaaatgac agtatttact atttcaagca     420
tgtgggaatt aaayttggag cataaaccaa gggctgacaa actatggcct cttggctggt     480
caaatcttgt cagctacttg ttttttaaaa aaantaattg gtataataat ttcacaccac     540
aaaattatac actttaagca tttaatcttt atgattcatt ggcatttaac acatttgaaa     600
tgttctgcca ctaccaccac tatctagatc caaattattt ttttcacttc aaaaggaagc     660
tttacaccca ttagagagtc atctcgcatt ctcccattat ccgtgccttg caacctggca     720
ttatgtgttg gcatcattgt atagcttatt gggtatataa cttcaacaaa gtgttttatt     780
ttttcttact tctaacatgt cctatttgtt tctaaacagc aattttatga tgcataaaat     840
taaacttcta tgttctgatt tctctgttat taaatatatt cagaggtgtt ctgatttaca     900
ttgttgtgag ttctctccaa ttttatattg aagtattttc ttgagaatgg ccataaacca     960
```

agatcctgga aagctctgaa taaggtgggg aagtgagttt c 1001

<210> 371
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 438
<223> 12-646-433 : polymorphic base G or T

<220>
<221> misc_binding
<222> 418..437
<223> 12-646-433.mis1, potential

<220>
<221> misc_binding
<222> 439..458
<223> 12-646-433.mis2, potential complement

<220>
<221> primer_bind
<222> 6..26
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 474..494
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 426..450
<223> 12-646-433 potential probe

<220>
<221> misc_feature
<222> 31..32,35,59,514
<223> n=a, g, c or t

<400> 371
ctacacttgg aaaatatctg taccccaaat nnganagtca atataacctg gtggttaana 60
gctggcactc tggatccaga tggccttgat tcaagtctta gaaaccactg tataatgatg 120
tgggactgga caagttactt gaacttcatt tgactcagct tcctcaccaa tgaaatggca 180
atagttgtca tcacattatc aatatcatgg gttgctgaaa gaacgaattc attaatattg 240
caaagcacta acaattgtgt gtacagcaaa ataaaattgt actattatca ttaaacaagt 300
caaaaaattt ccacaataat aattttagtg ttcatataat tgcataatat attatagttt 360
caaaacatgc tatgtttcta atgcaaatga taaaaatgac agtatttact atttcaagca 420
tgtgggaatt aaacttgkag cataaaccaa gggctgacaa actatggcct cttggctggt 480
caaatcttgt cagctacttg tttttttaaaa aaantaattg gtataataat ttcacaccac 540
aaaattatac actttaagca tttaatcttt atgattcatt ggcatttaac acatttgaaa 600
tgttctgcca ctaccaccac tatctagatc caaattattt ttttcacttc aaaaggaagc 660
tttacaccca ttagagagtc atctcgcatt ctcccattat ccgtgccttg caacctggca 720
ttatgtgttg gcatcattgt atagcttatt gggtatataa cttcaacaaa gtgttttatt 780
ttttcttact tctaacatgt cctatttgtt tctaaacagc aattttatga tgcataaaat 840
taaacttcta tgttctgatt tctctgttat taaatatatt cagaggtgtt ctgatttaca 900
ttgttgtgag ttctctccaa ttttatattg aagtattttc ttgagaatgg ccataaacca 960
agatcctgga aagctctgaa taaggtgggg aagtgagttt c 1001

<210> 372
<211> 1001

<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 12-647-145 : polymorphic base A or G

<220>
<221> misc_binding
<222> 483..502
<223> 12-647-145.mis1, potential

<220>
<221> misc_binding
<222> 504..523
<223> 12-647-145.mis2, potential complement

<220>
<221> primer_bind
<222> 359..378
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 788..808
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 12-647-145 potential probe

<220>
<221> misc_feature
<222> 351,951
<223> n=a, g, c or t

<400> 372
```
gcatcattgt atagcttatt gggtatataa cttcaacaaa gtgttttatt ttttcttact     60
tctaacatgt cctatttgtt tctaaacagc aattttatga tgcataaaat taaacttcta    120
tgttctgatt tctctgttat taaatatatt cagaggtgtt ctgatttaca ttgttgtgag    180
ttctctccaa ttttatattg aagtattttc ttgagaatgg ccataaacca agatcctgga    240
aagctctgaa taaggtgggg aagtgagttt cagatatatg agtccggtaa aatataacga    300
aatgagaaag aaagaacaaa atgcaaaggt agaagaaatt tattactcac nagttcctaa    360
gtgatgttag ggatgatgat aggaaactga cagaaagtcc agaggtggta gagagctcaa    420
ccagctgcct agaagtgcga gggggaaccc ttgtaggaag gcttttatta aggaccttag    480
gtattatttc ctaggcttct ccrcaggagt tgaggaatgg ctagcttaag ggaacacaca    540
tgaaggggaa aattatcata tgactctggt attgatcatt aggttatatc atggtcatca    600
cctctgtgat gtgttgcgtt tctgggtcat taggatgaga aacatgtaga ctctatctca    660
aagaagggaa gttttaacaa aggcaatagt gacaacctat gactaggtct taagcaactc    720
atgttaagcc taaaaatcaa tgctgaggca aaacaaactt acgacgagaa ggtagacaga    780
cattttagaa gaaatgtgac ctagctgctt ctggattggt agtataaaaa gtaccatgaa    840
tcagcttcta aatgtaacaa gaataaatag tgaaaattgt ttttagagac aactatgcaa    900
acatattagg agaagttgac tgcagtggca tgcacctata gttccagcta nctcaggagg    960
ctgaggaagg tggattactt gagcccagga gttcaaggcc a                       1001
```

<210> 373
<211> 751
<212> DNA
<213> Homo Sapiens

<220>

<221> allele
<222> 251
<223> 12-648-123 : polymorphic base A or G

<220>
<221> misc_binding
<222> 231..250
<223> 12-648-123.mis1, potential

<220>
<221> misc_binding
<222> 252..271
<223> 12-648-123.mis2, potential complement

<220>
<221> primer_bind
<222> 129..147
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 607..627
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 239..263
<223> 12-648-123 potential probe

<220>
<221> misc_feature
<222> 14,23,28,31..32,35,44,49,67,106,113,124
<223> n=a, g, c or t

<400> 373
```
atttcttttt tggngggaaa gtncatcnag nnacntggga attnctcgnt ttacagaaag     60
aaattgnatt ttaaaacctc gtaagtagaa gggatcacaa gtaagnataa ttntcaaaca    120
aatncaggaa aacaagtctt tagcaggagt tttctgaagc gtgaagtgag ctgctcaaga    180
gagtgaccgg atcttttctg gagaaaagcc tggtggacct ctcccactga agtgtgcatg    240
tgcatcctcc rcataggaca tggtgaggtg atgatgagag tccctcgaag ccagttgtac    300
ataacacatt ccatgagggt gccaatttta cagtaagata tcagagtaac aggtgtcacc    360
cataaacaaa cccagaaata tgtaactata catgtttact tatggattat cagtaggatt    420
ttgaggacga gttcacagaa attcaaaacc atacaccagt caaaaccatg caccaggctt    480
cgggatgtca gcaattctta ccttatgtga tgaaggagtg atttagaagc aaggtttggg    540
aaattctgac aaattttaag ataggttaga aataattata cagttgagag aaatatataa    600
tatcttccca atcataagtg acttttcctt agtagcataa tcaaggaaat gaaattataa    660
tgactacatt aaagtaatga tttagaaaac ctccctgaaa taaaaacaag ttacttagga    720
gaacaataac aatataaaat taaagagaag t                                   751
```

<210> 374
<211> 928
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 428
<223> 12-648-300 : polymorphic base C or T

<220>
<221> misc_binding
<222> 408..427
<223> 12-648-300.mis1, potential

<220>
<221> misc_binding
<222> 429..447
<223> 12-648-300.mis2, complement

<220>
<221> primer_bind
<222> 129..147
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 607..627
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 416..440
<223> 12-648-300 potential probe

<220>
<221> misc_feature
<222> 14,23,28,31..32,35,44,49,67,106,113,124
<223> n=a, g, c or t

<400> 374
```
atttcttttt tggngggaaa gtncatcnag nnacntggga attnctcgnt ttacagaaag    60
aaattgnatt ttaaaacctc gtaagtagaa gggatcacaa gtaagnataa ttntcaaaca   120
aatncaggaa aacaagtctt tagcaggagt tttctgaagc gtgaagtgag ctgctcaaga   180
gagtgaccgg atctttttctg gagaaaagcc tggtggacct ctcccactga agtgtgcatg   240
tgcatcctcc gcataggaca tggtgaggtg atgatgagag tccctcgaag ccagttgtac   300
ataacacatt ccatgagggt gccaatttta cagtaagata tcagagtaac aggtgtcacc   360
cataaacaaa cccagaaata tgtaactata catgtttact tatggattat cagtaggatt   420
ttgaggayga gttcacagaa attcaaaacc atacaccagt caaaaccatg caccaggctt   480
cgggatgtca gcaattctta ccttatgtga tgaaggagtg atttagaagc aaggtttggg   540
aaattctgac aaattttaag ataggttaga aataattata cagttgagag aaatatataa   600
tatcttccca atcataagtg acttttcctt agtagcataa tcaaggaaat gaaattataa   660
tgactacatt aaagtaatga tttagaaaac ctccctgaaa taaaaacaag ttacttagga   720
gaacaataac aatataaaat taaagagaag taaacagtgg tagtcttcct aagaatctat   780
attagtgatt acaagagctt ggttcccata tttttaactg tatctttccc tcactactgt   840
gtaaagatac taatttattt cttactttac atacttaatc aaatacatac acacacacac   900
gcacatgcac acacttacat aactacag                                       928
```

<210> 375
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-648-402 : polymorphic base G or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-648-402.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-648-402.mis2, potential complement

<220>
<221> primer_bind
<222> 100..118
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 578..598
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-648-402 potential probe

<220>
<221> misc_feature
<222> 2..3,6,15,20,38,77,84,95,910..911,996..997
<223> n=a, g, c or t

<400> 375
```
gnnacntggg aattnctcgn tttacagaaa gaaattgnat tttaaaacct cgtaagtaga     60
agggatcaca agtaagnata attntcaaac aaatncagga aaacaagtct ttagcaggag    120
ttttctgaag cgtgaagtga gctgctcaag agagtgaccg gatcttttct ggagaaaagc    180
ctggtggacc tctcccactg aagtgtgcat gtgcatcctc cgcataggac atggtgaggt    240
gatgatgaga gtccctcgaa gccagttgta cataacacat tccatgaggg tgccaatttt    300
acagtaagat atcagagtaa caggtgtcac ccataaacaa acccagaaat atgtaactat    360
acatgtttac ttatggatta tcagtaggat tttgaggacg agttcacaga aattcaaaac    420
catacaccag tcaaaaccat gcaccaggct tcgggatgtc agcaattctt accttatgtg    480
atgaaggagt gatttagaag saaggtttgg gaaattctga caaattttaa gataggttag    540
aaataattat acagttgaga gaaatatata atatcttccc aatcataagt gacttttcct    600
tagtagcata atcaaggaaa tgaaattata atgactacat taaagtaatg atttagaaaa    660
cctccctgaa ataaaaacaa gttacttagg agaacaataa caatataaaa ttaaagagaa    720
gtaaacagtg gtagtcttcc taagaatcta tattagtgat tacaagagct tggttcccat    780
atttttaact gtatctttcc ctcactactg tgtaaagata ctaatttatt tcttacttta    840
catacttaat caaatacata cacacacaca cgcacatgca cacacttaca taactacaga    900
ttaataatan ngagaaaatt gatgttgtat aacataagtc tttccaaagg aactgagcga    960
tgtcgtattt aaaaaactgg cactactaga agtcanngta t                       1001
```

<210> 376
<211> 798
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 298
<223> 12-652-115 : polymorphic base C or T

<220>
<221> misc_binding
<222> 278..297
<223> 12-652-115.mis1, potential

<220>
<221> misc_binding
<222> 299..318
<223> 12-652-115.mis2, potential complement

<220>
<221> primer_bind
<222> 184..203

<223> upstream amplification primer

<220>
<221> primer_bind
<222> 615..635
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 286..310
<223> 12-652-115 potential probe

<220>
<221> misc_feature
<222> 43..44,341
<223> n=a, g, c or t

<400> 376
```
aaataattgg ttaaaaattt ttatgccaca aaattaaaca ctnnaaccat ttaatgtgta     60
caattcattg gcgtttaata tatttgcaat attttgccac taccaccact ctctagatcc    120
aaagtatttt gtcacttcaa aaggaagctt tatacccatt agacagtcat ctcgcattct    180
cccatcctcc atctcctgca acctggcatt atctgttggc atcattctat agcctagtag    240
ataatgtttt tttaaaggca aataggtaca taacttcaac aaagtgtttt atttttcytt    300
atttttacat ctcctatttg ttcctaaatg aaaattctgt ngatgtataa gaattagtta    360
ttatttccta gttgctctgt tattaaatat attcagcagt gttgtgattt atattgttac    420
agtttctgtc caattttgta ttgaagtctg tccctttaga attgcaataa accaagctct    480
gatggaggtg aggaagtgaa attcagatgt gtgtgtcagg taaaatacaa tgaaatgtaa    540
aataaaacca aaatgcatga aatagaagaa atgtattaca gttcctagag atattaagga    600
taatgacata aaacggacag aaaattcaga agtggcagag agctcaacca gctgcctgga    660
agtgatagag agaatccctg tgtgggggc tgtgggggtg cttttcttaa ggtctatgag    720
cattatttcc tagtcttgtc tgccggagtt gtggagtggc tatcttaaga aaacacacat    780
gaagagggaa aattatta                                                  798
```

<210> 377
<211> 886
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 386
<223> 12-652-203 : polymorphic base A or C

<220>
<221> misc_binding
<222> 367..385
<223> 12-652-203.mis1

<220>
<221> misc_binding
<222> 387..406
<223> 12-652-203.mis2, potential complement

<220>
<221> primer_bind
<222> 184..203
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 615..635
<223> downstream amplification primer, complement

```
<220>
<221> misc_binding
<222> 374..398
<223> 12-652-203 potential probe

<220>
<221> misc_feature
<222> 43..44,341
<223> n=a, g, c or t

<400> 377
aaataattgg ttaaaaattt ttatgccaca aaattaaaca ctnnaaccat ttaatgtgta      60
caattcattg gcgtttaata tatttgcaat attttgccac taccaccact ctctagatcc     120
aaagtatttt gtcacttcaa aaggaagctt tatacccatt agacagtcat ctcgcattct     180
cccatcctcc atctcctgca acctggcatt atctgttggc atcattctat agcctagtag     240
ataatgtttt tttaaaggca aataggtaca taacttcaac aaagtgtttt atttttcttt     300
atttttacat ctcctatttg ttcctaaatg aaaattctgt ngatgtataa gaattagtta     360
ttatttccta gttgctctgt tattamatat attcagcagt gttgtgattt atattgttac     420
agtttctgtc caattttgta ttgaagtctg tccctttaga attgcaataa accaagctct     480
gatggaggtg aggaagtgaa attcagatgt gtgtgtcagg taaaatacaa tgaaatgtaa     540
aataaaacca aaatgcatga aatagaagaa atgtattaca gttcctagag atattaagga     600
taatgacata aaacggacag aaaattcaga agtggcagag agctcaacca gctgcctgga     660
agtgatagag agaatccctg tgtgggggc tgtgggggtg cttttcttaa ggtctatgag      720
cattatttcc tagtcttgtc tgccggagtt gtggagtggc tatcttaaga aaacacacat     780
gaagagggaa aattattatt tgattctggt gttgaccatt aggttatctc atggtaatca     840
gctctgtggt atgttgcatt tctgggtcag tgggatgaga aacaag                    886

<210> 378
<211> 957
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 457
<223> 12-652-274 : polymorphic base G or T

<220>
<221> misc_binding
<222> 437..456
<223> 12-652-274.mis1, potential

<220>
<221> misc_binding
<222> 458..477
<223> 12-652-274.mis2, potential complement

<220>
<221> primer_bind
<222> 184..203
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 615..635
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 445..469
<223> 12-652-274 potential probe

<220>
```

<221> misc_feature
<222> 43..44,341
<223> n=a, g, c or t

<400> 378
aaataattgg ttaaaaattt ttatgccaca aaattaaaca ctnnaaccat ttaatgtgta 60
caattcattg gcgtttaata tatttgcaat attttgccac taccaccact ctctagatcc 120
aaagtatttt gtcacttcaa aaggaagctt tatacccatt agacagtcat ctcgcattct 180
cccatcctcc atctcctgca acctggcatt atctgttggc atcattctat agcctagtag 240
ataatgtttt tttaaaggca aataggtaca taacttcaac aaagtgtttt atttttcttt 300
atttttacat ctcctatttg ttcctaaatg aaaattctgt ngatgtataa gaattagtta 360
ttatttccta gttgctctgt tattaaatat attcagcagt gttgtgattt atattgttac 420
agtttctgtc caattttgta ttgaagtctg tcccttkaga attgcaataa accaagctct 480
gatggaggtg aggaagtgaa attcagatgt gtgtgtcagg taaaatacaa tgaaatgtaa 540
aataaaacca aaatgcatga aatagaagaa atgtattaca gttcctagag atattaagga 600
taatgacata aaacggacag aaaattcaga agtggcagag agctcaacca gctgcctgga 660
agtgatagag agaatccctg tgtgggggc tgtgggggtg cttttcttaa ggtctatgag 720
cattatttcc tagtcttgtc tgccggagtt gtggagtggc tatcttaaga aaacacacat 780
gaagagggaa aattattatt tgattctggt gttgaccatt aggttatctc atggtaatca 840
gctctgtggt atgttgcatt tctgggtcag tgggatgaga aacaagtgta ctctgtaaca 900
aacaactaca caaggaaggg aagtttcaca aagccaaaag tgacaggcta tgacttg 957

<210> 379
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-652-371 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-652-371.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-652-371.mis2, potential complement

<220>
<221> primer_bind
<222> 131..150
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 562..582
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-652-371 potential probe

<220>
<221> misc_feature
<222> 288
<223> n=a, g, c or t

<400> 379

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atgtgtacaa ttcattggcg tttaatatat ttgcaatatt ttgccactac caccactctc     60
tagatccaaa gtattttgtc acttcaaaag gaagctttat acccattaga cagtcatctc    120
gcattctccc atcctccatc tcctgcaacc tggcattatc tgttggcatc attctatagc    180
ctagtagata atgttttttt aaaggcaaat aggtacataa cttcaacaaa gtgttttatt    240
tttctttatt tttacatctc ctatttgttc ctaaatgaaa attctgtnga tgtataagaa    300
ttagttatta tttcctagtt gctctgttat taaatatatt cagcagtgtt gtgatttata    360
ttgttacagt ttctgtccaa ttttgtattg aagtctgtcc ctttagaatt gcaataaacc    420
aagctctgat ggaggtgagg aagtgaaatt cagatgtgtg tgtcaggtaa aatacaatga    480
aatgtaaaat aaaaccaaaa ygcatgaaat agaagaaatg tattacagtt cctagagata    540
ttaaggataa tgacataaaa cggacagaaa attcagaagt ggcagagagc tcaaccagct    600
gcctggaagt gatagagaga atccctgtgt ggggggctgt gggggtgctt ttcttaaggt    660
ctatgagcat tatttcctag tcttgtctgc cggagttgtg gagtggctat cttaagaaaa    720
cacacatgaa gagggaaaat tattatttga ttctggtgtt gaccattagg ttatctcatg    780
gtaatcagct ctgtggtatg ttgcatttct gggtcagtgg gatgagaaac aagtgtactc    840
tgtaacaaac aactacacaa ggaagggaag tttcacaaag ccaaaagtga caggctatga    900
cttgctctta aacaactcaa gttaagtcta aaaatggatg tggaatcaat aactatattc    960
aacaaatgta tgacaagaag gtagaaaagg gatgggtcca g                       1001
```

<210> 380
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 499
<223> 12-653-423 : polymorphic base T or A

<220>
<221> misc_binding
<222> 479..498
<223> 12-653-423.mis1, potential

<220>
<221> misc_binding
<222> 500..519
<223> 12-653-423.mis2, potential complement

<220>
<221> primer_bind
<222> 903..921
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 390..410
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 487..511
<223> 12-653-423 potential probe

<400> 380

```
aaaaactgtg taaaaactgt tatctccaga gaaaaaccaa tgctaaggaa gcatccagtg     60
tagataatag agagtatcct ggagtcactg atattaataa tttagatgag agctgaacta    120
tatgcaggaa taggtaaaag aatgaagaag agaaaaaaac acaaaaagaa aagcaggtaa    180
agtgttcagg acagttctca agactcaaag tttagtttgc aaggaagata ctgagtaaga    240
atcagatgat gctgataggc aagataagag ccagatactc ctcaggagtt gaaatattta    300
ttaagcacat ttagggacta ctaaaaagag ttaagaaaag aaaatatggg ataagattat    360
actttttaaa aaaagattcc aagatgttcg atggattaaa ttgtggaagg gccaaactag    420
aaagagctga ccattgagga aattttgtat gaattcaggt agcagatgat ggaaaaatgg    480
actagaaagt ggatagaawt acctatgcct acttttacag taatatgact aacttcatat    540
```

```
tgtgttgtgt ggaaaaaagt taatacaaat aaaccactta aaatgtctct ggcatatagt    600
tagtgattca gaaatattat tttgcaatta tggttatttt tgttattact aatactatga    660
attacttaac atgtgtaagt cacttgagat attattcctc atttaataga aactaattat    720
tcagcatttc aagattatat tctctaacaa agtcctatgg tcttctatat gacagatacc    780
ctgtagactt gtttaaaata agacatatca gttttgacag taagatgagc aaaatgaaat    840
tgtaaaattc taccacaagt gacaaggatc ttcatcagta ttctaactta taagaaaata    900
atcccttacc gatataaatg tgtgattcta ttagtatttg cagccagacc cagtgttcac    960
ttgattttac taaagcattt aaatcattct gcgttgagat c                       1001
```

<210> 381
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 499
<223> 12-654-115 : polymorphic base T or C

<220>
<221> misc_binding
<222> 479..498
<223> 12-654-115.mis1, potential

<220>
<221> misc_binding
<222> 500..519
<223> 12-654-115.mis2, potential complement

<220>
<221> primer_bind
<222> 595..613
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 76..96
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 487..511
<223> 12-654-115 potential probe

<400> 381

```
ccatcaggaa gacccactac gttatctgag acaatggcaa aagctgacat atggcttatt     60
cgaaactact gggattttca atttcctcac ccactcttac caaatgttga gttcgttgga    120
ggactccact gcaaacctgc caaacccccta ccgaaggtaa actattactg tttgttttgt    180
ctgctttgaa gtttcagtac gaatggttct atattcattc aaagtgtttg acttacactg    240
gaagaaaggt ggaagtggga agagtaaagc agataccaat tagaaactga cgtacatgtt    300
gatactatca caagtttatg aatttcatca ttattaccaa taaagaggga tactaaagag    360
actttgaaaa tagggttggt aaattaaagc tttgattatg caacatgtaa gaaggtactg    420
gccattcatt caaagaatat ttataaagag attagcacac accacaggta cgtgtatggg    480
acacagtttc tatcccaaya caccttacat tctattttga aagatagaat atatgcaagt    540
aataaaaact gtgtaaaaac tgttatctcc agagaaaaac caatgctaag gaagcatcca    600
gtgtagataa tagagagtat cctggagtca ctgatattaa taatttagat gagagctgaa    660
ctatatgcag gaataggtaa aagaatgaag aagagaaaaa aacacaaaaa gaaaagcagg    720
taaagtgttc aggacagttc tcaagactca aagtttagtt tgcaaggaag atactgagta    780
agaatcagat gatgctgata ggcaagataa gagccagata ctcctcagga gttgaaatat    840
ttattaagca catttaggga ctactaaaaa gagttaagaa aagaaaatat gggataagat    900
tatacttttt aaaaaaagat tccaagatgt tcgatggatt aaattgtgga agggccaaac    960
tagaaagagc tgaccattga ggaaattttg tatgaattca g                       1001
```

<210> 382
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 499
<223> 12-654-207 : polymorphic base G or A

<220>
<221> misc_binding
<222> 479..498
<223> 12-654-207.mis1, potential

<220>
<221> misc_binding
<222> 500..519
<223> 12-654-207.mis2, potential complement

<220>
<221> primer_bind
<222> 687..705
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 168..188
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 487..511
<223> 12-654-207 potential probe

<400> 382
```
tgcctacatt tttgcccaca ttattctaac ttctttcaga aaattaccta gtttaattat      60
cttgtgtcat ctatcttttc tttttttttc ccccatcagg aagacccact acgttatctg     120
agacaatggc aaaagctgac atatggctta ttcgaaacta ctgggatttt caatttcctc     180
acccactctt accaaatgtt gagttcgttg gaggactcca ctgcaaacct gccaaacccc     240
taccgaaggt aaactattac tgtttgtttt gtctgctttg aagtttcagt acgaatggtt     300
ctatattcat tcaaagtgtt tgacttacac tggaagaaag gtggaagtgg gaagagtaaa     360
gcagatacca attagaaact gacgtacatg ttgatactat cacaagttta tgaatttcat     420
cattattacc aataaagagg gatactaaag agactttgaa aatagggttg gtaaattaaa     480
gctttgatta tgcaacatrt aagaaggtac tggccattca ttcaaagaat atttataaag     540
agattagcac acaccacagg tacgtgtatg ggacacagtt tctatcccaa tacaccttac     600
attctatttt gaaagataga atatatgcaa gtaataaaaa ctgtgtaaaa actgttatct     660
ccagagaaaa accaatgcta aggaagcatc cagtgtagat aatagagagt atcctggagt     720
cactgatatt aataatttag atgagagctg aactatatgc aggaataggt aaaagaatga     780
agaagagaaa aaaacacaaa aagaaaagca ggtaaagtgt tcaggacagt tctcaagact     840
caaagtttag tttgcaagga agatactgag taagaatcag atgatgctga taggcaagat     900
aagagccaga tactcctcag gagttgaaat atttattaag cacatttagg gactactaaa     960
aagagttaag aaaagaaaat atgggataag attatacttt t                        1001
```

<210> 383
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 12-657-396 : polymorphic base A or G

<220>
<221> misc_binding
<222> 483..502
<223> 12-657-396.mis1, potential

<220>
<221> misc_binding
<222> 504..523
<223> 12-657-396.mis2, potential complement

<220>
<221> primer_bind
<222> 108..128
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 566..586
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 12-657-396 potential probe

<220>
<221> misc_feature
<222> 74,84,232,860,993
<223> n=a, g, c or t

<400> 383
ctgtataatt atcgggttgt gtgctgcttc tagtaaataa ttattatata ctgaagctat 60
atgtttctaa cacnaaactt tatnaatttc tgttctaaca tgcatctcag aatataggga 120
caatatagct atatgtatga caacttcaaa attttatttt aaaagtatac ataaactata 180
ttattttatg tggtattgca tctttataat gaagacaatt ttttctctgg angaaaatgg 240
aagaatttgc ccagagctct gatgaagacg gtgttgtgtt ttctctggag tcagctgtgc 300
aaaaccttac agaagaaaaa gctgatctta tcacttcggc cctggctcag attccacaaa 360
aagtcagtac aacctccaat ccttataaga aactattcac acaatggaga aagtatggct 420
ttccacctgg aacttgaatc tcatttttca atttgcataa caggcactag atttatgtaa 480
caatttggaa agtattatgg tartttatgt gagcacaact gattatttgt ctagtgatct 540
ttgctattac tttagtaaca catctcttgg ttgtcgtttg ttaataataa agtaaaaata 600
aagcattaag tccctatttc acgttgcagg atttgaaatc ttaagaccta ttctgatgac 660
tccaaaggaa acttcttaag tatactagct caaaggaacc taaactttgg gggatgatat 720
aagaaagata gagaagaatc atgctcaata ttatcttcaa catattttat tgtataggag 780
ctctattcag tgtgtttgaa cataaaagta gaagcttaga tttatgtagt ctttctaatg 840
aactggagtt ttctatagtn tacaaggcaa ttatgatttt aatattacag tctaacaacc 900
tgcatgtaat actttatgat attcaattaa ttttattact gtaattctag ttttcctctc 960
tttagttagt gctatttata cactagcctc aangggttac t 1001

<210> 384
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 12-658-120 : polymorphic base A or T

<220>
<221> misc_binding
<222> 483..502

<223> 12-658-120.mis1, potential

<220>
<221> misc_binding
<222> 504..523
<223> 12-658-120.mis2, potential complement

<220>
<221> primer_bind
<222> 384..404
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 863..883
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 12-658-120 potential probe

<220>
<221> misc_feature
<222> 418,551
<223> n=a, g, c or t

<400> 384
```
atttttcaat ttgcataaca ggcactagat ttatgtaaca atttggaaag tattatggta      60
gtttatgtga gcacaactga ttatttgtct agtgatcttt gctattactt tagtaacaca     120
tctcttggtt gtcgtttgtt aataataaag taaaaataaa gcattaagtc cctatttcac     180
gttgcaggat ttgaaatctt aagacctatt ctgatgactc caaaggaaac ttcttaagta     240
tactagctca aaggaaccta aactttgggg gatgatataa gaaagataga gaagaatcat     300
gctcaatatt atcttcaaca tattttattg tataggagct ctattcagtg tgtttgaaca     360
taaaagtaga agcttagatt tatgtagtct ttctaatgaa ctggagtttt ctatagtnta     420
caaggcaatt atgattttaa tattacagtc taacaacctg catgtaatac tttatgatat     480
tcaattaatt ttattactgt aawtctagtt ttcctctctt tagttagtgc tatttataca     540
ctagcctcaa ngggttactt tttaaaattt tatgtttaaa tttcaaaaca ctcaataaaa     600
gccagtatgc taattaggaa tgtgaaatta gttttgatta tgagattctc tttttgggag     660
ttcagaatat ctatgtaatc ctttgttttc aagtgtaaga ttttcatata ggtttccaga     720
aagaaaaaag tatggaatta aggtacaaat acaaacaaaa ttcagccttg aacaatgaag     780
tataggtaac ttctgtctct ttcttttttg attaaaaata aatgaaataa aggagagaat     840
gaagcataaa gagaaaagac aaccaactat ccaaaaccag acaaaagcca aagcaatgtt     900
tgtctctggg aaactgtaaa tttgataata gagctagaat ggccaagtga tttacattta     960
cacagcagtt gtgtgtccac aaggatattt aacttccata t                        1001
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<210> 385
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-659-382 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-659-382.mis1, potential

<220>
<221> misc_binding

<222> 502..521
<223> 12-659-382.mis2, potential complement

<220>
<221> primer_bind
<222> 120..139
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 552..572
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-659-382 potential probe

<220>
<221> misc_feature
<222> 21,546
<223> n=a, g, c or t

<400> 385
atattgagat aataaatgaa ncattcaaat atttaagtaa tcattaggca gacataattc 60
cagtgtaaag atgagtaaaa aattactaat ggtccccacc ctttttatta atgtatttac 120
tacattcact ttcaacttcc aaataatgtt aagcttttca tttctaaagc aatgaaaagg 180
gagtgagttt acttatattc acttgtttca taagttatat tcccatatct gatgatttac 240
aaagaaagca aatctatcaa tcatctatgt ctgagaaata cattaatctg cttaaaaggc 300
acatataatt tgtttccgat tacaaattat taagcacttt ttccaagaaa aaaattcaag 360
tgactttttt tcccatatgt gcagaataat atcgcatgtg ctacaattgg aaattattta 420
aaggtggaaa agactgattg gcagttcttt aataataggt ctgtttaaaa tatcccaaat 480
ttgtggtgat gctaaatttc rttctgctgg ctcttaactc ttcagtggca caatccaaag 540
cgttgncagc agtggtttat atggtctgct atagctaagc catgtagtac atgcctagta 600
ccaacatgtg gtactgattt tggaattacc aagcaatctt cataaactag tgtataatct 660
acaagttttt aacgtgtact tgctatctga gttttaaaag taactacaca tttgcatcaa 720
aaaattagta taggtgatta caagaatgtt atacaggata taaaactaaa aactgcttta 780
taaatattca aatatcaaag ttgctgcatc agctcagaga cgctgaagct gtgctggagg 840
cagcagagtt aatggcggca agtccctgtg gagggacctt cactaaccca cattcctcct 900
tcctgccctc catccttccc gatctcccgc tcctcttggt gtcatttctt actgcaatag 960
agttttgcgt ccacatacct acctagggct attattaaca a 1001

<210> 386
<211> 983
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 306
<223> 12-660-134 : polymorphic base A or G

<220>
<221> misc_binding
<222> 286..305
<223> 12-660-134.mis1, potential

<220>
<221> misc_binding
<222> 307..326
<223> 12-660-134.mis2, potential complement

<220>

<221> primer_bind
<222> 173..193
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 692..712
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 294..318
<223> 12-660-134 potential probe

<220>
<221> misc_feature
<222> 880..881,889,925..926,930
<223> n=a, g, c or t

<400> 386
agtgtagtta catctcacaa ataatttttt caatcatttt ctgggttgtc tgtctactaa 60
ttcaaatgtt acacctacct ttttctccta atagctagat attccaaatg taactgaaat 120
ataacagccc ttcttttatt accagtgaca gcacttttta tgggaataaa tccccagtct 180
ttattatgaa gtggtaacac attttgtcat ggagtgtggc ctgtccttct actactggag 240
catcaccacc accccactcc ctgctgccgt ggacaccatg ccctatcaca ctcagtgact 300
tcactrtttc tctaagagaa tatgttctag catgcatcct gctttttggg ggctagagtg 360
ggggatatgc agtttttttt gtctgcagtg tgctctttct atttgtccac ttgacaatct 420
tgtattcatt cttcaagtct caagtcacat accacttctt caatatgtag ccatcactta 480
tcgccccaga ggacttggtg cttctttctc tgagatctga aagtaatttt aatgcagttt 540
tactgttaca gtaatttgtt acctagagaa ccatgcccat ttcattgcct catattgagc 600
attgctcatt ttaagactca ccacgaataa ttattcaaaa atttatctaa tcctaggtca 660
tctaacaacc aaagctttta tacctcatgg tggaggcaat gacatctatg agaggatcta 720
ccatgggatc cctatggtgg gccttccttt gtttgtagat caacccgata agttggttca 780
catgaaggct aagggggaag ctgttacagt agactcaaaa acgatgtcat ctacaaattt 840
gctcaatgca taaaaagcag tcattaatga ctcttcatgn ntgtaattnt tttaactacg 900
tagcatgtat ttgctgacta cattnntttn tggtaatgct taaaggcaat cgtcaattaa 960
ccactatgag tatcacgatc tgt 983

<210> 387
<211> 1000
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 497
<223> 12-662-80 : polymorphic base G or C

<220>
<221> misc_binding
<222> 477..496
<223> 12-662-80.mis1, potential

<220>
<221> misc_binding
<222> 498..517
<223> 12-662-80.mis2, potential complement

<220>
<221> primer_bind
<222> 418..435
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 979..1000
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 485..509
<223> 12-662-80 potential probe

<220>
<221> misc_feature
<222> 24,726,739
<223> n=a, g, c or t

<400> 387
atatagtcag tgactcagaa atgnttatta attttgcaat tatggttatt ttattactaa 60
tactactaac tacttaacat gtgcatgtca cttgagatat cattcctcat ttaagagaac 120
cagattattc agcacatcaa ggttatattg tcttggaaag tcatagatga cagataccct 180
tggacttgat taaaagtaga catatcagtt gtgacagcaa gataagctag ttgaaatttt 240
aaaattcttc cataagtaat aaggatcttc accagtattc cagcttaaaa cacttcctca 300
acaatataaa tgtgtgcctc aaatatgtgc agacaaacac agggttcaca tgattttaat 360
aaagcattta aatcattctg cattgagatc ccagaatttt acattttaga gcataaacat 420
atcctattag agcagatgat ttctgcctta tgacaggcca ctcaataaag cttcctgggg 480
gaactcgtct tgacatsata ggtgtctgac agagaagcac agagataatg aacaatgcat 540
gtataataaa gaccaaataa tttctgccac ttgtttctga atagtgccct tagtttcaat 600
acgaaaaaaa attccgtcag catataagat tatattcttt tcgaaggaat acaagaactt 660
catatatttt aattaacatc acattttaag gcatatgtaa aaagtaaggc ttcttcaatg 720
gattanttat gcaatctcnt taaaagatca tttttgcttg cataaaactg agaatttgtt 780
ccattgttaa aactcagtat ctatgtttaa tgcaagttgt ataggcttta tagagtcagt 840
ttcttaagag acaaaagttg aggtaagact aatgaaaaat atataccact ctaccctact 900
cttgaaagat ttccccactc acactaaggg aaactgacag tgccagtaga aggaggaaga 960
gagtaagaca atgtagaagg acaagaaaaa aaggttgact 1000

<210> 388
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-906-149 : polymorphic base A or G

<220>
<221> misc_binding
<222> 482..500
<223> 12-906-149.mis1

<220>
<221> misc_binding
<222> 502..521
<223> 12-906-149.mis2, potential complement

<220>
<221> primer_bind
<222> 353..372
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 809..829
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-906-149 potential probe

<220>
<221> misc_feature
<222> 750,853..854,860,942,945
<223> n=a, g, c or t

<400> 388
taattttata actgattgcc aggttgttaa gcctggcaag acattcagag ctaggtcaac 60
aaatatttca tttttttctg ttttatcctg tggcatatgg accacctcaa atttcagtgc 120
agaaggcttc ctgtagtcaa ttaacaaaga ctttgagtga gtcaatactg ttacctcatg 180
gcccctcact atgatctcct ctagaatgac cttgacatta agccaatggc tcatgtcaca 240
gggccacacc aggaccttct cacagaattc acaactagca cagaagagtt gcaggagccg 300
aaataccaaa gctgacttct cgggcctcat gatgacattt ccctcacaca ctgatctgca 360
ctagctttgt agttactaag catgaaattg aaatgacaat ataagcacag aagttaaaaa 420
ttaatatttt aagtgtaaat aaagttcatt ggttggttgc cagcttcaca tttattgaag 480
atatcaaaaa gaaatgcaat rttgcaatgt atcagggaaa atttgttcca accttctaga 540
gcttagaaat aaaacacata aagatacttt tattatctgg attgatgata aagaaatttt 600
ttaaaattct ttagatttaa taattcatgt gcagaaacat atgcacacaa ccacatttac 660
attcattcca cactaaatcc aaggtgtcag atggtttaga agaactcatg tttcacatcc 720
tttgctcaca aggacaatac aaagaattan ctgggaatac acttggagac tttgggtaac 780
tattttcatt aattctatat actaagtgca aagtgttcag tatttcagag gagaaaaatg 840
cacaattgct ttnnaatatn ctgataatta ataaaagctt tagtaagaca tttgacttag 900
gaggtgagat gaaagcttca ttaggattta ttgttgccaa anggnaagca tttcacaatc 960
aatacaagca tgacgaaagt ataggatatt taaaagtcat t 1001

<210> 389
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-906-154 : polymorphic base A or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-906-154.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-906-154.mis2, potential complement

<220>
<221> primer_bind
<222> 348..367
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 804..824
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513

<223> 12-906-154 potential probe

<220>
<221> misc_feature
<222> 745,848..849,855,937,940
<223> n=a, g, c or t

<400> 389
ttataactga ttgccaggtt gttaagcctg gcaagacatt cagagctagg tcaacaaata 60
tttcattttt ttctgtttta tcctgtggca tatggaccac ctcaaatttc agtgcagaag 120
gcttcctgta gtcaattaac aaagactttg agtgagtcaa tactgttacc tcatggcccc 180
tcactatgat ctcctctaga atgaccttga cattaagcca atggctcatg tcacagggcc 240
acaccaggac cttctcacag aattcacaac tagcacagaa gagttgcagg agccgaaata 300
ccaaagctga cttctcgggc ctcatgatga catttccctc acacactgat ctgcactagc 360
tttgtagtta ctaagcatga aattgaaatg acaatataag cacagaagtt aaaaattaat 420
attttaagtg taaataaagt tcattggttg gttgccagct tcacatttat tgaagatatc 480
aaaaagaaat gcaatgttgc matgtatcag ggaaaatttg ttccaacctt ctagagctta 540
gaaataaaac acataaagat acttttatta tctggattga tgataaagaa atttttttaaa 600
attctttaga tttaataatt catgtgcaga aacatatgca cacaaccaca tttacattca 660
ttccacacta aatccaaggt gtcagatggt ttagaagaac tcatgtttca catcctttgc 720
tcacaaggac aatacaaaga attanctggg aatacacttg gagactttgg gtaactattt 780
tcattaattc tatatactaa gtgcaaagtg ttcagtattt cagaggagaa aaatgcacaa 840
ttgctttnna atatnctgat aattaataaa agctttagta agacatttga cttaggaggt 900
gagatgaaag cttcattagg atttattgtt gccaaanggn aagcatttca caatcaatac 960
aagcatgacg aaagtatagg atatttaaaa gtcattccag t 1001

<210> 390
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-906-251 : polymorphic base A or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-906-251.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-906-251.mis2, potential complement

<220>
<221> primer_bind
<222> 251..270
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 707..727
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-906-251 potential probe

<220>
<221> misc_feature

<222> 648,751..752,758,840,843
<223> n=a, g, c or t

<400> 390
cacctcaaat ttcagtgcag aaggcttcct gtagtcaatt aacaaagact ttgagtgagt 60
caatactgtt acctcatggc ccctcactat gatctcctct agaatgacct tgacattaag 120
ccaatggctc atgtcacagg gccacaccag gaccttctca cagaattcac aactagcaca 180
gaagagttgc aggagccgaa ataccaaagc tgacttctcg ggcctcatga tgacatttcc 240
ctcacacact gatctgcact agctttgtag ttactaagca tgaaattgaa atgacaatat 300
aagcacagaa gttaaaaatt aatattttaa gtgtaaataa agttcattgg ttggttgcca 360
gcttcacatt tattgaagat atcaaaaaga aatgcaatgt tgcaatgtat cagggaaaat 420
ttgttccaac cttctagagc ttagaaataa aacacataaa gatactttta ttatctggat 480
tgatgataaa gaaatttttt waaattcttt agatttaata attcatgtgc agaaacatat 540
gcacacaacc acatttacat tcattccaca ctaaatccaa ggtgtcagat ggtttagaag 600
aactcatgtt tcacatcctt tgctcacaag gacaatacaa agaattanct gggaatacac 660
ttggagactt tgggtaacta ttttcattaa ttctatatac taagtgcaaa gtgttcagta 720
tttcagagga gaaaaatgca caattgcttt nnaatatnct gataattaat aaaagcttta 780
gtaagacatt tgacttagga ggtgagatga aagcttcatt aggatttatt gttgccaaan 840
ggnaagcatt tcacaatcaa tacaagcatg acgaaagtat aggatattta aaagtcattc 900
cagtgagtag tgatcacaga gaaagttcag ggcaggacgt tacagaacaa agttagtttg 960
aaataggaga aattagtttt aaataaacaa ttattagtct g 1001

<210> 391
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-906-451 : polymorphic base A or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-906-451.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-906-451.mis2, potential complement

<220>
<221> primer_bind
<222> 52..71
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 508..528
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-906-451 potential probe

<220>
<221> misc_feature
<222> 449,552..553,559,641,644
<223> n=a, g, c or t

<400> 391

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aataccaaag ctgacttctc gggcctcatg atgacatttc cctcacacac tgatctgcac     60
tagctttgta gttactaagc atgaaattga aatgacaata taagcacaga agttaaaaat    120
taatatttta agtgtaaata aagttcattg gttggttgcc agcttcacat ttattgaaga    180
tatcaaaaag aaatgcaatg ttgcaatgta tcagggaaaa tttgttccaa ccttctagag    240
cttagaaata aaacacataa agatactttt attatctgga ttgatgataa agaaattttt    300
taaaattctt tagatttaat aattcatgtg cagaaacata tgcacacaac cacatttaca    360
ttcattccac actaaatcca aggtgtcaga tggtttagaa gaactcatgt ttcacatcct    420
ttgctcacaa ggacaataca aagaattanc tgggaataca cttggagact ttgggtaact    480
attttcatta attctatata mtaagtgcaa agtgttcagt atttcagagg agaaaaatgc    540
acaattgctt tnnaatatnc tgataattaa taaaagcttt agtaagacat ttgacttagg    600
aggtgagatg aaagcttcat taggatttat tgttgccaaa nggnaagcat ttcacaatca    660
atacaagcat gacgaaagta taggatattt aaaagtcatt ccagtgagta gtgatcacag    720
agaaagttca gggcaggacg ttacagaaca aagttagttt gaaataggag aaattagttt    780
taaataaaca attattagtc tgaatgataa tttataggta aataattact tactcaagtt    840
ttaaaggaca gtcacaagat cgagcttttc cttagcaaga aattcttgca tctcaacata    900
gagtgatatg taaagataag agtttagaaa cagggaaaat gataaaaatt gtatattagt    960
tactgagaca tgtcaacctt atggaataaa acataaattg t                       1001

<210> 392
<211> 744
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 244
<223> 12-907-199 : polymorphic base G or T

<220>
<221> misc_binding
<222> 224..243
<223> 12-907-199.mis1, potential

<220>
<221> misc_binding
<222> 245..263
<223> 12-907-199.mis2, complement

<220>
<221> primer_bind
<222> 46..65
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 533..553
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 232..256
<223> 12-907-199 potential probe

<400> 392
tgactttagg aacatttaga aagtttaaag taaacaatgc tcaatgtaat tgagcatgag     60
gagtggttga attatgattt aaaaccagcc ttgtcttttt ttatagtgac ttgaagaggt    120
ttagtaattc cttcatgttt tggaccgaga ccgattccag gaacaaacgt catgttttcc    180
attatatata gactgggaac actataagag ctatgtggaa tattaattgc agccccccat    240
tgtkccagct aatctctgcc tcaaagatta atggggattg gtgtgatata aggctgaatt    300
gtacctttg accatcaggg ccagtgcaag gcaagataaa tgtgctctgg tgaacttcat    360
cagcttttcc aacccctact tatcccatgt tagtgggatg tttaagccag aaggaaggcc    420
atacattaga ggaaataata gaaacatcag ccccagcatc cactatgccc tcaaaccttt    480
ttccttgaat gtgtatggtg caggtgggcc attgtttaga aattacttta atccaataag    540
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cggctttttc actgttggag cctatcccag agccccctgt cttatctcct ttgtttaaaa 600
caatattagg taataaaagt aattgagcaa ttgactcacc aactggaatg gaaacaggaa 660
ccttggcaga caccataagt ttaatctcat cagaggaatc agaattaatg agaccagtag 720
gaactatgat acctttagca gagg 744

<210> 393
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-907-482 : polymorphic base A or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-907-482.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-907-482.mis2, potential complement

<220>
<221> primer_bind
<222> 20..39
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 507..527
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-907-482 potential probe

<400> 393
aaagtaaaca atgctcaatg taattgagca tgaggagtgg ttgaattatg atttaaaacc 60
agccttgtct ttttttatag tgacttgaag aggtttagta attccttcat gttttggacc 120
gagaccgatt ccaggaacaa acgtcatgtt ttccattata tatagactgg gaacactata 180
agagctatgt ggaatattaa ttgcagcccc ccattgttcc agctaatctc tgcctcaaag 240
attaatgggg attggtgtga tataaggctg aattgtacct tttgaccatc agggccagtg 300
caaggcaaga taaatgtgct ctggtgaact tcatcagctt ttccaacccc tacttatccc 360
atgttagtgg gatgtttaag ccagaaggaa ggccatacat tagaggaaat aatagaaaca 420
tcagccccag catccactat gccctcaaac ctttttcctt gaatgtgtat ggtgcaggtg 480
ggccattgtt tagaaattac wttaatccaa taagcggctt tttcactgtt ggagcctatc 540
ccagagcccc ctgtcttatc tcctttgttt aaaacaatat taggtaataa aagtaattga 600
gcaattgact caccaactgg aatggaaaca ggaaccttgg cagacaccat aagtttaatc 660
tcatcagagg aatcagaatt aatgagacca gtaggaacta tgatagcttt agcagaggtg 720
gatgtcctac ctaacaccag gcccatggaa ccttgaggta aagggccagt gacccctgtg 780
gggacaatta aaagacaaga attaggtagt aaatttagag gaatggtact atggagatca 840
accaccctgc cccctactgt ggaggtagac aagcagtgta ctgtgacaga agaagaggct 900
gggacccatc tgggtttgct gtaggtaaat ttgtttgtac tgggggctgc gttaggaccg 960
cttcaattgg aaatgcaaca ttggtctgag tctgaggtgt g 1001

<210> 394
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 53
<223> 12-909-36 : polymorphic base A or G

<220>
<221> misc_binding
<222> 33..52
<223> 12-909-36.mis1, potential

<220>
<221> misc_binding
<222> 54..73
<223> 12-909-36.mis2, potential complement

<220>
<221> primer_bind
<222> 18..38
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 505..525
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 41..65
<223> 12-909-36 potential probe

<220>
<221> misc_feature
<222> 480,526,538..539,545,554..556,573
<223> n=a, g, c or t

<400> 394
taacttgtgt tttgactcca ggaaaagtaa aatgttagtt tgagctcgag aargaatctg 60
gatactggta actttaccca gaccttggga atcttccccc tcagtacatt taattaatga 120
agtgttacaa tgaattctca aaagatctaa gagatttgtt ttcacttcat tcgctgtgat 180
catgggccta atcagagtca ctgcactggc aaccactgct ggagtggcat tataccaatc 240
tattcaaaca gctcattttg tcaatgatta gcaagtcaat tccacccaaa tgtggaattc 300
tcaacaagac attgatcaaa aattagctaa tcaaattaat gatttaagac agtctgttat 360
ttggcttgga aatcagctga tgagtctcga acatcacatg caaatgcagt gtgatttgaa 420
tacttctgat ttctgtatca caccatattc ctacaatgag actgatcatt catggaaaan 480
tggtcaaagg acaccttctg ggtagggaag ataatttatt cttggnacat aactaaannt 540
taaangaaac aaannntttc tgaagcctct cangctcatt tacccattgt gtctggagct 600
gaggcgttag atcaggtggc agaaagtatt tctggactaa accccacgac ttggattaag 660
tctactgggg gctccatggt agtaaatttt ggaataatat ttctctgttt aatcgacttg 720
tttttagtgt gctggaccag tcaaagattc ccgtgtcaaa acctagagaa caaacaagac 780
tttgcaccat ggcacattta tataaaaaga aagggaggga tgttgtggga agtcagggac 840
cctgaatgga gggactggct ggagctgtgg cagaggaaca taaattgtga agatttcatt 900
ttaatatgga cctttgtcag ttcccaaata atacttttct aatttcttat gcctgtctta 960
ctttaatctc ttaatcctgt tatcttcata acctgaggat g 1001

<210> 395
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 193

<223> 12-909-176 : polymorphic base C or T

<220>
<221> misc_binding
<222> 173..192
<223> 12-909-176.mis1, potential

<220>
<221> misc_binding
<222> 194..213
<223> 12-909-176.mis2, potential complement

<220>
<221> primer_bind
<222> 18..38
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 505..525
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 181..205
<223> 12-909-176 potential probe

<220>
<221> misc_feature
<222> 480,526,538..539,545,554..556,573
<223> n=a, g, c or t

<400> 395
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taacttgtgt tttgactcca ggaaaagtaa aatgttagtt tgagctcgag aaggaatctg      60
gatactggta actttaccca gaccttggga atcttccccc tcagtacatt taattaatga     120
agtgttacaa tgaattctca aaagatctaa gagatttgtt ttcacttcat tcgctgtgat     180
catgggccta atyagagtca ctgcactggc aaccactgct ggagtggcat tataccaatc     240
tattcaaaca gctcattttg tcaatgatta gcaagtcaat tccacccaaa tgtggaattc     300
tcaacaagac attgatcaaa aattagctaa tcaaattaat gatttaagac agtctgttat     360
ttggcttgga aatcagctga tgagtctcga acatcacatg caaatgcagt gtgatttgaa     420
tacttctgat ttctgtatca caccatattc ctacaatgag actgatcatt catggaaaan     480
tggtcaaagg acaccttctg ggtagggaag ataatttatt cttggnacat aactaaannt     540
taaangaaac aaannntttc tgaagcctct cangctcatt tacccattgt gtctggagct     600
gaggcgttag atcaggtggc agaaagtatt tctggactaa accccacgac ttggattaag     660
tctactgggg gctccatggt agtaaatttt ggaataatat ttctctgttt aatcgacttg     720
tttttagtgt gctggaccag tcaaagattc ccgtgtcaaa acctagagaa caaacaagac     780
tttgcaccat ggcacattta tataaaaaga aagggaggga tgttgtggga agtcagggac     840
cctgaatgga gggactggct ggagctgtgg cagaggaaca taaattgtga agatttcatt     900
ttaatatgga cctttgtcag ttcccaaata atacttttct aatttcttat gcctgtctta     960
ctttaatctc ttaatcctgt tatcttcata acctgaggat g                        1001
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<210> 396
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-909-484 : polymorphic base G or T

<220>
<221> misc_binding

<222> 481..500
<223> 12-909-484.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-909-484.mis2, potential complement

<220>
<221> primer_bind
<222> 18..38
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 505..525
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-909-484 potential probe

<220>
<221> misc_feature
<222> 480,526,538..539,545,554..556,573
<223> n=a, g, c or t

<400> 396
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taacttgtgt tttgactcca ggaaaagtaa aatgttagtt tgagctcgag aaggaatctg     60
gatactggta actttaccca gaccttggga atcttccccc tcagtacatt taattaatga    120
agtgttacaa tgaattctca aaagatctaa gagatttgtt ttcacttcat tcgctgtgat    180
catgggccta atcagagtca ctgcactggc aaccactgct ggagtggcat tataccaatc    240
tattcaaaca gctcattttg tcaatgatta gcaagtcaat tccacccaaa tgtggaattc    300
tcaacaagac attgatcaaa aattagctaa tcaaattaat gatttaagac agtctgttat    360
ttggcttgga aatcagctga tgagtctcga acatcacatg caaatgcagt gtgatttgaa    420
tacttctgat ttctgtatca caccatattc ctacaatgag actgatcatt catggaaaan    480
tggtcaaagg acaccttctg kgtagggaag ataatttatt cttggnacat aactaaannt    540
taaangaaac aaannntttc tgaagcctct cangctcatt tacccattgt gtctggagct    600
gaggcgttag atcaggtggc agaaagtatt tctggactaa accccacgac ttggattaag    660
tctactgggg gctccatggt agtaaatttt ggaataatat ttctctgttt aatcgacttg    720
tttttagtgt gctggaccag tcaaagattc ccgtgtcaaa acctagagaa caaacaagac    780
tttgcaccat ggcacattta tataaaaaga aagggaggga tgttgtggga agtcagggac    840
cctgaatgga gggactggct ggagctgtgg cagaggaaca taaattgtga agatttcatt    900
ttaatatgga cctttgtcag ttcccaaata atacttttct aatttcttat gcctgtctta    960
ctttaatctc ttaatcctgt tatcttcata acctgaggat g                        1001
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<210> 397
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 347
<223> 12-910-76 : polymorphic base A or G

<220>
<221> misc_binding
<222> 327..346
<223> 12-910-76.mis1, potential

<220>

<221> misc_binding
<222> 348..366
<223> 12-910-76.mis2, complement

<220>
<221> primer_bind
<222> 272..292
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 704..724
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 335..359
<223> 12-910-76 potential probe

<220>
<221> misc_feature
<222> 17,38,54,57,59,62,69,76,87,95,106,109,115,118,122,128,857,876,888
<223> n=a, g, c or t

<400> 397
aataattata cagaacnttt aagtgagaaa tgtccagntt gtttaatatt tggnagncnt 60
cnaattctna aaacanaatg gtttgcnaac tcatnaaact atttcnacna tatcnagngt 120
cnatttgntg acattttgtg atgtcaacaa aatgataaaa ttttagaaac ccaacatcaa 180
ttccctcaca aaagtacaac cagtagctat ccaaatacaa aaatgccact ctgaattcac 240
cagatctcaa ggcagaagga gaaaacccga agactcacag acatgagaaa acttatgatt 300
ggtaagatga ttaatttttt tggactgtac caccccgctt ccacaarcca aaatgacacc 360
actgtgaggg aacttccttt cacctgcagt tattgaaatg ggaggaggga atttcaagtg 420
gacatttaat ttcttcatgg atctgtaaat ttgaggggaa agcccacatt tgtcccaccc 480
cacagacggt attaagagtg ttcagagggc tgaaccacct ggggtaaatt ggggacagga 540
gatggagtag taatcacagt gatcaccaca cagatcttgg catctgcttt gtgttcctag 600
atacggggat gccacacaga ggagtctcac cagaaccata gcactgcagg gggcaaaatc 660
ttaaggaagg cctgaatctt tgacaaaatt ttacaattcc caggtagtca tgtggagatt 720
ttccatgact gggaaacaag tataagactt gaaattaagt tccaaggctt gtttaaatgt 780
ctcccagatc tagaaatcac tgcaagtctg ggtttaagta ccagtgcagc atttaagttc 840
agatgctcac aataagntct cccaagactg gaaaancaac attaaagnaa atactgagtt 900
ttggtgcagt attaaattct ggtggcaaat attcagtcct tgcctaaaca aaaagcaact 960
ggtggcaagg aattagattc caatattaag tagtaaaggt t 1001

<210> 398
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 12-910-295 : polymorphic base C or T

<220>
<221> misc_binding
<222> 483..502
<223> 12-910-295.mis1, potential

<220>
<221> misc_binding
<222> 504..523
<223> 12-910-295.mis2, potential complement

<220>
<221> primer_bind
<222> 209..229
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 641..661
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 12-910-295 potential probe

<220>
<221> misc_feature
<222> 6,13,24,32,43,46,52,55,59,65,794,813,825
<223> n=a, g, c or t

<400> 398
attctnaaaa canaatggtt tgcnaactca tnaaactatt tcnacnatat cnagngtcna 60
tttgntgaca ttttgtgatg tcaacaaaat gataaaattt tagaaaccca acatcaattc 120
cctcacaaaa gtacaaccag tagctatcca aatacaaaaa tgccactctg aattcaccag 180
atctcaaggc agaaggagaa aacccgaaga ctcacagaca tgagaaaact tatgattggt 240
aagatgatta atttttttgg actgtaccac cccgcttcca caagccaaaa tgacaccact 300
gtgagggaac ttcctttcac ctgcagttat tgaaatggga ggagggaatt tcaagtggac 360
atttaatttc ttcatggatc tgtaaatttg aggggaaagc ccacatttgt cccaccccac 420
agacggtatt aagagtgttc agagggctga accacctggg gtaaattggg gacaggagat 480
ggagtagtaa tcacagtgat caycacacag atcttggcat ctgctttgtg ttcctagata 540
cggggatgcc acacagagga gtctcaccag aaccatagca ctgcaggggg caaaatctta 600
aggaaggcct gaatctttga caaaatttta caattcccag gtagtcatgt ggagatttc 660
catgactggg aaacaagtat aagacttgaa attaagttcc aaggcttgtt taaatgtctc 720
ccagatctag aaatcactgc aagtctgggt ttaagtacca gtgcagcatt taagttcaga 780
tgctcacaat aagntctccc aagactggaa aancaacatt aaagnaaata ctgagttttg 840
gtgcagtatt aaattctggt ggcaaatatt cagtccttgc ctaaacaaaa agcaactggt 900
ggcaaggaat tagattccaa tattaagtag taaaggttga acaacacaag aatacaccta 960
taaaagttag aacatgtgga tatctcttta agtatggaaa c 1001

<210> 399
<211> 740
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 240
<223> 12-911-22 : polymorphic base G or C

<220>
<221> misc_binding
<222> 221..239
<223> 12-911-22.mis1

<220>
<221> misc_binding
<222> 241..260
<223> 12-911-22.mis2, potential complement

<220>
<221> primer_bind
<222> 219..237
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 653..673
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 228..252
<223> 12-911-22 potential probe

<220>
<221> misc_feature
<222> 354,703,732,739
<223> n=a, g, c or t

<400> 399
atatttcca ctgtaatatt ttatcttagc tatatagcct aaaatttaaa caattaatct 60
cggggggag tgtcgcattc ttttgttgta ttttcctagg cgatttgatc cttttctaat 120
acattgctga cacaagatca ctaacaattc taaaatgtcc tattcatgat atcactattt 180
ttatgatgtc acatttttta aaccttagtt gatatgttta ttcacaatat gctggtccts 240
tgtagtgcat aaatatgaac tgacatcaat agatgtaaag aagtcaaaag cataaaattc 300
acaggaggca atagactata caagtcatgg aagtgttcta tgatattagt ttgntattaa 360
aaacataaca atgttccctt tttgataaaa ataagccatt ttacatagcc aacagtactg 420
ggcttagacc atgaattggt aatgataata atgatagtgc attactctgg aaaaggttta 480
gtatatttct ctagaactca tctagatatt atggcctaca tttctgcctt tagtccaata 540
ttttttgtgt cctcaatgag aaagagatag ttatcatcaa tgtgttcaaa caaaagggta 600
agtgatcctt tcttagggag agaatatgtc aacaaggtga tcaagttgaa cagattattt 660
taggagaggt aacgacagga aacattttat taaaaatact aanttttaaa aaactttgat 720
cgtttacttg ancaaagant 740

<210> 400
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-912-65 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-912-65.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-912-65.mis2, potential complement

<220>
<221> primer_bind
<222> 437..457
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 908..928
<223> downstream amplification primer, complement

<220>
<221> misc_binding

<222> 489..513
<223> 12-912-65 potential probe

<220>
<221> misc_feature
<222> 24,47,131,137,440
<223> n=a, g, c or t

<400> 400
acaacaggaa gctgcaccct tctnctgcat tcagacagaa gtgaganctg ctgggccgga 60
agctctagca aggatgatag caatacaagt tgattcttaa ttaattaaag cacattgaga 120
agctgatcca naaaagncaa acactattaa atctctcaga ctttaaaaat acagtcatat 180
tccaggagtt aaggggtcca gctcaccaac atggcacatg tatacatacg taacaaacct 240
gtacgttgtg cacatgtacc ctagaactta aagtataata aaaaatatat atatacatag 300
tcatattcat ttttcacaac atagcatatt gtgacaggtc tttcttgatt tactaagttt 360
acttattatc ctgtgaagta tattttcata cctgaatttt acctagcttc agccttccat 420
taacgttgca ttcattcttn aacatttgta aaccaccata ttttctagaa attggtgact 480
atattctaaa atcattgtag ycacgaaatc atatgaatac ctgcttggcc tctccggata 540
gggtcaagtt tctcacataa gcaaaattta cttatttggc atatacaatg tgaacataat 600
cttaaaacct gactttggct tttggtgtta ttaataaggt tcttaatcca atttttgttt 660
tttttttaca gaagtgatac agctatactg taatcctagc attcctgagt tttgtatata 720
gcttggaaat aatatttatt gtcaaatatt tttaaatact tcactttctt ctaatatatt 780
tattaacctt agcatctttt tttgcatttt ttccctgtga agtgtcattc actctatcaa 840
ttactatcag aaaaatctgt tatcatcttg cctatttatg caaagcaaat gattctccaa 900
ctgttgactc taatccttcc tctcaaatag gttctgctaa ataaatgacc ctgagtctct 960
gagacatttg ttgtatcaaa gcacaacaac attaacagta a 1001

<210> 401
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 384
<223> 12-914-106 : polymorphic base C or T

<220>
<221> misc_binding
<222> 365..383
<223> 12-914-106.mis1

<220>
<221> misc_binding
<222> 385..404
<223> 12-914-106.mis2, potential complement

<220>
<221> primer_bind
<222> 279..298
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 773..793
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 372..396
<223> 12-914-106 potential probe

<220>

<221> misc_feature
<222> 536,990
<223> n=a, g, c or t

<400> 401
aactcctatt atatggaggt agttttctta ataatgtttg atactttcca tatgcctact 60
tcactaattt taattatttc tcttttttg ctcttctgat tgggtaatta catatgtttt 120
atctttagga ttgctgattc cttactctgt ttgaccaagt ctgctgttga agttttctac 180
tgagtttttc aattcacttc acatattttt tattaattgg atttcttttt atttttaaaa 240
catttccact tctttgcaaa atttatcatc attttcctgg attattctct aaagtgtgtt 300
ttttttcaac tctctattca tatgtgctgt gatttctgaa cttttaaaat aggtgtgcac 360
tgaatttctt gtcaaaaatt ttayggagca tctgaacctt aattctgcac tgtaacttaa 420
aactagactt gcagtgattt ctaggtctgt gagatactta agcaataact ggagcttaat 480
ctcaaatgtt atacttgttt gcaggtcata gaaaagctcc gtatgagtaa ctgggnatta 540
taaaaatacc tgccaaagat tcaggccttc ctttggattt tggcccctgc agtgttatgg 600
aactggtcag actcctcagc gtggcattcc tgctaatagg aacaccaagc agttgctgag 660
atgtgtgtgc ctgtcactgt gattagtact tccactcttg tttccaattc accccaggtc 720
attcaactct atagccactc ctaatgcctc tcctgaggta ggacaaaagt gggcttccca 780
aaccaaaaag attcacagat ccatgaagaa actgaacatt cacttcaaat ttcctcctct 840
gatcttggca actgcaggta aaataaagtt ctgtcacagt ggtgtcttct tggtgtgtgg 900
aaggggtgcc ataatccaaa aaattattca ttttacagat catgagtttt cccatgtcta 960
tgagtcttgg gattttcttc ttctcttttn agctctggtg a 1001

<210> 402
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 12-914-252 : polymorphic base A or T

<220>
<221> misc_binding
<222> 483..502
<223> 12-914-252.mis1, potential

<220>
<221> misc_binding
<222> 504..523
<223> 12-914-252.mis2, potential complement

<220>
<221> primer_bind
<222> 252..271
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 746..766
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 12-914-252 potential probe

<220>
<221> misc_feature
<222> 509,963
<223> n=a, g, c or t

<400> 402
ttaataatgt ttgatacttt ccatatgcct acttcactaa ttttaattat ttctcttttt 60
ttgctcttct gattgggtaa ttacatatgt tttatcttta ggattgctga ttccttactc 120
tgtttgacca agtctgctgt tgaagttttc tactgagttt ttcaattcac ttcacatatt 180
ttttattaat tggatttctt tttattttta aaacatttcc acttctttgc aaaatttatc 240
atcattttcc tggattattc tctaaagtgt gttttttttc aactctctat tcatatgtgc 300
tgtgatttct gaacttttaa aataggtgtg cactgaattt cttgtcaaaa attttatgga 360
gcatctgaac cttaattctg cactgtaact taaaactaga cttgcagtga tttctaggtc 420
tgtgagatac ttaagcaata actggagctt aatctcaaat gttatacttg tttgcaggtc 480
atagaaaagc tccgtatgag tawctgggna ttataaaaat acctgccaaa gattcaggcc 540
ttcctttgga ttttggcccc tgcagtgtta tggaactggt cagactcctc agcgtggcat 600
tcctgctaat aggaacacca agcagttgct gagatgtgtg tgcctgtcac tgtgattagt 660
acttccactc ttgtttccaa ttcaccccag gtcattcaac tctatagcca ctcctaatgc 720
ctctcctgag gtaggacaaa agtgggcttc ccaaaccaaa aagattcaca gatccatgaa 780
gaaactgaac attcacttca aatttcctcc tctgatcttg gcaactgcag gtaaaataaa 840
gttctgtcac agtggtgtct tcttggtgtg tggaaggggt gccataatcc aaaaaattat 900
tcattttaca gatcatgagt tttcccatgt ctatgagtct tgggattttc ttcttctctt 960
ttnagctctg gtgaattcag tgtggctttt tgtatttaca t 1001

<210> 403
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 10-448-266 : polymorphic base A or C

<220>
<221> misc_binding
<222> 483..502
<223> 10-448-266.mis1, potential

<220>
<221> misc_binding
<222> 504..523
<223> 10-448-266.mis2, potential complement

<220>
<221> primer_bind
<222> 238..257
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 660..679
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 10-448-266 potential probe

<220>
<221> misc_feature
<222> 772,907,915
<223> n=a, g, c or t

<400> 403
gaattatcac attgcacaag gatggctctg aaatggacta cagttctgct gatacaactc 60
agtttttact ttagctctgg gagttgtgga aaggtgctgg tatgggccgc agaatacagc 120
ctttggatga atatgaagac aatcctgaaa gaacttgttc agagaggtca tgaggtgact 180

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gtactggcat cttcagcttc cattcttttt gatcccaacg actcatccac tcttaaactt    240
gaagtttatc ctacatcttt aactaaaact gaatttgaga atatcatcat gcaattggtt    300
aagagattgt cagaaattca aaaagataca ttttggttac ctttttcaca agaacaagaa    360
atcctgtggg caattaatga cataattaga aacttctgta aagatgtagt ttcaaataag    420
aaacttatga aaaaactaca agagtcaaga tttgacatcg tttttgcaga tgcttattta    480
ccctgtggtg agctgctggc tgmgctattt aacataccct ttgtgtacag tcacagcttc    540
agtcctggct actcatttga aaggcacagt ggaggattta ttttccctcc ttcctacgta    600
cctgttgtta tgtcaaaatt aagtgatcaa atgactttca tggagagggt aaaaaatatg    660
ctctatgtgc tttattttga cttttggttc caaatattta atatgaagaa gtgggatcag    720
ttttacagtg aagttttagg taagattttt ttcagttagt aacatgaagc tnctaactta    780
tttgtgtctt tgaagcacaa cttgcataaa gccataaagt cagggaagtg gagtttttga    840
taaatgaatt tatgaaatga aaatacaaga tgatctacca atctcacaaa tattatagaa    900
aagcttnaaa ttatnggggt cagtgaaaac gctgtgacca tcactcatac agaacacccc    960
aggaaatcat aaacctatat attagtacac ctaagacttt a                       1001
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<210> 404
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 10-453-330 : polymorphic base C or T

<220>
<221> misc_binding
<222> 483..502
<223> 10-453-330.mis1, potential

<220>
<221> misc_binding
<222> 504..523
<223> 10-453-330.mis2, potential complement

<220>
<221> primer_bind
<222> 172..189
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 578..597
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 10-453-330 potential probe

<220>
<221> misc_feature
<222> 19,31,101,212,337,520,661
<223> n=a, g, c or t

<400> 404

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cattagtcca actggaaant cttgtattaa ngttttgcag tctgaagtca caccaccata     60
tagccttcag ttacatctcc aacacaagta cctgtttttt ncctctgaaa tctgaaaagt    120
aatagcaaat tagttcagtg tgttatctag aaaacactgt cactttcaga gcctttcatt    180
gtgcatctca ttttattcct atgaataatt tntgctaaaa ttcatccaat cctaggtcat    240
ccaaaaacca gagcttttat aactcatggt ggagccaatg gcatctatga ggcaatctac    300
catgggatcc ctatggtggg cattccattg ttttttngat caacctgata atattgctca    360
catgaaggcc aagggagcag ctgttagagt ggacttcaac acaatgtcga gtacagacct    420
```

```
gctgaatgca ctgaagacag taattaatga tccttcgtga gtagaacaat atttttcact    480
agatggtatt aatagatagc ttytcttgtc agtagtgagn catgagtttc atccttttta    540
taagagagtg attttgaaag aatttaaatg atttaaccaa tccgaaatct gcttttactt    600
tttatctgtt atttaaaaat tgtatttgaa ccccatacat ctaatgagta accagttagt    660
ngaaacagtt ttctaaataa aaataatttt aaaatgatat agataatata aaaaaataca    720
tttcttaaaa atttgacata atgaatccat agtagaaagg aagaataatc ttgaaataat    780
ataataaaat gttttaatta aatatctaaa atgtctcaga atataactat tttcttgcag    840
aaaaattaat ttttattatt atctttattg taacagactt gaaaatgaga tttaattttg    900
atagcataaa acccacctat ttatggcaaa aattccaaat atttttacta tgtttacaga    960
gtcatgaagt catcaccagt gtataagttt ggaacatttt t                       1001
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<210> 405
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 10-455-367 : polymorphic base C or T

<220>
<221> misc_binding
<222> 483..502
<223> 10-455-367.mis1, potential

<220>
<221> misc_binding
<222> 504..523
<223> 10-455-367.mis2, potential complement

<220>
<221> primer_bind
<222> 135..152
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 545..564
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 10-455-367 potential probe

<220>
<221> misc_feature
<222> 161,248
<223> n=a, g, c or t

<400> 405

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tttaaaagcc aaactttgta tgatgactca aattaaaata cataaattct atatcaattc     60
tttgacattt actttgaatt atttgacact ttaaaagcct ttcatagact tgatatctac    120
aggcaaatta acttactttc agtgtcggta tctttatttt ntatccttca gatataaaga    180
gaatattatg aaattatcaa gaattcaaca tgatcaacca gtgaagcccc tggatcgagc    240
agtcttcntg gattgaattt gtcatgcgcc acaaaggagc caaacatctt cgagttgcag    300
cccacaacct cacctggttc cagtaccact ctttggatgt gattgggttc ctgctggctt    360
gtgtggcaac cgtgctattt atcatcacaa agtgttgtct gttttgtttc tggaagtttg    420
ctagaaaagg aaagaaggga aaaagggatt agttatatct gagatttgaa gctggaaaac    480
ctgatagata ggaatacttc agytgattcc agcaataaat attgtgatgc aagatttctt    540
tcttcctgtg acaaaaaaaa atcctttcga agtctacctt gtcaagtaaa aatttgtttt    600
tcagagattt accacccagt taatggttag aaatattctg tggcaatgaa gaaaacacta    660
```

```
ggggaaataa aaaataatat aaagccatat gagcttgtat tgaaatttgt tgcacttata     720
ttgaaatgtg atcatggctc acttcagcct caacttacta agctcaagag gttctctcac     780
ctcagccccc caagtagctg ggaccatagg tgcatgtcac catgtccaac taattttta      840
tttttgtag tgatgagatc tcattgtgtt ctccatgctg atttcaaact cctgggctca      900
aacaatcctc ccattttagc atcccaaagg gatgagatta caggtatgta ccaccataac     960
tttacaaaat gagattttta tataagaatg attcaaatgt t                        1001

<210> 406
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 12-5-158 : polymorphic base C or T

<220>
<221> misc_binding
<222> 484..502
<223> 12-5-158.mis1

<220>
<221> misc_binding
<222> 504..523
<223> 12-5-158.mis2, potential complement

<220>
<221> primer_bind
<222> 346..366
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 801..821
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 12-5-158 potential probe

<220>
<221> misc_feature
<222> 314,336,793
<223> n=a, g, c or t

<400> 406
caaaggatga aggtcctctg gaccagaagc acccaaccag attattcagc aacaggactg      60
agggtgcctg gggcaagtgc cagctcatgc catcaccctc acagagcccc gggtaagttt     120
aaccattgag ggccaggaag tggacttcct cctgggcact ggcgcggcct tctcaatttt     180
aatcccctga cccagatgac tgttctcaaa gtccgttact atctgaggaa tcttaggaca     240
gcctgtaacc aggtatttct ctcgcctcct cagctgcaat tgagagactt tgctctttca     300
catgcctttt ctgnttatgt ctgaaagtcc cacacncttt attagggaga gacatatttg     360
ccaaagctgg ggccattatc tacatgaata tggggaacaa gtgacccatt tgttgtcccc     420
tacttgaaga agaaatcaac tttgagctct gggccttaga aggacaattt ggaagggcaa     480
agaatatcca tccagtccac atyaagctaa aagacaccac cacttttcct tatcaaagga     540
aatatcactt aaggcctgaa gttctcaaag gattacagga tattgttaga aatttaaaag     600
ctcaaggttt agtaaaaaaa tgtagcagtc tttgaaacac cccaatccta ggaatacaaa     660
aaccaaatag tggagactag ggcaagacct caggtttcac ctatctacct tcaggaaatt     720
tttttcatct gtgataacac agcctatcga tgccaaaatg gcactccaaa agaactatgc     780
tatgtctcat ttnctagcac ctcccatgtc catatatact gaacaagagt tacaaagtct     840
ccttataccc caatctcgcc acacccgagc ccttattgtc ccttttacag taggagcagg     900
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aatactaggc aggcttggga ctggaattgg aggcataacc tcctccaccc aattctatta 960
taaattatca tgagaattaa atgatgacat ggaatgagtt g 1001

<210> 407
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 499
<223> 12-9-367 : polymorphic base G or A

<220>
<221> misc_binding
<222> 500..518
<223> 12-9-367.mis1, complement

<220>
<221> misc_binding
<222> 479..498
<223> 12-9-367.mis2, potential

<220>
<221> primer_bind
<222> 847..865
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 386..406
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 487..511
<223> 12-9-367 potential probe

<220>
<221> misc_feature
<222> 231,891
<223> n=a, g, c or t

<400> 407
gggagcaaca agcagctagg ggaaccccac cctcccaggg aagcattgag taattgtgca 60
accacaggaa accatacttc tcccaagaat ctttgcaacc ctcaagtcaa gaagtctacc 120
tgtgaactca catcaacagg gccttcattc tgacagccag aaaaaggtgg agtctcagca 180
gagcatctac tcaggcatgc gaggtgaccc tggaacctta gctatgtggg nctttctggc 240
aaaagtaact gcagctttgg caaattagga gattagaacc acatacatat ccctaggaaa 300
aaggctgaat ccaagggact gagaagatac agcctgcagg ccccactttc acagcacctc 360
acaggtgagc acccactggc ttaaaattcc agcaagccac caatagcggc attgcacctc 420
cataagaagg agctctcagt gggagtggca ggctgccacc tttgctggcc tttattctta 480
gtttttctct cccatcacrg aaattccatc ctatgagtgg actggggcaa tggctatttg 540
gtactcagta ttctttgtgc cgttcttgag ttgaatctct gagttatgac tgtggctgaa 600
tgaaagatgt gagacccttc ttagccacac ttgcctagaa ttaagcttct ggagcatatg 660
cctgagtcta tatatataaa aaaatcagag agacaccttt tctcaactgc ataccctgac 720
actcaactgg gagctttgaa gagtgagagc cctgtggtag catcagcacc tccctggaag 780
agagggagtt tctgtcactg aactaggagg gggggcaaat gagcatgttg tggcttaaat 840
gccaaagaca cttgctgttt tcactacaaa ttactggatt ttcttcagtg naatgttact 900
ttattatatg cctttaggat tattgccagg gacaccaaat ggttgtttta aaaaacaatt 960
ttcaccagtt attcctgttt cccttgaaat ttcctccatg g 1001

<210> 408

<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-10-303 : polymorphic base T or C

<220>
<221> misc_binding
<222> 502..521
<223> 12-10-303.mis1, potential complement

<220>
<221> misc_binding
<222> 482..500
<223> 12-10-303.mis2

<220>
<221> primer_bind
<222> 787..807
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 335..355
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-10-303 potential probe

<220>
<221> misc_feature
<222> 67,85,89,608,657,722..723,752,854,885
<223> n=a, g, c or t

<400> 408
agttgcccca ccttttcaga ccaaacccat gtatcattta catgtattga ttgatgtgga 60
acatctnctc taaattgtat aaaanccang gttgtagcct gaggacattg ggcacatgtt 120
ctaaacagct gaaggctgtg ttatgggcca ttagtcactc atatttggct cagaataaat 180
ctctttgaat atttacaga gtttgactca tttcctcaca ataatttgac acttgaacat 240
gtgggaactc ccagaaaacc caggaccccc aaaatgtttc ctgaacttga aactaaagta 300
ccagaagggg cccattgaag gcctttcaaa ctttaagctc ctctgatgga actggtcagt 360
cctcttgagc cctggatctc cctttggttg acagacatca atttttcctg aacttatttt 420
tttcctagga agttgttgtt taggattcta attctagttc tggggtgcat tctgaagagt 480
cttctccatt gccttttatc yaaaagataa actcaattgg cttgtctgca catttgcatg 540
aagatagaac tgtcatttta tagataaatg agggactgag ctcctcagct ttgaagagaa 600
agaacatntt tgctcctccc agaaaatgag ccctggatga ccagaggcta agtgggnaac 660
atctagatgt ttgactccca ttcccgttat gtgcagtgcc cctacagaag atgccccaac 720
anntaattag tttcttctgt gtttaaatgt tntttaactg ctgagatatt taaaagcttg 780
tagaatcaat ctctaagaag cagacacatc atattattgc aatttttgta gttcaattta 840
ctatggaatt tttnatgact ctccatcaag tataccttca tgttncatat attttcctaa 900
gtatatatgt acatatcact ttatgtagaa agtcttcctc aaattaaact agtgaaaata 960
ttacttgttc actcatggat agacatagat ttatgtatct g 1001

<210> 409
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-14-264 : polymorphic base C or T

<220>
<221> misc_binding
<222> 482..500
<223> 12-14-264.mis1

<220>
<221> misc_binding
<222> 502..521
<223> 12-14-264.mis2, potential complement

<220>
<221> primer_bind
<222> 237..257
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 680..700
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-14-264 potential probe

<220>
<221> misc_feature
<222> 307,577,897
<223> n=a, g, c or t

<400> 409
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tgaaatgtta acttcataca atatagtaaa tggtcacata tcactgttcc tgttatcttt     60
actgggggct ggaaaaaatg ggaagaactg ggcctccaga cttttcttgg atgcctcatt    120
gtcaaatgtt aataaagagc acagtgggac tttgtgtttt ctatttttga tggtgcccaa    180
atggtctgta ctttcagatg tattgcacat ttacattctc aataaagtat attaatgata    240
aaagacttgt aacatggaga ataactcaag gagaaagtct tttattagtt ttctgttgct    300
gcattancaa actacctcat ttcttaatat cttaaaaaaa aaactgttta actcatggtt    360
tcatggttct tctcacaatt ttgatctagg ctagtatagc tgatctcagc aggtcctgcc    420
cactttcagg tgcatatgaa actataggaa cctggctgat cctaaaagcc gttagttgca    480
tgctttgcat ttgcctgagc ygtgtctttg taggtatatg tcatgtgggt gtctctcatc    540
atcacaatgt gtaactgtag tacaagtgct aataggnaaa gtctcataca ctaaagtaaa    600
caacattaag catactatat ttatgtaata aatgtatgat tgtgcaccat atgtcctact    660
ggaaacaatt tttaaaattc tcaaactact gcctttcaat ttaagactct actgggctac    720
ataatttaaa gaaatttaga aatttctctc atgaaaaaat atacatttcg tgaaaaatat    780
ccatacacgt taaataaata tgaagagtgt tttaataggc cccagatttt taggacagtc    840
cagattacac cttttctgct tgagtcactt taatgatgcc tcaaaaattg gataatnttt    900
aacattccac atgaaacttt gtaataaatt atatatatcg cacatatttt acatacatat    960
aactttatat aaaaacttta aaaatagtaa atatacagat a                       1001
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<210> 410
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 499
<223> 12-17-86 : polymorphic base T or A

<220>
<221> misc_binding
<222> 500..518
<223> 12-17-86.mis1, complement

<220>
<221> misc_binding
<222> 479..498
<223> 12-17-86.mis2, potential

<220>
<221> primer_bind
<222> 565..584
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 121..140
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 487..511
<223> 12-17-86 potential probe

<220>
<221> misc_feature
<222> 44,197,388..389,398,407,627,852,856,941
<223> n=a, g, c or t

<400> 410
gaagttgagg tgtacaggtg aggcaacttg ccaaacccca catnaattct ctagaggttt 60
tgcagggact tgaatccagg ctaactggat ccagagtgca ggagctctta accaccatgc 120
tacgctgact cccctttctg agttagttat tttcaaaatg tcacatttgt agtttccatt 180
ttcttgtctc tatattnaag tgtatattat tatgaatgta taattaaatt tttagaaata 240
tccttgtagc tatttatcac ttcctaacaa actaccctca atcatgggga ctttgaaaaa 300
caattagcat tttattacaa tttccatagc atgagtgttg ggtaggttca gcaagatggt 360
tcatacacag tatttctcag gtcattannc tttaatangg gtggctnggg gatgtaatca 420
tctgaaggtc attcattcac gtacttggtg atggatgtca aaagactcaa attcctgtgg 480
gactgaataa tcatgactwc ttagtctctt ctttgcatca ttccccgagt tgtcatttat 540
catcaggact ttgggtgtaa cactgggctc caaagtatat agagggagaa aaagggaaag 600
agggaggaga gagagagaga gagaaangag gtataagtaa aagacataga cagacagaca 660
aacggagaca gactgccttt tctaacacag tcttcaaaac tatgctgtca cttccagtat 720
actttctttg ctgagaaagc cacgagtctt gccaaaattc aaggggaggg accacggttt 780
gataagaatg tcaaagtgtt tgcagtgatg tctcaaaatt ccacaaatat aacctattga 840
gttagtcaac angaangcct ctaagcaact atgaaattca ttacatatgg acattaaaaa 900
cacaataaaa tcctaaaaag tgtgaattta tattttttac naactactga aacattaagc 960
attttaaaat atttactcat agatttttat atatgaaata g 1001

<210> 411
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-19-163 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500

<223> 12-19-163.mis1, potential

<220>
<221> misc_binding
<222> 502..520
<223> 12-19-163.mis2, complement

<220>
<221> primer_bind
<222> 339..357
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 781..801
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-19-163 potential probe

<220>
<221> misc_feature
<222> 612,814,950
<223> n=a, g, c or t

<400> 411
accttgaaaa gaggttagat gaatttctaa ctagaataac cagtgtttga cttcttcctg 60
gtttaagctt gggaaagtgt acgtgtccag gaatttatca atttgttcta aattttctag 120
tttatttgcg tacaggtgtt tatagtattc tctgatggca gtttgtattt ctgtgggatc 180
agtggtgata tcccccatat cattttttat tgcgtctatt tgattctgcc aattcatagc 240
acatacagca ttctggagaa ctttggccca gccatgaaaa gtactgttac ctagctgaca 300
ctgtaactat aacttctaaa ggccatttca ctatagtaca aaggcagttg cttcaggaga 360
atgaggaaca tggtaaaacc agtaaatttc atgagcatga gctcattgtt gcacttcttt 420
gtcagtaaag ccagttcctt agtcagaaac aatactgtgt ggaagaccat gatagagaat 480
taggcatcca gtaaatttat rgatggtagt tttgacagat gtatatgttc agagaagata 540
aatccatatt caaaataagt atgtattcca gtaagaaaaa aatgcagctc cttctatgat 600
ggaggtggtc tnaaggtaat caatctgcca ctgggaagct ggttgattat cttggagaat 660
gatgccatat caggggctta gcatggctct ctgttcctgc atattgggca cacagtggtg 720
gctttagcca ggttgaactt agtgagtgaa agattatgtt gcttaaccca tgcataactt 780
ccatcaatgc catcatagcc actttgctca tgangcccat tgggtgataa caggggtagc 840
tgaggaaaga gtctgacccc agatctacag gaggggtcat cccatccact ttattattaa 900
aattttcttc tagtgatgtc attctttgaa gaacattcac atgactcacn aaatgtcttc 960
atatattttg ccccctcaaa gaggtttatc cagatagttt t 1001

<210> 412
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 10-457-284 : polymorphic base G or T

<220>
<221> misc_binding
<222> 483..502
<223> 10-457-284.mis1, potential

<220>
<221> misc_binding

<222> 504..523
<223> 10-457-284.mis2, potential complement

<220>
<221> primer_bind
<222> 220..238
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 621..639
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 10-457-284 potential probe

<220>
<221> misc_feature
<222> 715
<223> n=a, g, c or t

<400> 412
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ggtcataaaa attattgctt gactagagta attgtaaaca taaaagaaca ccaaacacac      60
taaaataaat atgaggtcat caatcttttg ttggtctcct tggcatgcac ctattcagac     120
tgttagtatt atgtatttac ttcaaatttt agcagttata ttttaacttg attgattttt     180
cctcagatat aagtatgaga aatgacagaa agaaacaaca actggaaaag aagcattgca     240
taagaccagg atgtctctga aatggacgtc agtctttctg ctgatacagc tcagttgtta     300
ctttagctct ggaagctgtg gaaaggtgct agtgtggccc acagaataca gccattggat     360
aaatatgaag acaatcctgg aagagcttgt tcagaggggt catgaggtga ctgtgttgac     420
atcttcggct tctactcttg tcaatgccag taaatcatct gctattaaat tagaagttta     480
tcctacatct ttaactaaaa atkatttgga agattctctt ctgaaaattc tcgatagatg     540
gatatatggt gtttcaaaaa atacattttg gtcatatttt tcacaattac aagaattgtg     600
ttgggaatat tatgactaca gtaacaagct ctgtaaagat gcagttttga ataagaaact     660
tatgatgaaa ctacaagagt caaagtttga tgtcattctg gcagatgccc ttaantccct     720
gtggtgagct actggctgaa ctatttaaca taccctttct gtacagtctt cgattctctg     780
ttggctacac atttgagaag aatggtggag gatttctgtt ccctccttcc tatgtacctg     840
ttgttatgtc agaattaagt gatcaaatga ttttcatgga gaggataaaa aatatgatac     900
atatgcttta ttttgacttt tggtttcaaa tttatgatct gaagaagtgg gaccagtttt     960
atagtgaagt tctaggtaag tcatgtgtct aactggtgct t                        1001
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<210> 413
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 10-460-221 : polymorphic base C or T

<220>
<221> misc_binding
<222> 483..502
<223> 10-460-221.mis1, potential

<220>
<221> misc_binding
<222> 504..523
<223> 10-460-221.mis2, potential complement

<220>

<221> primer_bind
<222> 283..301
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 686..704
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 10-460-221 potential probe

<220>
<221> misc_feature
<222> 128,707,966
<223> n=a, g, c or t

<400> 413
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atggggatta taattcaaga tgagaggaga tttgggtggg gacagtcaaa ccatattagt     60
gacttatttt aataattatt tatgattgtg aatatactga tgttacatta aagatgtgat    120
ttcttctnac agatctctga atacatttgc cttccttata tatacatatg agcaacatat    180
gcaataaata aaatctaaat tatgactata tataaatgta tttatatata ttttatcaat    240
gcacagacat tttatatatg tttgggtatg ttattccaag tcctttcagg aaaatacctg    300
catattcaaa taacaattct cgtgttagct accttttgtt ttgttttgtt tttttccatc    360
aggaagaccc actacattat ttgagacaat ggggaaagct gaaatgtggc tcattcgaac    420
ctattgggat tttgaatttc ctcgcccatt cttaccaaat gttgattttg ttggaggact    480
tcactgtaaa ccagccaaac ccytgcctaa ggtaaatgta ttcttgtttc atttgtttgc    540
ttgacatttt cagaaggaat ggctggatat gtttctttca gagtgtttaa ctcagagtga    600
ggggaatatg ggaggtcaaa aacaaggact tgccattaga aaatcatata tttctgtagt    660
atcacaagta tgtgaatgtt attatcatta aagaccaaag aggtttnact agggagattt    720
tgaaaacagg gttggttaaa gtaaggcctt cattgtgcca cccaaaagat agtatgattc    780
atttcttcaa aaaatatttg tagagtgatt aatacaaacc acaggtaagt gctggatttt    840
cagagaataa aggtagcaca gtttctgctc cctcatgcct tacattgtac tttgaaagat    900
agaataaaaa caagtgaaaa agaaaagtct aaaaagtgtt ataaggaaag accacaatga    960
taaagnaaat atgcagaaga gatcccaaac tcattgacaa t                       1001
```

<210> 414
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 10-460-232 : polymorphic base A or G

<220>
<221> misc_binding
<222> 483..502
<223> 10-460-232.mis1, potential

<220>
<221> misc_binding
<222> 504..523
<223> 10-460-232.mis2, potential complement

<220>
<221> primer_bind
<222> 272..290
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 675..693
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 10-460-232 potential probe

<220>
<221> misc_feature
<222> 117,696,955,992
<223> n=a, g, c or t

<400> 414
aattcaagat gagaggagat ttgggtgggg acagtcaaac catattagtg acttatttta 60
ataattattt atgattgtga atatactgat gttacattaa agatgtgatt tcttctnaca 120
gatctctgaa tacatttgcc ttccttatat atacatatga gcaacatatg caataaataa 180
aatctaaatt atgactatat ataaatgtat ttatatatat tttatcaatg cacagacatt 240
ttatatatgt ttgggtatgt tattccaagt cctttcagga aaatacctgc atattcaaat 300
aacaattctc gtgttagcta ccttttgttt tgttttgttt ttttccatca ggaagaccca 360
ctacattatt tgagacaatg gggaaagctg aaatgtggct cattcgaacc tattgggatt 420
ttgaatttcc tcgcccattc ttaccaaatg ttgattttgt tggaggactt cactgtaaac 480
cagccaaacc cctgcctaag gtraatgtat tcttgtttca tttgtttgct tgacattttc 540
agaaggaatg gctggatatg tttctttcag agtgtttaac tcagagtgag gggaatatgg 600
gaggtcaaaa acaaggactt gccattagaa aatcatatat ttctgtagta tcacaagtat 660
gtgaatgtta ttatcattaa agaccaaaga ggtttnacta gggagatttt gaaaacaggg 720
ttggttaaag taaggccttc attgtgccac ccaaaagata gtatgattca tttcttcaaa 780
aaatatttgt agagtgatta atacaaacca caggtaagtg ctggattttc agagaataaa 840
ggtagcacag tttctgctcc ctcatgcctt acattgtact ttgaaagata gaataaaaac 900
aagtgaaaaa gaaaagtcta aaaagtgtta taaggaaaga ccacaatgat aaagnaaata 960
tgcagaagag atcccaaact cattgacaat tnaaagtgag t 1001

<210> 415
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 10-460-235 : polymorphic base C or T

<220>
<221> misc_binding
<222> 483..502
<223> 10-460-235.mis1, potential

<220>
<221> misc_binding
<222> 504..523
<223> 10-460-235.mis2, potential complement

<220>
<221> primer_bind
<222> 269..287
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 672..690
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 10-460-235 potential probe

<220>
<221> misc_feature
<222> 114,693,952,989
<223> n=a, g, c or t

<400> 415
tcaagatgag aggagatttg ggtggggaca gtcaaaccat attagtgact tattttaata 60
attatttatg attgtgaata tactgatgtt acattaaaga tgtgatttct tctnacagat 120
ctctgaatac atttgccttc cttatatata catatgagca acatatgcaa taaataaaat 180
ctaaattatg actatatata aatgtattta tatatatttt atcaatgcac agacatttta 240
tatatgtttg ggtatgttat tccaagtcct ttcaggaaaa tacctgcata ttcaaataac 300
aattctcgtg ttagctacct tttgttttgt tttgtttttt tccatcagga agacccacta 360
cattatttga gacaatgggg aaagctgaaa tgtggctcat tcgaacctat tgggattttg 420
aatttcctcg cccattctta ccaaatgttg attttgttgg aggacttcac tgtaaaccag 480
ccaaacccct gcctaaggta aaygtattct tgtttcattt gtttgcttga cattttcaga 540
aggaatggct ggatatgttt ctttcagagt gtttaactca gagtgagggg aatatgggag 600
gtcaaaaaca aggacttgcc attagaaaat catatatttc tgtagtatca caagtatgtg 660
aatgttatta tcattaaaga ccaaagaggt ttnactaggg agattttgaa aacagggttg 720
gttaaagtaa ggccttcatt gtgccaccca aaagatagta tgattcattt cttcaaaaaa 780
tatttgtaga gtgattaata caaaccacag gtaagtgctg gattttcaga gaataaaggt 840
agcacagttt ctgctccctc atgccttaca ttgtactttg aaagatagaa taaaaacaag 900
tgaaaaagaa aagtctaaaa agtgttataa ggaaagacca caatgataaa gnaaatatgc 960
agaagagatc ccaaactcat tgacaattna aagtgagtac t 1001

<210> 416
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 10-460-236 : polymorphic base A or G

<220>
<221> misc_binding
<222> 483..502
<223> 10-460-236.mis1, potential

<220>
<221> misc_binding
<222> 504..523
<223> 10-460-236.mis2, potential complement

<220>
<221> primer_bind
<222> 268..286
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 671..689
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515

<223> 10-460-236 potential probe

<220>
<221> misc_feature
<222> 113,692,951,988
<223> n=a, g, c or t

<400> 416
caagatgaga ggagatttgg gtggggacag tcaaaccata ttagtgactt attttaataa 60
ttatttatga ttgtgaatat actgatgtta cattaaagat gtgatttctt ctnacagatc 120
tctgaataca tttgccttcc ttatatatac atatgagcaa catatgcaat aaataaaatc 180
taaattatga ctatatataa atgtatttat atatatttta tcaatgcaca gacattttat 240
atatgtttgg gtatgttatt ccaagtcctt tcaggaaaat acctgcatat tcaaataaca 300
attctcgtgt tagctacctt ttgttttgtt ttgttttttt ccatcaggaa gacccactac 360
attatttgag acaatgggga aagctgaaat gtggctcatt cgaacctatt gggattttga 420
atttcctcgc ccattcttac caaatgttga ttttgttgga ggacttcact gtaaaccagc 480
caaacccctg cctaaggtaa atrtattctt gtttcatttg tttgcttgac attttcagaa 540
ggaatggctg gatatgtttc tttcagagtg tttaactcag agtgagggga atatgggagg 600
tcaaaaacaa ggacttgcca ttagaaaatc atatatttct gtagtatcac aagtatgtga 660
atgttattat cattaaagac caaagaggtt tnactaggga gattttgaaa acagggttgg 720
ttaaagtaag gccttcattg tgccacccaa aagatagtat gattcatttc ttcaaaaaat 780
atttgtagag tgattaatac aaaccacagg taagtgctgg attttcagag aataaaggta 840
gcacagtttc tgctccctca tgccttacat tgtactttga aagatagaat aaaaacaagt 900
gaaaaagaaa agtctaaaaa gtgttataag gaaagaccac aatgataaag naaatatgca 960
gaagagatcc caaactcatt gacaattnaa agtgagtact c 1001

<210> 417
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 10-460-285 : polymorphic base A or T

<220>
<221> misc_binding
<222> 483..502
<223> 10-460-285.mis1, potential

<220>
<221> misc_binding
<222> 504..523
<223> 10-460-285.mis2, potential complement

<220>
<221> primer_bind
<222> 219..237
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 622..640
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 10-460-285 potential probe

<220>
<221> misc_feature

<222> 64,643,902,939
<223> n=a, g, c or t

<400> 417
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tattttaata attatttatg attgtgaata tactgatgtt acattaaaga tgtgatttct     60
tctnacagat ctctgaatac atttgccttc cttatatata catatgagca acatatgcaa    120
taaataaaat ctaaattatg actatatata aatgtattta tatatatttt atcaatgcac    180
agacatttta tatatgtttg ggtatgttat tccaagtcct ttcaggaaaa tacctgcata    240
ttcaaataac aattctcgtg ttagctacct tttgttttgt tttgtttttt tccatcagga    300
agacccacta cattatttga gacaatgggg aaagctgaaa tgtggctcat tcgaacctat    360
tgggattttg aatttcctcg cccattctta ccaaatgttg attttgttgg aggacttcac    420
tgtaaaccag ccaaacccct gcctaaggta aatgtattct tgtttcattt gtttgcttga    480
cattttcaga aggaatggct ggwtatgttt ctttcagagt gtttaactca gagtgagggg    540
aatatgggag gtcaaaaaca aggacttgcc attagaaaat catatatttc tgtagtatca    600
caagtatgtg aatgttatta tcattaaaga ccaaagaggt ttnactaggg agattttgaa    660
aacagggttg gttaaagtaa ggccttcatt gtgccaccca aaagatagta tgattcattt    720
cttcaaaaaa tatttgtaga gtgattaata caaaccacag gtaagtgctg gattttcaga    780
gaataaaggt agcacagttt ctgctccctc atgccttaca ttgtactttg aaagatagaa    840
taaaaacaag tgaaaaagaa aagtctaaaa agtgttataa ggaaagacca caatgataaa    900
gnaaatatgc agaagagatc ccaaactcat tgacaattna aagtgagtac tcaataatgt    960
gcagagatag gtgaaacgat gaggggttga taaacaccca a                       1001
```

<210> 418
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-605-58 : polymorphic base G or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-605-58.mis1, potential

<220>
<221> misc_binding
<222> 502..520
<223> 12-605-58.mis2, complement

<220>
<221> primer_bind
<222> 444..464
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 901..921
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-605-58 potential probe

<400> 418
```
gttcagcaga acagcagaca aattactttt atttttaatt tcaatactct ttgctttaga     60
aacaattttg ctgtggcact tcctagtctg tgactctgtc ttgaaaaggg ctggaactca    120
ggctgcgtag acatacatat ttcatttatc tggtcttcaa cttaaacatt cacctcttta    180
taaaaacttc tctgtaattc tgaaggtaat tcccctttttt ttgatggagt tcaaaaattg   240
ctgacttgca ctgttgggaa atcatcactg actgtgattt cattttccat actttcatat    300
```

```
ttacatccac ctgctttttc tgttcagtgg gagacaagca gttggagcca accttctgag     360
cttcttcaaa aaggctatca acaaaatatt cacaatttgt tgattatcac tgagagattg     420
attgtcagat actgtttcac aaacccatct tcttttatac tttcgagatt atctacctct     480
ttcattctct tttgtcttat kctgggcagg gtctcctggc ctcagcctca ctcagctcag     540
aggccacgag caccctttgg ccccgggctc cgtctggagc ccgctgctcc agacctcctt     600
aggttccgcc gcggcacagc taggatcctg acggactctc taggtctctg ccaggcacca     660
gacaccaaaa gcatgctgat gtagtctcaa ttgatttgtt tttaaattgg taattaaacc     720
tccaccttta ttgaaagatc atttggaaga ttttgttctc atactcggtc agttaataaa     780
catatgattt gtcaaaagat agattttaga aacattttat gaattcaaaa aatttgaggg     840
aaatatttgg gttgttttag aagctctgtc aagatgtagt tttaatcaag aaacttatgt     900
caaaagttta agaatcaagc cttaatatta ttcttgcaga tgtccttggt aaaatctgct     960
ggtggggata attaaaatac acattgtata tactttgtat t                        1001
```

<210> 419
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-607-207 : polymorphic base G or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-607-207.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-607-207.mis2, potential complement

<220>
<221> primer_bind
<222> 689..707
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 179..199
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-607-207 potential probe

<220>
<221> misc_feature
<222> 531,558
<223> n=a, g, c or t

<400> 419

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atgtacatgt atatatgtgt tcacttcttc caaaacaagg cacagaatta ttgagctgcc      60
ttacagatgt ttgtgaaact gaatgtgttt gtagaagaca gttaaaaatg ataattattc     120
tatataaccc tattttatat aaggatgtct catgtttctc tctttcctca gaagcctgta     180
actctattca tcccataaca ctaatatgaa aacataagtc atttagcatg accaaaaata     240
ggataatgat tttttaaaat gtaagcatat tgcaactaat cataatcagt aacaattaaa     300
agaccacaaa aattaccaaa aattggcaaa taataaaatc tcaggaattc tcaaggccct     360
cttaaaagct acacatcaag gaaacacttt atgatcaaag tagtatgggt taacacaaac     420
ctatgtgtct ttattggtaa gaagaccatc atccaagtct cacaataacc actctatgac     480
ctatggcatg aatgtattct raaaataaat taaaattttg atgctaaggg naattattgg     540
```

```
aagagattgc agcaacantt tttataaaat gtatctagat aaatgaaaca tttttaagaa    600
aaattgaatg aatatagtgt catagtagat aatattgcta aatcatgcat acaaacctaa    660
agtaatttac atcaagctta tcctgcaaca catagataaa ggactggtat ctcttgtata    720
gtgagagcta ttatatatca ccaaccaaaa agacaaacag accaatatga aaatagatga    780
aggatatgaa ttgacaattc acagaagtaa aaatggccaa tcacatcaaa aagatggcta    840
cttgtactag aaagttggac attataattt agtaagtcaa taaccttaag tcaatgaatt    900
tattttaact tttattttaa gctcaggggt acatgtgcaa gtttgttaca taggtaaata    960
tgtgtcaaca cccaggtatt aagcctagta cccactaatt a                        1001
```

<210> 420
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 499
<223> 12-609-119 : polymorphic base T or G

<220>
<221> misc_binding
<222> 500..518
<223> 12-609-119.mis1, complement

<220>
<221> misc_binding
<222> 479..498
<223> 12-609-119.mis2, potential

<220>
<221> primer_bind
<222> 597..615
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 114..134
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 487..511
<223> 12-609-119 potential probe

<220>
<221> misc_feature
<222> 454
<223> n=a, g, c or t

<400> 420

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ttttaaaaat acttaccaat atatggtctg aattgacata ttttagaatt tcttttttta     60
tttgtaaaca gttttataaa gaaatttccc ccaatgatta ggaccagaaa gtatatttgt    120
tatgacagaa ggggttggtc attattttac tgagaaaaag agaatttaga acaaaaggga    180
caacagcaac aaaaagatga gtatacaatt ttgatatgat atccaggaaa cttatgggtc    240
tacatttctt ttcctctttc tctctctctt ttttttttt ttggtgtgag aatacattga    300
gcgatgtggc attagagaat ggatttaagt ttaaaaacag ggacacatca ggaaacacaa    360
gtcagaataa ttctcattca tttcaaagca aacacatatt caccaggagc ttcatatagt    420
gtgagggagc tactctaggg ggtgagcaga tctnccactg gagaaagtcc tggtgacctc    480
tcccactgtg gttcaagtkc cccctgtgag acacagcaaa gtgatgatga gggtccccca    540
cattcagtta tacatagcac atcaaattca cagtgtgatt tcaggacaaa aggtgtcata    600
gtcataccta agcaatgacc tgagaaataa gatcacttaa ttatgtaact atatagtata    660
taatactgta ttataaatgg aattctcaga actatttccc agaaattcca aaccacaata    720
ccagactgct gaatgtcagt gattcttata cttcagcttt taaggtgttt ttggggggtg    780
```

```
ggggtgtcgg gggcagtgag gggtagtggg gtaagactag gaaaccctaa ctttaagtga    840
aatataaagg gttagagagc tagaagctaa ataaatgtag atataatatc attccaattg    900
taactaactt ttcctcaatg ctcatagtca tgtaatggct ccaatgactc ctaactaaaa    960
gaactgaaca gaaaaaaata aaataaaata aaactacccc a                       1001
```

<210> 421
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 499
<223> 12-609-180 : polymorphic base T or G

<220>
<221> misc_binding
<222> 479..498
<223> 12-609-180.mis1, potential

<220>
<221> misc_binding
<222> 500..519
<223> 12-609-180.mis2, potential complement

<220>
<221> primer_bind
<222> 658..676
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 175..195
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 487..511
<223> 12-609-180 potential probe

<220>
<221> misc_feature
<222> 34,53..54,515
<223> n=a, g, c or t

<400> 421

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ggtgacagag aaagactcca tctggaaaaa aaanaaagat gtcataaagt tannttatat      60
tttttaaaaa tacttaccaa tatatggtct gaattgacat attttagaat ttcttttttt     120
atttgtaaac agttttataa agaaatttcc cccaatgatt aggaccagaa agtatatttg     180
ttatgacaga aggggttggt cattatttta ctgagaaaaa gagaatttag aacaaaaggg     240
acaacagcaa caaaaagatg agtatacaat tttgatatga tatccaggaa acttatgggt     300
ctacatttct tttcctcttt ctctctctct tttttttttt tttggtgtga gaatacattg     360
agcgatgtgg cattagagaa tggatttaag tttaaaaaca gggacacatc aggaaacaca     420
agtcagaata attctcattc atttcaaagc aaacacatat tcaccaggag cttcatatag     480
tgtgagggag ctactctakg gggtgagcag atctnccact ggagaaagtc ctggtgacct     540
ctcccactgt ggttcaagtg ccccctgtga gacacagcaa agtgatgatg agggtccccc     600
acattcagtt atacatagca catcaaattc acagtgtgat ttcaggacaa aaggtgtcat     660
agtcatacct aagcaatgac ctgagaaata agatcactta attatgtaac tatatagtat     720
ataatactgt attataaatg gaattctcag aactatttcc cagaaattcc aaaccacaat     780
accagactgc tgaatgtcag tgattcttat acttcagctt ttaaggtgtt tttgggggt     840
gggggtgtcg ggggcagtga ggggtagtgg ggtaagacta ggaaacccta actttaagtg     900
aaatataaag ggttagagag ctagaagcta aataaatgta gatataatat cattccaatt     960
gtaactaact tttcctcaat gctcatagtc atgtaatggc t                        1001
```

<210> 422
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 499
<223> 12-609-233 : polymorphic base G or A

<220>
<221> misc_binding
<222> 479..498
<223> 12-609-233.mis1, potential

<220>
<221> misc_binding
<222> 500..519
<223> 12-609-233.mis2, potential complement

<220>
<221> primer_bind
<222> 711..729
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 228..248
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 487..511
<223> 12-609-233 potential probe

<220>
<221> misc_feature
<222> 87,106..107,568
<223> n=a, g, c or t

<400> 422
ctgggaggca gaggttgcaa tgagccaaga ttgcatcatt gcactccagc ctgggtgaca 60
gagaaagact ccatctggaa aaaaaanaaa gatgtcataa agttanntta tattttttaa 120
aaatacttac caatatatgg tctgaattga catattttag aatttctttt tttatttgta 180
aacagtttta taaagaaatt tcccccaatg attaggacca gaaagtatat ttgttatgac 240
agaaggggtt ggtcattatt ttactgagaa aaagagaatt tagaacaaaa gggacaacag 300
caacaaaaag atgagtatac aattttgata tgatatccag gaaacttatg ggtctacatt 360
tcttttcctc tttctctctc tctttttttt ttttttggtg tgagaataca ttgagcgatg 420
tggcattaga gaatggattt aagtttaaaa acagggacac atcaggaaac acaagtcaga 480
ataattctca ttcatttcra agcaaacaca tattcaccag gagcttcata tagtgtgagg 540
gagctactct agggggtgag cagatctncc actggagaaa gtcctggtga cctctcccac 600
tgtggttcaa gtgccccctg tgagacacag caaagtgatg atgagggtcc cccacattca 660
gttatacata gcacatcaaa ttcacagtgt gatttcagga caaaaggtgt catagtcata 720
cctaagcaat gacctgagaa ataagatcac ttaattatgt aactatatag tatataatac 780
tgtattataa atggaattct cagaactatt tcccagaaat tccaaaccac aataccagac 840
tgctgaatgt cagtgattct tatacttcag cttttaaggt gtttttgggg ggtgggggtg 900
tcgggggcag tgaggggtag tggggtaaga ctaggaaacc ctaactttaa gtgaaatata 960
aagggttaga gagctagaag ctaaataaat gtagatataa t 1001

<210> 423
<211> 1001
<212> DNA

<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-611-294 : polymorphic base G or A

<220>
<221> misc_binding
<222> 502..520
<223> 12-611-294.mis1, complement

<220>
<221> misc_binding
<222> 481..500
<223> 12-611-294.mis2, potential

<220>
<221> primer_bind
<222> 776..795
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 251..271
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-611-294 potential probe

<220>
<221> misc_feature
<222> 406,571,773,943..944
<223> n=a, g, c or t

<400> 423
```
taaatcgtgc acactggacc aaaacttgta agtaccaaat ttcaattaat cttttgagag     60
atgagacaat aaataattca ttcgaatggg ctagatatag ggaaagtaaa tcttgcagag    120
ccattcatct ctaatgtctt ttagcaacat gccgaagcac acaagtaaag ggccactaat    180
ccaaagacaa atgaggaatg tgaaagttaa aaatctcagg accatcaagc aaggtctctg    240
caaagaaaca gtaagtatag tcagcagtca gaaaattggc agacagcaga cagtctttag    300
tgaatgacag agagcacagg gagggctaat tgaaagggag tagtaattaa cattttgtag    360
cattgaaccc atttcttgtt gtgaagggct tctaaccccc ttagcntttc ggaaaggcct    420
ctaaacctct tatctgtcag aagggcctct aactgtccta agttgggcct ctaaaccgat    480
tttgaacagt gtctctgttc ragtataaaa atatgttcca ccacttaccc aaatcagcca    540
attggtgttg catagtctat ttcctttggg nttggaatct cacctcattt aggtcccagc    600
agagtcacca gaggaaaata ttactggaaa agtggtcttg tcccagacgt taagggtggg    660
tttgtggatc tcatgtggga aagaatgcaa ggtgagtcgc agagtacagt aaaattaaca    720
gtttgttaga gactactcta ttacagaata gggcatcctc agaaagcaag aangagaaat    780
acccctacct taaacttagt gcttgcttat ataggttgtt aagaatactg tactttatta    840
caaaggtttg tgatcagctt gtgacaggct attaatattg ttattttcct atgtattatt    900
gatttcagca agattttaca agtggctag tttttaaag gannaaacta attcttaaat     960
taagaagttt ttgttttcaa actattggga cattttcata a                       1001
```

<210> 424
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele

<222> 501
<223> 12-612-41 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-612-41.mis1, potential

<220>
<221> misc_binding
<222> 502..520
<223> 12-612-41.mis2, complement

<220>
<221> primer_bind
<222> 461..481
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 981..1001
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-612-41 potential probe

<220>
<221> misc_feature
<222> 383
<223> n=a, g, c or t

<400> 424
```
gtagaagctg agaaactagt taggagacat ttcaccagtt gtgacacaat tcttctttaa      60
atatgtcaaa atgggctggg cacagtggtt catgtctgta gggccaacac tttgggagac     120
agaggcagaa tgattagacc acaggagttc cagatgagta tgggcactac agcaagacct     180
catatctaaa aatgtaaaaa ataaaaaata tagccaggca tggtggtgcg cagctgtagc     240
cccagcttct catgaggctg aggtggagga ttacctgaga ccgaaacgga aaggctgcac     300
tgagccatga tcatgtgact gcactcagcc tgtgtaatgg agcaaaagcc tgtctcaaaa     360
aaaaataaaa actaaaaata tcnaaaatga tcattcccag attctatttc cactatctta     420
cttatagcac ttagaatggc tcacaatatt ttctgctcta gaaaaacatt aactttccca     480
ccgaaaattc catttttcat ytttaaaggt atttgtcaat gataaaactc caatttaaaa     540
accaaacttt ctgtaatgac atacattaaa acattaatat tttatgtcaa ttcaatgaca     600
cttactttga atcacttgtg tggcgctttt caaagaccat ccatagactt gatatgctta     660
agcaataaat ttacttttaa tgttgatatc tttatattta tccttcagct ataaagagaa     720
tatcatgaaa ttatcaagaa ttcatcatga tcaaccggtg aagcccctgg atcgagcagt     780
cttctggatt gagtttgtca tgcgccataa aggagccaag caccttcggg tcgcagccca     840
caacctcacc tggatccagt accactcttt ggatgtgata gcattcctgc tggcctgcgt     900
ggcaactatg atatttatga tcacaaaatg ttgcctgttt tgtttccgaa agcttgccaa     960
aacaggaaag aagaagaaaa gggattagtt atatcaaaag c                         1001
```

<210> 425
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 499
<223> 12-613-302 : polymorphic base C or G

<220>

<221> misc_binding
<222> 479..498
<223> 12-613-302.mis1, potential

<220>
<221> misc_binding
<222> 500..519
<223> 12-613-302.mis2, potential complement

<220>
<221> primer_bind
<222> 781..799
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 343..363
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 487..511
<223> 12-613-302 potential probe

<220>
<221> misc_feature
<222> 309
<223> n=a, g, c or t

<400> 425
agaaagtgat agtgccagta gcagggggaa gagagtagca gaataaggac aagggataaa 60
tgactagtag tacaatagtg attattactg atactagcat gatctcggct cactgaaacc 120
tccacccccc aggttcaagc gatctgattc tcctgcctca gcctcccgag tagctgggat 180
tacaggcacc tgccaacaca tctgactaat ctttgtgttt ttagtagaga cagagtttca 240
ccatgttggc caggctggtc ttgaactcct gacctcaggt gatccacatg cctcagcctc 300
ccaaagtgnc tgggattaca agtgtgagcc tccgttgttg ttaacttgca gaaggtagac 360
ttgaatccaa gtaaataatt gtgaaactga ttctctaatt cttttgtaca caaaataatt 420
gttgcgacaa atttgcttgc ttttccatta tgtattagat tctcagataa tgtttgtata 480
tttcaaaaga ataagactst tgccaaaaag tatcaagtgt ttgaaaaatg catataggca 540
ttgcctttat aatatactca catgaaactg tacagagaat aaatcatgat ggtaagattc 600
aatatcggta gcaaatactc attaaaaaaa ctctggaaat aattcaaata tcttacatta 660
agaaatggtt aaaaacttac ataatgtgca taccaagcca ttacaatcct tttttcaaaa 720
caatgtttaa ttacactgtc agccgtggta caggtatagt tggaaactaa ggaacaaaat 780
gatgagtaga acaagatcac agttttttg tagaataaaa aggcatatac aatgagaata 840
aaattttcta aataaacatc acatatgtac attgagttat ataaatagaa ttaaacccat 900
aatgaaatgg cacacatttt aaattgagat agagatatgg gtaaatgatt ttctttttct 960
aaattttcat acttttataa aactacttac attgatcttc t 1001

<210> 426
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-614-471 : polymorphic base T or A

<220>
<221> misc_binding
<222> 502..520
<223> 12-614-471.mis1, complement

<220>
<221> misc_binding
<222> 481..500
<223> 12-614-471.mis2, potential

<220>
<221> primer_bind
<222> 952..971
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 424..442
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-614-471 potential probe

<220>
<221> misc_feature
<222> 109,479
<223> n=a, g, c or t

<400> 426
gagctggatt ggtaaagtaa aatgaggaca tgcacgttgc aagagtcaag atagaatgaa 60
accaaaattg agataaaatc aaaattgaga taaacacatg aaatatttnc acaaatactt 120
cagtgaaaca tagcatgaat gattaagacc agtaaaacaa ttagaaataa gagagttttg 180
ggaataaagc aggcaatcgg gagagcacta attcagcttt tttttctttt ttaacaaata 240
acacttttat attttaatca ccttagtggc aattcctaga gtattaggtg attcctattg 300
gggctctatg agtcaagatt cagggagaaa aatagaaaga ttcactagtt ctttctactg 360
ctgttattgt ttgttctttt gttcattcat tcagttccat tttatttcat gttatcaatt 420
acattttagt gtaaccagtg agtttatttc taatttctag aattgatgtg tttcttttnt 480
atgtttatgg ttctcgtcat wttccataca tatattatat gaactatttt tcatctctgg 540
acatttgaac tatgtttatt ataaaacatc attttgattt attttctata tctataatcc 600
tttggtgcaa atgttactat tatacatagt atatagttgt atactattgt aaactattgt 660
atattgtata tagttgtata ctattgtata ttgtatatag ttggttattt cttcatttgg 720
ttttcattag ttaatcttca acaggtattg atttctgcaa acattcttca tattctgcat 780
tgtgagaaca tcagaataat ttattgattg cctctgctgt aacctaggca gatcactttc 840
attacaattt ggcttttctt gtcatttttt ttacaattta ttgttacaat taatttttat 900
agcagaaatt ccctgaactc tgtagataca ttttttttcct agttttaagg tctttgtctc 960
attttgattc cttccaaaac cacttctttt tatagctcct a 1001

<210> 427
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 12-620-192 : polymorphic base G or T

<220>
<221> misc_binding
<222> 483..502
<223> 12-620-192.mis1, potential

<220>
<221> misc_binding
<222> 504..522
<223> 12-620-192.mis2, complement

<220>
<221> primer_bind
<222> 309..326
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 777..797
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 12-620-192 potential probe

<220>
<221> misc_feature
<222> 461..463
<223> n=a, g, c or t

<400> 427
tatgagaaaa ctacaagagt caaaatttga tgtccttctg gcagatgccg ttaatccctg 60
tggtgagctg ctggctgagc tacttaacat accctttctg tacagtctcc gcttctctgt 120
tggctacaca gttgagaaga atggtggagg atttctgttc cctccttcct atgtacctgt 180
tgttatgtca gaattaagtg atcaaatgat tttcatggag aggataaaaa atatgatata 240
tatgctttat tttgactttt ggtttcaagc atatgatctg aagaagtggg accagtttta 300
tagtgaagtt ctaggtaagt cgtgtgtcca attggtgttt attaagttct aatttcctg 360
tgcctttgaa ggtgggctta tataaatata atgtcagaag atagtgtttt tatgggaaat 420
tatgaattgc aaatgtaaga tgatctatga gtctcaaaaa nnntatagaa tgttgacctt 480
atagaatcag ttagaaccct ggkgccatca ctgctacagg acaccaagag agtcataaac 540
cttcaatgta aaacacttat gatttcttta agccatcaca tatcatttg ctatacattt 600
tttcatcttt aaaaaagtca atagatactt caagaaacat cttcatgaag gcagacatac 660
aaattttata tttacacata tttctaaaaa tattatcaat gcaggattga ggaacttgta 720
cctgagtacc tcagtttcct catttagaaa ttaaattttg tttttcatat aagaaggatt 780
ccttcacagt tgagaaatat agtggctcta ctccagaaac agaagcctaa aacttgagat 840
ttctaatgtt tatacattcc ttcaataaca acttcacaat tatttccttc aaaaactgaa 900
atcttgttga aagtgaacat ctaagtttta atctatattt tattaaactg catctctcca 960
tcaaagaaaa taggggccaa aataaggaag agcacatatc t 1001

<210> 428
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 503
<223> 12-621-49 : polymorphic base A or G

<220>
<221> misc_binding
<222> 483..502
<223> 12-621-49.mis1, potential

<220>
<221> misc_binding
<222> 504..523
<223> 12-621-49.mis2, potential complement

<220>
<221> primer_bind
<222> 455..473

<223> upstream amplification primer

<220>
<221> primer_bind
<222> 907..927
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 491..515
<223> 12-621-49 potential probe

<220>
<221> misc_feature
<222> 634
<223> n=a, g, c or t

<400> 428
aacttggaaa tggtttgtga gatataaaat caaaaataaa agcaaccaaa ttaaaattga 60
ttagttggac ttcatcaaaa tcaatacttt tgtgcttcaa tgaacaccgt taagaaagta 120
aaaggacagc ccaaagaata aaaaaaaaac aaggaaatca tatatgtgat aaggttctta 180
tatcagaaag atattaaaaa cacaagtcca taagaagaca aataattcaa ccaaaattag 240
gcaaaacatg ctcaacatga tttcatatca aagaaaggta aagcataacc agatatcact 300
tcattcacac tggctataat caaacgaaat ataatcccaa gtgttggcaa ggttgggaag 360
aaattaaaat tcttatacat tgctggtgag aatggaaatt gaagcatcca ctgtgaaaaa 420
caatctggaa attcctatgg taatttagaa attatatggt aacagacaat tcctatggta 480
atttagaaat tatatggtaa ctrctacttt gaattgtagc agttatactt tcacttgatt 540
gatttatctt cagatataag taggagaaaa acagaaagaa acagcgattt gaaaagaagc 600
attgcattgc accaggagaa ctatgaaatc gatngtcaaa tattctcctg atacaactca 660
gttgtcactt tagttctggg agttgtggaa aggtgctagt gtggcccaca gaatacagcc 720
attggatgaa tataaagaca atcctggatg aacttgtttg gagaggccat aagatgactg 780
tgctgtcatc tttggcttcc attattattc accctagtaa atcatctgct attagatttg 840
aggtttatcc aacatctcta attaaaaata attttgaggg tcttgttgtg aaactgatca 900
atagatggat atacgatctt cagaaagatg cattttggtc atatttctca caagcacaag 960
aactcttttg ggaatctaca gactgtgtta ataatctctg t 1001

<210> 429
<211> 710
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 364
<223> 12-622-325 : polymorphic base C or T

<220>
<221> misc_binding
<222> 344..363
<223> 12-622-325.mis1, potential

<220>
<221> misc_binding
<222> 365..384
<223> 12-622-325.mis2, potential complement

<220>
<221> primer_bind
<222> 40..59
<223> upstream amplification primer

<220>
<221> primer_bind

<222> 551..569
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 352..376
<223> 12-622-325 potential probe

<220>
<221> misc_feature
<222> 333,685,688
<223> n=a, g, c or t

<400> 429
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tattgttaga gttcatgttc ccttctcctt cactgatctc tcaaactaac aagactcagt     60
tcatttccag aagaccctac ctcttatatt agggagtttc agtaccttac ccagtcttat    120
gcactaacct ggtatgacct ctacttatcc tgtcttccac cctcaccttc tacttatcct    180
ctcttccacc ctcaccccag aagacaggga ccatatttgg accctggttc aggagcatgc    240
taatacaatt catcatcaag ctcctgccca gcctactggc acggaggcag tccccaacca    300
ggagccccac caggattatc aagacagggc ctnctggaca ctgccatcaa gaccacatga    360
ttgygtatct ccttgcagga ctcaaaaagg gtgcccataa agtggtaaac tataaaaacc    420
tttcagaaat cacccaaggt cctgacagaa acccagcctt ttttctctct tgtttaactg    480
aagccatgag aaaatatacc aacctagacc cagccaaccc agaaggaatc actattttaa    540
acctttggtt cctcatccaa tctacccctg atatttggtg caagattcag aagcttgaca    600
atggccctga aaccccacaa tgacaccttc ttaatttagt cttcaaagtc tttaacagtt    660
ataacgagga aagtaaaaag aaaanaanaa aagacagagt ttcaaatgct                710
```

<210> 430
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-624-82 : polymorphic base T or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-624-82.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-624-82.mis2, potential complement

<220>
<221> primer_bind
<222> 562..582
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 114..134
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-624-82 potential probe

<220>

<221> misc_feature
<222> 464,639
<223> n=a, g, c or t

<400> 430
tgtcttatgt caacatttta tgaattctac agtagtttag tgatttcttc taatttttaa 60
ggttatattt gcagtaattt tgagatgtga ttacaaatgc attggcaatc ctctcatcaa 120
gtcatatacc cttcctgtga aatttagcaa attttgtggc tgtctcaaaa aagagaatat 180
agtggaagtg aggagcttaa cttccaaagc tcaaaaaaat tgttaataca ttttctctgt 240
ctgtccttct gtccttttct ctgtgtttct gtcattcttt tttccttttt ctctgtctct 300
ccactcgctt tggagccctg tgctatatcc acagtcccca ggagaaatat accatttggt 360
gtagaaatac atatgtatgc ctaataagtc acaattggcc cagcactgca gtagcttgag 420
acttttaata ctaatcacca gatatgtgag tgattaacct tcangatgat tagcccaagc 480
taccttagga cagtaaccaa ytgagaaatg ctgtgccata aacacctaat tgagcctggc 540
caacaaccta gaattaaaac agatgatgat aaaatgttgc tgttctaagc accttcattt 600
cagagcagtt ggttaagcag tgatagacaa ccagaaaana tatttttaca tatttgagtt 660
atactcctgt aataatatta aaattaatat atacctacaa aaaaagtgaa tctatattac 720
attttgtaac tacctgtaac ccagaaagag tagtcagcat aggatggtgg gtaagagctt 780
gcactctgaa tccagataac ctatatcatc tttgcaaaac cattacagaa tcatgtatag 840
ttaagcaaat tacttatcag gtctatgcct cacattctcc ttcagtgaaa tgtagatgaa 900
gcaatgtcac tacctactta atagcattgc tgagactaaa agagttgctg tatgtaattg 960
ctgtatatag caaaattcaa tttgctataa ctattattat t 1001

<210> 431
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-624-83 : polymorphic base G or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-624-83.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-624-83.mis2, potential complement

<220>
<221> primer_bind
<222> 563..583
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 115..135
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-624-83 potential probe

<220>
<221> misc_feature
<222> 465,640
<223> n=a, g, c or t

<400> 431
atgtcttatg tcaacatttt atgaattcta cagtagttta gtgatttctt ctaattttta 60
aggttatatt tgcagtaatt ttgagatgtg attacaaatg cattggcaat cctctcatca 120
agtcatatac ccttcctgtg aaatttagca aattttgtgg ctgtctcaaa aaagagaata 180
tagtggaagt gaggagctta acttccaaag ctcaaaaaaa ttgttaatac attttctctg 240
tctgtccttc tgtccttttc tctgtgtttc tgtcattctt ttttcctttt tctctgtctc 300
tccactcgct ttggagccct gtgctatatc cacagtcccc aggagaaata taccatttgg 360
tgtagaaata catatgtatg cctaataagt cacaattggc ccagcactgc agtagcttga 420
gacttttaat actaatcacc agatatgtga gtgattaacc ttcangatga ttagcccaag 480
ctaccttagg acagtaacca rctgagaaat gctgtgccat aaacacctaa ttgagcctgg 540
ccaacaacct agaattaaaa cagatgatga taaaatgttg ctgttctaag caccttcatt 600
tcagagcagt tggttaagca gtgatagaca accagaaaan atatttttac atatttgagt 660
tatactcctg taataatatt aaaattaata tatacctaca aaaaaagtga atctatatta 720
cattttgtaa ctacctgtaa cccagaaaga gtagtcagca taggatggtg ggtaagagct 780
tgcactctga atccagataa cctatatcat ctttgcaaaa ccattacaga atcatgtata 840
gttaagcaaa ttacttatca ggtctatgcc tcacattctc cttcagtgaa atgtagatga 900
agcaatgtca ctacctactt aatagcattg ctgagactaa aagagttgct gtatgtaatt 960
gctgtatata gcaaaattca atttgctata actattatta t 1001

<210> 432
<211> 989
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 489
<223> 12-624-107 : polymorphic base T or C

<220>
<221> misc_binding
<222> 469..488
<223> 12-624-107.mis1, potential

<220>
<221> misc_binding
<222> 490..509
<223> 12-624-107.mis2, potential complement

<220>
<221> primer_bind
<222> 575..595
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 127..147
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 477..501
<223> 12-624-107 potential probe

<220>
<221> misc_feature
<222> 477,652
<223> n=a, g, c or t

<400> 432
tttaaaattt taatgtctta tgtcaacatt ttatgaattc tacagtagtt tagtgatttc 60
ttctaatttt taaggttata tttgcagtaa ttttgagatg tgattacaaa tgcattggca 120
atcctctcat caagtcatat acccttcctg tgaaatttag caaattttgt ggctgtctca 180

aaaaagagaa tatagtggaa gtgaggagct taacttccaa agctcaaaaa aattgttaat 240
acattttctc tgtctgtcct tctgtccttt tctctgtgtt tctgtcattc ttttttcctt 300
tttctctgtc tctccactcg ctttggagcc ctgtgctata tccacagtcc ccaggagaaa 360
tataccattt ggtgtagaaa tacatatgta tgcctaataa gtcacaattg gcccagcact 420
gcagtagctt gagactttta atactaatca ccagatatgt gagtgattaa ccttcangat 480
gattagccya agctacctta ggacagtaac caactgagaa atgctgtgcc ataaacacct 540
aattgagcct ggccaacaac ctagaattaa aacagatgat gataaaatgt tgctgttcta 600
agcaccttca tttcagagca gttggttaag cagtgataga caaccagaaa anatattttt 660
acatatttga gttatactcc tgtaataata ttaaaattaa tatataccta caaaaaaagt 720
gaatctatat tacattttgt aactacctgt aacccagaaa gagtagtcag cataggatgg 780
tgggtaagag cttgcactct gaatccagat aacctatatc atctttgcaa aaccattaca 840
gaatcatgta tagttaagca aattacttat caggtctatg cctcacattc tccttcagtg 900
aaatgtagat gaagcaatgt cactacctac ttaatagcat tgctgagact aaaagagttg 960
ctgtatgtaa ttgctgtata tagcaaaat 989

<210> 433
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-624-146 : polymorphic base T or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-624-146.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-624-146.mis2, potential complement

<220>
<221> primer_bind
<222> 627..647
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 179..199
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-624-146 potential probe

<220>
<221> misc_feature
<222> 529,704
<223> n=a, g, c or t

<400> 433
tagaatgtta attaaaattt ttaattatgg ctaaaatttt agtaaacaaa tttttaaaat 60
tttaatgtct tatgtcaaca ttttatgaat tctacagtag tttagtgatt tcttctaatt 120
tttaaggtta tatttgcagt aattttgaga tgtgattaca aatgcattgg caatcctctc 180
atcaagtcat atacccttcc tgtgaaattt agcaaatttt gtggctgtct caaaaaagag 240
aatatagtgg aagtgaggag cttaacttcc aaagctcaaa aaaattgtta atacattttc 300
tctgtctgtc cttctgtcct tttctctgtg tttctgtcat tctttttttcc tttttctctg 360
tctctccact cgctttggag ccctgtgcta tatccacagt ccccaggaga aatataccat 420

ttggtgtaga aatacatatg tatgcctaat aagtcacaat tggcccagca ctgcagtagc 480
ttgagacttt taatactaat yaccagatat gtgagtgatt aaccttcang atgattagcc 540
caagctacct taggacagta accaactgag aaatgctgtg ccataaacac ctaattgagc 600
ctggccaaca acctagaatt aaaacagatg atgataaaat gttgctgttc taagcacctt 660
catttcagag cagttggtta agcagtgata gacaaccaga aaanatattt ttacatattt 720
gagttatact cctgtaataa tattaaaatt aatatatacc tacaaaaaaa gtgaatctat 780
attacatttt gtaactacct gtaacccaga aagagtagtc agcataggat ggtgggtaag 840
agcttgcact ctgaatccag ataacctata tcatctttgc aaaaccatta cagaatcatg 900
tatagttaag caaattactt atcaggtcta tgcctcacat tctccttcag tgaaatgtag 960
atgaagcaat gtcactacct acttaatagc attgctgaga c 1001

<210> 434
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-624-288 : polymorphic base T or G

<220>
<221> misc_binding
<222> 481..500
<223> 12-624-288.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-624-288.mis2, potential complement

<220>
<221> primer_bind
<222> 769..789
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 321..341
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-624-288 potential probe

<220>
<221> misc_feature
<222> 113,671,846
<223> n=a, g, c or t

<400> 434
gttttaatat aatattatca atccattagt gccatttaga aaacttaaat tgaccagcaa 60
tccggtgctc tctatctgat aaatttacag cctgtttttg gacacctact tgnatatttt 120
aaatatttat taataaatat attagaatgt taattaaaat ttttaattat ggctaaaatt 180
ttagtaaaca aatttttaaa attttaatgt cttatgtcaa cattttatga attctacagt 240
agtttagtga tttcttctaa tttttaaggt tatatttgca gtaattttga gatgtgatta 300
caaatgcatt ggcaatcctc tcatcaagtc atataccctt cctgtgaaat ttagcaaatt 360
ttgtggctgt ctcaaaaaag agaatatagt ggaagtgagg agcttaactt ccaaagctca 420
aaaaaattgt taatacattt tctctgtctg tccttctgtc cttttctctg tgtttctgtc 480
attctttttt ccttttctc kgtctctcca ctcgctttgg agccctgtgc tatatccaca 540
gtccccagga gaaatatacc atttggtgta gaaatacata tgtatgccta ataagtcaca 600
attggcccag cactgcagta gcttgagact tttaatacta atcaccagat atgtgagtga 660

ttaaccttca ngatgattag cccaagctac cttaggacag taaccaactg agaaatgctg 720
tgccataaac acctaattga gcctggccaa caacctagaa ttaaaacaga tgatgataaa 780
atgttgctgt tctaagcacc ttcatttcag agcagttggt taagcagtga tagacaacca 840
gaaaanatat ttttacatat ttgagttata ctcctgtaat aatattaaaa ttaatatata 900
cctacaaaaa aagtgaatct atattacatt ttgtaactac ctgtaaccca gaaagagtag 960
tcagcatagg atggtgggta agagcttgca ctctgaatcc a 1001

<210> 435
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-624-293 : polymorphic base T or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-624-293.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-624-293.mis2, potential complement

<220>
<221> primer_bind
<222> 774..794
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 326..346
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-624-293 potential probe

<220>
<221> misc_feature
<222> 118,676,851
<223> n=a, g, c or t

<400> 435
cttgggtttt aatataatat tatcaatcca ttagtgccat ttagaaaact taaattgacc 60
agcaatccgg tgctctctat ctgataaatt tacagcctgt ttttggacac ctacttgnat 120
attttaaata tttattaata aatatattag aatgttaatt aaaattttta attatggcta 180
aaattttagt aaacaaattt ttaaaatttt aatgtcttat gtcaacattt tatgaattct 240
acagtagttt agtgatttct tctaattttt aaggttatat ttgcagtaat tttgagatgt 300
gattacaaat gcattggcaa tcctctcatc aagtcatata cccttcctgt gaaatttagc 360
aaattttgtg gctgtctcaa aaaagagaat atagtggaag tgaggagctt aacttccaaa 420
gctcaaaaaa attgttaata cattttctct gtctgtcctt ctgtcctttt ctctgtgttt 480
ctgtcattct tttttccttt ytctctgtct ctccactcgc tttggagccc tgtgctatat 540
ccacagtccc caggagaaat ataccatttg gtgtagaaat acatatgtat gcctaataag 600
tcacaattgg cccagcactg cagtagcttg agacttttaa tactaatcac cagatatgtg 660
agtgattaac cttcangatg attagcccaa gctaccttag gacagtaacc aactgagaaa 720
tgctgtgcca taaacaccta attgagcctg gccaacaacc tagaattaaa acagatgatg 780
ataaaatgtt gctgttctaa gcaccttcat ttcagagcag ttggttaagc agtgatagac 840
aaccagaaaa natattttta catatttgag ttatactcct gtaataatat taaaattaat 900

atatacctac aaaaaaagtg aatctatatt acattttgta actacctgta acccagaaag 960
agtagtcagc ataggatggt gggtaagagc ttgcactctg a 1001

<210> 436
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-421-135 : insertion T

<220>
<221> misc_binding
<222> 481..500
<223> 12-421-135.mis1, potential

<220>
<221> primer_bind
<222> 367..385
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 797..817
<223> downstream amplification primer, complement

<400> 436
gttcttgtct cattttgata cagatgaacc tagtgtcaaa tgagttggag gaagcatcct 60
gttctacttt ctcagataat tttaataagg ttggaagagt gtgttccttc aaggttgtgt 120
agaacttgcc ttaaaataat ctgggcctaa tgtttttctg gtgggaaatt tttaaattat 180
gggatttgca ttctttaatg attattggac taggcaggct ttttgttaca tcttgaatca 240
attttggtag gccttggtcc ttgagatgat aacattggtc tcttgattat ccacttgctc 300
caaggagggt tttacagact actccctagg cttgaaagcg tggggtgaat accaccggga 360
gtacacgaga taattgtaag aggtgtgtag acttggtttt aaataacatt gaactacatg 420
atgagaagtc attctcattt caattatctt tgaatcctta tggttaagtc aagtggaaag 480
tattggtttg gagccagcat gtcccacacc tcaaaattaa tgtttatttt tatcaaagta 540
atttatgtac gtgatctgaa gataaagtgg gattacaggt tttatgacaa caaataactc 600
ttccttgtcc ctacctcccc tctccctcta tccctagaga taacccttttt tgattactac 660
tttgggtatt tacttctgta tttctaaaca ttatactttc actgctattt attgattcac 720
aaattttaga cattgtcagt tggcttcttt ttatggaaga aataatttca tgctccttta 780
cttcttcttt tccttacctc atccttccag taacattata tcactctgtt aggttaaatc 840
aatagccaat gtttataatt attgtgatta agaaaataat gttgaaagca gggccttata 900
gtatactgtg gttacatttc cttcttgtgc aatttttttt ccctagggtt aataattgct 960
ctttatttct ttgtttgctt agtttcatgc ccaaatcttc t 1001

<210> 437
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-442-133 : insertion C

<220>
<221> misc_binding
<222> 502..520
<223> 12-442-133.mis1, complement

<220>

<221> primer_bind
<222> 616..633
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 184..203
<223> downstream amplification primer

<220>
<221> misc_feature
<222> 94,734
<223> n=a, g, c or t

<400> 437
ttagaattct ttttggcatt aatcaaaact ttacagagga cataaacact gattttttcc 60
ccccattcat ttaactattt gcacacagag acangaagcc agaaatctga ctgggaagaa 120
attcctaccc ttttgccagc atgctaagct tctgggttct ctttccctga gtggccctag 180
tgatctggct tgtggcacaa ctgcctttgg gggccaagcc gcatcataaa ggaaaagtat 240
ttctttttgt tctggccaaa gcaaaatacg cgtaataaaa catagatatt aaccaggctg 300
cttagcatcc aatatcaaac tggcaaggct taaatttgcc ctcaggtggg ccctgtcatc 360
tttaatctaa cctccgacta ggagtttcaa catgtggtct ctgggcaaga tggtcgccct 420
gagtaataga aaagaaagag aaaggagaga gagaaaaaca ttgcctgtgg cagggcgggg 480
aaggtgaaat gatcagggag gcagagaaag aaccacccat tgcagcgaca ctaaaaagtt 540
caggtggctg ctgtcggtgg agcaaggatc ttttccagta atcctaccag ctctcaaatt 600
tcccttgtta gggaggaaaa agctccccat gtcccaggat cctgtacatt cctaattctg 660
tcacccatag ccatcagcaa agtacaaggg agattaatcc aaagagaata gcagttaaca 720
tcccatagtg ccgnaacctg ttcttagccg agagggactt taccgaagag gggcctctaa 780
cccgctaaat cttagaaggg actctaactc tcctaagtcg ggcctctaac cagaggtcag 840
tcaagcatcc ttgcctttta ttaaggggga gcctttaacc acctctatct taggagagac 900
tctaactcca ctaagctggg cctctaaccc aatcccattc tttacccagg taccccacca 960
cttacccaaa gtcttccaat cagtgctgca gtctatttcc t 1001

<210> 438
<211> 756
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-449-63 : insertion AT

<220>
<221> misc_binding
<222> 481..500
<223> 12-449-63.mis1, potential

<220>
<221> primer_bind
<222> 546..563
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 86..106
<223> downstream amplification primer

<220>
<221> misc_feature
<222> 123,277
<223> n=a, g, c or t

<400> 438
ggggacggaa gaaaggaaaa gaaaaaatag tttatatgta tatacatttg tatcaaaata 60
agaaataaat actcataatt attacaattt tcctctgaaa gtagtcacat ggttatacct 120
ggntatttat ttattttta ttattattat tattatttga gacagggtct caccctgtca 180
cacaggctgg agtgcagtgg tgcaattatg gctcactgct acctctgcca cctgggctca 240
agccatcctc tcaccttagc cttctgaaca gctgggnata catgtgcact aatttttttt 300
tttttgaaac aaaaatattt gtgtagaagg cacaaaagct acaatcacag actccactgt 360
gcaaaggcgc aacctgcctc attgatctct agtgtacacc aacccagctt ccctttccat 420
tcagcctgtg aaaggagata gtgcttgggc catttggtaa aagaagggga tgggagatga 480
tcaaaacccc aagtaaggtt catccaatat ggtgtctaag cagcaaatga ctaattgctg 540
aagaaggaga ctagacagag gattagaggc agccatgggg ccagtgcagc tgtggagagc 600
tctgagcaaa gaaacaaggt tggcaggtga ggaggcctag gatagaggcc agaaggccaa 660
gcctggggct gcatgtgcac taatttttgt attttttgc ttttttgata gagatgagat 720
ttcatcatgt tgcacaggtg ggtcttgaag tcctgg 756

<210> 439
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-454-242 : deletion AT

<220>
<221> misc_binding
<222> 481..500
<223> 12-454-242.mis1, potential

<220>
<221> primer_bind
<222> 260..279
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 755..773
<223> downstream amplification primer, complement

<220>
<221> misc_feature
<222> 795..800
<223> n=a, g, c or t

<400> 439
caaatggaaa aaatgaaaac tgtcacactt cttacataac ttcttttatt atctgtattg 60
taaatacaga gtctcaatta ttgactaatt tatactaata gtgggaagca gtgtctagat 120
aatcccagat gattactaat ttaaaactac tttacatttt atttagtaat gtgtttggaa 180
cagttacatt ttgtagctac ttacaatttt actttaactg aaataataag acaaggccat 240
aaatattggc ctccctggct ggggagttgt gtgggtttcc tttccaggca gttgaggttt 300
tccatggagc ctactctaca gtgtcagcag gagtataaca tagaaggctt ccaggtcagg 360
tggcccagag tcaaatcaaa gccccatccc tttttagcaa atttctcagc cttacttagc 420
tgtgccggcc tgcctctttc taaaatgagg aaaataataa tacccacttc actggtttat 480
tgagaggatt aaatgaggac atgtgttatt tcacaccatt attgcttctg ttgttattat 540
tttaaaatct aggttggtga ttgcatcagt ttcttagggc tgctctaaag aaagtaccac 600
aagctgagtg acttacatag cagaaaagtg ttttcttaca ggttaagagg ctggaagtct 660
gaaatcaagg tgtcagcagg gccatgctcc cactgaaacc catagcgggg aatccttttct 720
tgcttctaag tttctagtgt ttccttggct tgtagatgtg tcacttcagt cacacggcca 780
tcttcttctt tcttnnnnnn cttcttcttc ttcttcttct tcttcttctt cttcttcttc 840
ttcttcttct tcttcttcct tcttcttctt cttcttcttc ttcttcttct tcttcttctt 900
cttcttcttc ttcttcttct tcttcttctt cttcttcttc ttcttcttct tcttcttctt 960
cttcttcttc ttcttcttct tcttcttctt ctttgagatg g 1001

<210> 440
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-463-230 : deletion CAT

<220>
<221> misc_binding
<222> 481..500
<223> 12-463-230.mis1, potential

<220>
<221> primer_bind
<222> 255..272
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 773..790
<223> downstream amplification primer, complement

<220>
<221> misc_feature
<222> 136,400,713,730
<223> n=a, g, c or t

<400> 440
aatcaatgca taaacaaaaa ggatgcccca gaaaacctgt gcttttcaga cacacacaca 60
catacacaca cactcactca ctcactcact ctgaattggg tcaagtaaaa aaaaattttt 120
tttaaaggaa ggaatncttt agcccaactg ggatttcgac gaaattgtat atatcaaaag 180
atagctacat ccaacctctc accagaatcc agaggctttc tcctgcaaag atactattga 240
aagttttatt agtaagtttg agaaggcgaa agtatgtatc agaggtgaaa gctaacatga 300
caattgcttg gccaaagagc gcagcagttt tatgttattg agcagcacag gatgaatcga 360
acacccacga tggctagaca gaggcgcctg gctgtgactn ccagaggttc aggcaagcca 420
tctgacctct ctcagtcccc accccctgaa atgaaaacca tactcataag actccttgac 480
aatggaaatt ttggaggtga catagttaat gaagtgtcat agaaaggaaa tagctaagaa 540
tactctaaaa cctccccatt cccagtatgg gcaatttggg aaaaatgagt aactaaaaat 600
taggggttct caaagtgtgg ttccaggatc aaatgcatta gtccccacct gggagcttgt 660
tagaaatgca aattcccagg ctcccctcta ggcctcctga attagaactt ttngggggtg 720
ttttaacaan gctctccagg tggttacgat gtcccataga gaatcattgg ggcaaataat 780
cctgtgccct gattagattg caaagctgca ctttcaaaag caagtcaggg tgctgagttg 840
cttagtttct attgcaaaat ttcctgcttt ggaacaaaat tttcaaaatt ttcagagggt 900
tgctcaggcc agtgatgttt gcaatgcaaa cccaagaatt ctgaaaggag cccatggctg 960
aaaggagcca attcttccag gacggactac tccagttgca a 1001

<210> 441
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-462-199 : deletion ATGTCCCACAGCTG

<220>
<221> misc_binding
<222> 481..500

<223> 12-462-199.mis1, potential

<220>
<221> primer_bind
<222> 303..322
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 736..756
<223> downstream amplification primer, complement

<220>
<221> misc_feature
<222> 255
<223> n=a, g, c or t

<400> 441
caaaagcaag tcagggtgct gagttgctta gtttctattg caaaatttcc tgctttggaa 60
caaaattttc aaaattttca gagggttgct caggccagtg atgtttgcaa tgcaaaccca 120
agaattctga aaggagccca tggctgaaag gagccaattc ttccaggacg gactactcca 180
gttgcaactg tgctgtggag gctgaggagc atccatgact gaggaagggc gagtccccta 240
taatgccctt gctangggga gcatcagaca tccctagact tacaagtccc tcgtgtaata 300
aggtgaacta tggaaagcta tgatttgagg aaagttccct ctgattgaaa gagttcttca 360
aatatgaaga atgtaacact tatggggcac ctactcattg caaaacactc tactaggggc 420
tttcacctgt atgtttaact cattttgttg attttttttt ttttaagccc aaatttctga 480
gaggttaagg aacttgtctg gtggtggcgt ctctgggatt ctgacttttc cactgaccat 540
aacatgcatc tggtctaaat tgagcggacc acccaggagg acgttggaat aaaaagaaat 600
gggaaggggg tggggagagg aatgggcata gaataaaaag gtagaaaccc ttgggatcaa 660
aggatgcaac tgaaagagca ccaaaatatg catcattttt tttaatatgt tgtctggtac 720
ccaaaattgg gatgcctctg tggtatcaac tttgacattt aaagaaaggg cataagatta 780
gatcattcaa ccataagtgg aaggaagaaa caaaataaaa taaaacctta caattccctt 840
tgaagttgat caggtgtcaa ggcagtgatt tggttttctt ttacaaactt tctttttcca 900
gaaaaatttt tactgtgggt ttggagaggt gtttacaata aattcatagc agagctccaa 960
aagggcccac cccatctaat atcctctgtc tcagcagatt a 1001

<210> 442
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-430-287 : insertion T

<220>
<221> misc_binding
<222> 481..500
<223> 10-430-287.mis1, potential

<220>
<221> primer_bind
<222> 215..233
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 617..635
<223> downstream amplification primer, complement

<220>
<221> misc_feature

<222> 938,965,972
<223> n=a, g, c or t

<400> 442
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cgaacaatat aattatttaa attatatttt gcatggccat ttgttaatgc tagttctcac     60
atgtctgtaa aattaggatt tttaatatca attaaatgaa ggactttgtt ttgttcactg    120
ttacatctcc attgcctaga acattgacat ataaatattt gttaaacgaa tgaatgaaat    180
aacattctga caattgaaga agagatttta agaatagctg taacacatca tacataaaaa    240
tgttaagcat aaatatttgt aatatatgta ccgaaattta ttgaccctca catgtttggc    300
agattcttaa tttttcttta ctggctttac ttagggacgt gcttccttaa cacaagagaa    360
agagaagttt gcccatgaac atgaagaaat gaagaaccta gaagccattg ttcaagaaat    420
aaaaccaact gccctcatag gtaagcattt tctcctctcc cttctcccct accccttatt    480
ttgacctgat tgtttttttt actaccaatt tttgaggtat aatttagcct ttttgaattc    540
aaaaaactac acgttcgctc aagcgacagt accctgtaga gacctagatt tttaacttta    600
gtcctgtcgt ctttctctta ctgatctgag atgaagcgta tggccccctc ctctaactca    660
gcctgttaat acctggcacg ttcagcactt ttctaggctt gattactcca gatagacagt    720
ggttctcaaa taagagggat ttttgccctg caggaaacat ttggcaatgt ctggaagctt    780
tgagttgtct taactagggt agcggggttg gaagggagta aagggagggg ctactgacat    840
ctagcagata gaggcagcgg aatgattcta ctaaatatcc tgtagtgcac tggacagccc    900
ctgcgacaag gaattatcca gcctaaaatg tcaatagntg ctgaggttga gaaatactgc    960
agtangataa gnaccctcct ggaagacagg gatcacatct c                       1001
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<210> 443
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-718-432 : deletion T

<220>
<221> misc_binding
<222> 481..500
<223> 12-718-432.mis1, potential

<220>
<221> primer_bind
<222> 913..932
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 479..499
<223> downstream amplification primer

<220>
<221> misc_feature
<222> 346,853..854,883..884
<223> n=a, g, c or t

<400> 443
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gtaaccttgg aaaaattact taccttcctc aaggcttaat tttcttgcct gtaaattggg     60
gtaaaatgct aatagtacct tcagtagtac cttcagacag ttgttatgat gattgagaga    120
aaacatataa aacaaattac ttttatcaag tgctataaat agtaactata atttttattt    180
ttcaggaagg attactagga ccataattta gttaaaagat gtaggctggc aaatttggct    240
taatattaaa tagagcattt aatagttgga attgtcccca aagaaaataa tgtatataaa    300
agtacttgca cataaaaatt actcagaggt tgttattcct tattgntttc tgttgttaat    360
attatttgtg aactctccat cactctgaga acatggacag atgtgcttaa agatataaag    420
atttctactt ttatgtgaga tgatggatta gaattaaatg tttctaaagt gttccaactt    480
taggattcta tgaaagtggt aaaaaaaaaa tcgtattttg tttcaacatt caggactggt    540
tgtttcataa aattcagtga ttcagccatg cttgtgatca ttatgagtca gttgaaattg    600
```

```
atcatcacaa tatatttgac ccagaggaat aaacttctca ttcaacattg taaattattt    660
tgttttgcat aacaaaacaa ctttaataaa cttcagtaag ctttagcttt cccttgctac    720
ccaaagttta tttcataaag agctcaagag acaattggca agttaaataa ttcaagagaa    780
aaaatgttca caagaagttt ttatttgctt tgcattctat tccctatgct acatattaat    840
tgtacagtta gcnncaaagt aagttttgta gtaaaaatta ctnncacaat aaaaaaggta    900
catagataca agcaactagc aaattaactt cgcaaagaat aagatgtggg tttacataag    960
ccatttatgc cagttaacta gaccagttct caactctctc t                        1001
```

<210> 444
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-269-301 : deletion T

<220>
<221> misc_binding
<222> 482..500
<223> 12-269-301.mis1

<220>
<221> primer_bind
<222> 204..222
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 634..654
<223> downstream amplification primer, complement

<220>
<221> misc_feature
<222> 626
<223> n=a, g, c or t

<400> 444

```
acacagaggc accatctgtg tcactctgtg tgtggtctgc catgttgtgg ggtggtcact      60
acagactcag gcagctgggc agacaatacc ttagccttag atgatgctga tgcagcccag     120
gagtcagaaa ctgtagtgca gacaatgccc tccttaggcc aacacaatta agtgcaatag     180
atgactggct tttctgttag cctcttcatt ggaaccaaaa gcagcattac tctaccaaac     240
agaggggagc tggaaagaaa ctacacagtt tgcccagcct agcctctgcc ttgacacgga     300
accatgtgag tctagacatt cacctagatc attccttggg gaccaatgct gctgacacat     360
taactcaata gtttgtcctg gcctgagagg tcatgtaact tgtagaaagt ttagaagcag     420
agattagtgt catttatttg ccatggctgt gacaacaaag gaaggaacag gagtgggaaa     480
acccaaggcc accctggttt tggtagatgg tgcacacgct tccactaact gttctggggc     540
aaagatccaa atgcactatt gggcctggct atgctgcttc tgctgggtcc cccaaacatg     600
agcctccacg ccatttctca gttgtnattt taccacatat tatcacagtc accggatttg     660
tacagaatat ttggaaccta tactgtctta agggctaccc tttaaagaag agaaaacaag     720
gttttaattc aactgtctgg aacattttat gtttacttat gtggaatact acatcttttg     780
ttataaacag gagggaatgt ggacattcga aggcccctac cttttagcta aaagcccata     840
tgaagcatat ggatccattt atacacacca tgcttttcag ctacattttc ctaatttgcc     900
tctctggggc caaccttgtg ggactagcag attcatggtt gagttgaagg atggtgacct     960
cttccatcag ctttcttct tcctccagtc ttccaaccct c                         1001
```

<210> 445
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>

<221> allele
<222> 501
<223> 2-13-398 : insertion G

<220>
<221> misc_binding
<222> 481..500
<223> 2-13-398.mis1, potential

<220>
<221> primer_bind
<222> 104..121
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 506..525
<223> downstream amplification primer, complement

<400> 445
```
tgagctccca tcccgcatcc tgtgtggcac tctgtccatc aagcccagtg tgaaggagtt     60
cacggaaacc tcagctgtgt ttgaggatgg gaccatgttt gaggctatcg actctgtcat    120
ctttgcaaca ggctatgatt attcctaccc cttccttgat gagaccatca tgaaaagcag    180
aaacaatgag gttaccttgt ttaaaggcat cttcccccca ctaatggaga agccaacctt    240
ggctgtgatt ggcttggttc agtcccttgg agctgccatc cccacagcag acctgcaagc    300
ctggtgggct gctaaagtat ttgcaagtag gtgggccatt ctgtctttca ttcattttat    360
caatgaacat ttactgaaca cctgctatat gcaaagcact gtgctaggga tacaatgaga    420
acaagacaaa catgttcctt gacctctcaa ggcttaaaat ggggtgtggg ggatgccata    480
ataggggaaa tttggggggg ttctagtgag gggagttgga ctgttgcaca gagcaaacag    540
tatacaggaa gtcataaagg tgagggaaag catgaaatgt gtaaggaccc agaaacattt    600
tggtggaagg gaatataaag cagaggcagg gagtggcaag aaatataggt ttataagcca    660
cgttaaagag cttaaacttc tcatagggat taaggacttc gcaagatttt aagcaagaaa    720
aaaatagcag aggataactg caatgtcagg ctacattata aagattggaa gggccctggt    780
gagggttgga ggtgtgccag aaacctcact ggtgtcaact tctgtcagaa taacaaagtc    840
aggccactct gattctcatg acaatcttct tcttctctcc ctctactcta gacctcatgg    900
tctccagggg ctacaagtat gcttatgtga ggaaatcaag aatatgagga ttacatggag    960
aaaggcaatg tctcaaatat attaatttac tccagtcata c                       1001
```

<210> 446
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 2-28-132 : insertion T

<220>
<221> misc_binding
<222> 481..500
<223> 2-28-132.mis1, potential

<220>
<221> primer_bind
<222> 370..387
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 769..793
<223> downstream amplification primer, complement

<400> 446
tattcaggga gttaaaggaa gacaaaggtt tttaaatggg gaaaaaatac aattacataa 60
ttgttttgaa ataattatat aaagagcaat aacaagggtg atgccagtct gagattggac 120
agttactgag cagatgttct tgtagaagtc atttttgtgt aagattatga tggtctttgt 180
gtaaggtggt ggtttttgta gtttttgtta tcaggcacac atcatgagaa cccgctcttt 240
ctggcctttc ccaattctat ttgtcgggtt tcttaacatt agtgactcca tctagattct 300
gacagttttc atgagaactt gcttttcttt tctctctcaa gtccttattc agtattcagc 360
acccttaaca gattagtccc actgctgagt caggcctctt gcatgaagca gcaatgagaa 420
agacacactt ggccaatgtt atcctggagt aattctcaat gatgccttct ctgtgtttct 480
tcaagacaac tgtccttagt gtgagaaaat gtccagattt ctcatcctct ggccaatgga 540
aggttgtcac tcagagcaac ggcaaggagc agagtgctgt ctttgacgca gttatggttt 600
gcagtggcca ccacattcta cctcatatcc cactgaagtc atttccaggt gagacccgct 660
gggattccca gcttttgga gtaggtttcc aggtacttta tatgtagttt ggattgacaa 720
gcaggattca ttgctgcaac tgggcagaac ttggctcaat aagattgaga cagagctaga 780
aagatgaaag acaccaaaca tcatctttgt ttctattggc ctctgagtct tcatcacaca 840
tagatctcag agccaacttc cttggaagtc actaagtcct tggcataatt ttagagaatt 900
cacatcaaac tggttctctg ttggagaggc ccttttagcc atgtgcctgc gttggccttt 960
ttctaccctg ccaaacaccg agcctttttc acagggccat a 1001

<210> 447
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 2-39-27 : deletion ACAATGACAGCATCATCATCA

<220>
<221> misc_binding
<222> 481..500
<223> 2-39-27.mis1, potential

<220>
<221> primer_bind
<222> 475..495
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 870..892
<223> downstream amplification primer, complement

<400> 447
ccagggacaa gttaagtccc accattagtg taccaaatcc cagtacttac atacttacct 60
tgatgtgtat atgctgcaca ccaaggtaaa ttacaaatca aacatattct gatttttgaa 120
aacatacttg aactaatagt cattttaaag gcttactctc tgggtataat taagcttgaa 180
atcatccaaa tattattatt ttcatagctg cagcaaagca gctgaatttc acagagctaa 240
caatgctgtc tctgtgctga atacttaata agccagaaat gaggcaaaag gtgagcccaa 300
tgagcaagca gtatactcag tgatacacag gacctccagg tcaaagggtt ataccatgtt 360
gaaaatcaag gaaaaagaca tattctttca gaaatttctc tctgcttcag tccaccaacc 420
tctcatggaa tttattctct gtacctgtgg gagtcatttc agtgttatga accagcaatc 480
aagacacctt atctggtcca acaatgacag catcatcatc atcatcatta tcatcattac 540
aatcatacac agtatttact atatatacac aaatctcttg acatagatta tctcatctaa 600
tccccaccac aactatctga tgcagatgtt attatgcctg ttttatttat tttttagaat 660
tttttatttt atttatttca atagcttttg ggggagcagg tggtgttttg ttacctggat 720
aagttcttta atggtgattt gtgggttttg gtgcacccat catctgagca gtgtacacta 780
tacccaatgt gtagtctttt atgcatcacc ccccactcca acacttaccc ccaagtcccc 840
aaagtccatt gtatcatttt tatgcctttg tattctcata gcctagctcc aacttatgag 900
tgagaacata gaatgttcag ttttccactc ccaagttact tcacttagga taatggtctg 960
caactccatc caggttgctg tgaatgccat tatttcatcc c 1001

<210> 448
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 2-45-155 : insertion GAC

<220>
<221> misc_binding
<222> 481..500
<223> 2-45-155.mis1, potential

<220>
<221> primer_bind
<222> 347..367
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 764..788
<223> downstream amplification primer, complement

<400> 448
```
ttatgttctc tgcccagtgt cccagggttt attggtttct aaagaggtag tgggtatata     60
cagcctcccc aaggggaatt taggaagtaa gctggttgtc acaaagactg gcattaaata    120
ggtagagacc taggatgcta atatcttgca atgtgccaaa ataattgtcc ctgtccccaa    180
cctcaccatt gccaatatta cccctacccc tcacagtgag cgtcacaggc aggcaacaaa    240
ctggtgtcgt cacagaatga ttgatggaac acatagactg cattcattac ctaaacattg    300
tcgtcacact gcagcaacca aagacaatcg cattacccag gggttagatg taggaagagt    360
aaaaaaacaaa aaatttttga atgcgtaatt atcactaatt attttatttg atccttcagg   420
agaatgtgga agatggccga gcaagtatct atcaatctgt cgttaccaac accagcaaag    480
aaatgtcctg tttcagtgac tttccaatgc ctgaagattt tccaaacttc ctgcataatt    540
ctaaacttct ggaatatttc aggatttttg ctaaaaaatt tgatctgcta aaatatattc    600
agttccaggt attgtatttt tggggaaatg ggtttctctg cattagttca gctcatattt    660
agatagaaaa gttactctga taatgaaagc aattatgaat gaagtatccc attctaagta    720
tttgttgaaa tataacagcc tcatataaaa cccaaaaagt agtgtcatta cccttggtat    780
tatagattat atacattaat tgaagaggaa aatcatctgt taaaattaaa ggtttgaata    840
ataatatatt gatgtcaaaa cttttttttt tttttttctc cctgagacag agtctcactc    900
tgttgctcag gctggagtgc agtggcatga tctcagctca ctgcaacctc tgccttccag    960
gctcaagtga ttctcctgcc tcggcctcca gagtagctgg g                       1001
```

<210> 449
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 2-4-391 : deletion G

<220>
<221> misc_binding
<222> 481..500
<223> 2-4-391.mis1, potential

<220>
<221> primer_bind
<222> 111..132
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 513..537
<223> downstream amplification primer, complement

<400> 449
ttatccctat atgttcattt gtgaatgaat atttattaca tcattataaa aaggattttt 60
aaactatctg tatgtttaag agtatatgtt gctactatgt aagagtatat gctgttactg 120
taaagacatt gcattactac tgttgacctc agagcacgcg cctcttgcct aattctagga 180
ctcctaacta agtctttgga gtttcagctg gaagaatgct ggaggaatac ggaactcctc 240
ccatttctca cagccacctc caactcttaa aaacgcttcc aactgcctcc cagcacacaa 300
ccaagggaga aaactattct gtcaaagaga cggtgccaaa aggcaaaaac aaaggtaagg 360
atgatcgctg gggaaagaag ctgaaaagga aaagctcaga actctagctg gaaatttggc 420
tcacatccct agtatgttac tgcatagtct ggctttgttc aatgggtcgc ttttaaatat 480
taaagctaga tgtaagcaag gtttgcaaca aagtccataa gaaactcagc ttttctcaaa 540
ggcaagaaga gagcaggatt tttgactggc tctttattca atagtgctgc ttattaaatt 600
accactgcta caatgtttaa agccaattac ctgagcacat cataaggatt ctcttaccgg 660
ttgtcccagt taagtaatgt tgattgatca actccttgac aggagctgat ggcaaagaag 720
gtagctgtga ttggagctgg ggtcagtggc ctaatttctc tgaagtgctg tgtggatgag 780
ggacttgagc ccacttgctt tgagagaact gaagatattg gaggagtgtg gaggttcaaa 840
gtaagtgaga ttttcttggg tcttgaacag gttgtgttgt tatttcaggg tgaatcacag 900
ttactgatgg gtcatattga gaaatttatt aaacaactct gatcagattt tatttctatt 960
tattgatgtg gccataatgg aactgaagtc ataggctggc a 1001

<210> 450
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-345-410 : deletion TAA

<220>
<221> misc_binding
<222> 481..500
<223> 12-345-410.mis1, potential

<220>
<221> primer_bind
<222> 96..113
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 601..621
<223> downstream amplification primer, complement

<400> 450
actcctaagc tgctaggaat gctaaaatgc taggtctcct tctcagatcc caatgggcag 60
ccctgccaag ctagcttgac tagatgggtt gtctcataat cctgagacaa cgcagacgct 120
ctgcatccct tatcaccacc tttcaaccta ctggggctct gtgattgatt tatttaacga 180
cttcagagca gggtgaaaca ctgctctgca tgtctcacta tatatctcac tatttctaga 240
tcctccattt ttaaaaggaa ttgggattca ctcattcatc aagtattgtt cagcatctac 300
tctagagcag atacagtggt gagggaaaaa aagtctcagc cttcatggaa cctataaatc 360
tagtgggaag aagagagact aaacaagtgc accaacaaat aattacaata tgctacttgc 420
tatgagggta catagagaac atgaaagacc aagttagaat acacagctga gacattaaaa 480
atgaatataa atcctcttaa taaccactac tgcatgcaca aatgaggcct tatacagtat 540
gtcgtattgg ggtaaaaaaa aaatctttta aattaaaaaa acgcaaagtt ggtaggaggg 600
cattcaccaa acattaactg aagtcatctc tggcttttaa caccagagta aagtgcattc 660
acttttttat tttaaattaa ataccgaagc tgggtgcggt ggctcatgcc tgtaatccca 720

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gcacttggga ggctgaggtg ggcagatcac ttgaggtcag gagttcgaga ccagcctggt      780
caacatggtg aaaccccatc tctactaaaa aaaaaaatac aaaaattagc cgggtatggt      840
ggtgggcgcc tgtaatccca gctacttgag agggtgaggc aggaaaatca cttgagctca      900
ggaggcggag gttgcagtga gccaagatca tgccactgca ctccagcctg ggcaacagag      960
cgagagactg tctcaaaaaa aaaaaaattg aatacctaaa a                         1001
```

<210> 451
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-358-353 : deletion AGCC

<220>
<221> misc_binding
<222> 481..500
<223> 10-358-353.mis1, potential

<220>
<221> primer_bind
<222> 149..167
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 577..596
<223> downstream amplification primer, complement

<400> 451

```
actggatgta tgtgttctca ttgcctgcct gcaacctaga attcctgccc aggaggagtt       60
cttcaaacgc tatgaaagat gttcccaccc cctgccatgc agctacacta aaaggacata      120
ttgatttctc tccagaattg tgtttatgct gaccactaaa tatcaactta ttaaaaaaaa      180
aacttacgtg gttttaattt ttttttcgct ccccccctcgc ccacaggaga actaatgaca     240
gttgccagat ggatgaggga gtttatcgca aaccatcctg actacaagca agacagtgtc      300
ataactgatg aaatgaatta tagccttatt ttgaagtgta accaaattgc aaatgaatta      360
tgtgaatgcc cagagttact tggatcagca tttaggaaag taaaatatag tggaagtaaa      420
actgactcat ccaactagac attctacaga aagaaaaatg cattattgac gaactggcta      480
cagtaccatg cctctcagcc agcccgtgtg tataatatga agaccaaatg atagaactgt      540
actgttttct gggccagtga gccagaaatt gattaaggct ttctttggta ggtaaatcta      600
gagtttatac agtgtacatg tacatagtaa agtatttttg attaacaatg tattttaata      660
acatatctaa agtcatcatg aactggcttg tacattttta aattcttact ctggagcaac      720
ctactgtcta agcagttttg taaatgtact ggtaattgta caatacttgc attccagagt      780
taaaatgttt actgtaaatt tttgttcttt taaagactac ctgggacctg atttattgaa      840
atttttctct ttaaaaacat tttctctcgt taattttcct ttgtcatttc ctttgttgtc      900
tacattaaat cacttgaatc cattgaaagt gcttcaaggg taatcttggg tttctagcac      960
cttatctatg atgtttcttt tgcaattgga ataatcactt g                         1001
```

<210> 452
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-360-190 : insertion T

<220>
<221> misc_binding
<222> 481..500

<223> 10-360-190.mis1, potential

<220>
<221> primer_bind
<222> 312..329
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 713..731
<223> downstream amplification primer, complement

<400> 452
gtataatatg aagaccaaat gatagaactg tactgttttc tgggccagtg agccagaaat 60
tgattaaggc tttctttggt aggtaaatct agagtttata cagtgtacat gtacatagta 120
aagtattttt gattaacaat gtattttaat aacatatcta aagtcatcat gaactggctt 180
gtacattttt aaattcttac tctggagcaa cctactgtct aagcagtttt gtaaatgtac 240
tggtaattgt acaatacttg cattccagag ttaaaatgtt tactgtaaat ttttgttctt 300
ttaaagacta cctgggacct gatttattga aatttttctc tttaaaaaca ttttctctcg 360
ttaattttcc tttgtcattt cctttgttgt ctacattaaa tcacttgaat ccattgaaag 420
tgcttcaagg gtaatcttgg gtttctagca ccttatctat gatgtttctt ttgcaattgg 480
aataatcact tggtcacctt gccccaagct ttcccctctg aataaatacc cattgaactc 540
tgatggctgt tatcaaagga acttttcttt gtttaaattt gctgatgcag gaattaagtt 600
taaacacaac tctatagaaa gaaaggagat tattacccag aattcacatg tagtgattat 660
taaggacaat tttttttttt aactaaaaaa gttggcggca ggggtggggg gtggcaatca 720
tttttcttcc tatacataca aaggatattg tcaaaaatgg cgttcttctc ttgtggcctg 780
ttattctgat tgctgctgta tacagttttg tcactcttta gtttttagtt aagcatactg 840
atagactttc ctctaaaagc cattcactcc agattttacc tggggaatat tctacatact 900
gcttactttc tctataaaac tcatcaataa atcatgaaag gcactgagtt ttgtaaatca 960
ggaccctaaa tgtttaattg taaataagtt tcagataatt a 1001

<210> 453
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-365-374 : deletion A

<220>
<221> misc_binding
<222> 481..500
<223> 10-365-374.mis1, potential

<220>
<221> primer_bind
<222> 128..145
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 530..548
<223> downstream amplification primer, complement

<400> 453
tcaaattctt cttttacacg atgactctta ggtgaccaat ttatgacgtt tggttgtctg 60
ttttagtacc ttaacaagaa atatccgaca taggagagga gaaaaggttg tcatcaatgt 120
accaagtaag tctactgaga ggtggtgggg tgggagagag acatgttgta ttgttgttta 180
atcctggatt ctaaaccatt tttattttg tatttttata atacagtatt taaggacaag 240
aatacaccat ctccatttat agaaacattt actgaggatg atgaagcttc aagggcttct 300
aagccggatc atatttacat ggatgccatg ggatttggaa tgggcaattg ctgtctccag 360

```
gtatagtttc aaatatacag agaggcaaag tgttccatcc atttctgttt tttaacttct     420
ttatatatgc atgtttcctg ttccaaaaat cacattttaa tgaggttgaa atggtagctg     480
gtatgccttt ctgaaaaaca atgaagttat attagtaaat tcattggaag ctgtctatga     540
ctaatagttc tacagactct gttgttcacc acaaaggtat atacggtata tataccttta     600
taactgtaat ttcagttaac ttaaaatgca atatattctg tcattgtttc ccttctcttt     660
ttatatgcct agtttttact gccatctcgt gacaggctag tgaggtggtt taaatattgt     720
tcaaaactct gaaaatgagc tctgatggaa gtattccaat gattttgtga tccaagggat     780
ttgtgcaaag ctgtctagcg gtacaaaaag aataaatatt tagcagcttg tgtttgtctt     840
gcccctgagt aaagtataca ggagcctgtc tctgtttacc catttaaaaa ttttcctgga     900
tctgtttaaa tgatggtgcc cctggcagtg agtgtgtcca agctcactta ggaccagagt     960
ggaagagcat ggaacccatc aggtggccac acacaagcct g                        1001
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<210> 454
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-367-58 : insertion GTGGAG

<220>
<221> misc_binding
<222> 481..500
<223> 10-367-58.mis1, potential

<220>
<221> primer_bind
<222> 444..461
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 855..874
<223> downstream amplification primer, complement

<400> 454

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tgcaattctt aaacaggtga cattccaagc ctgcagtata tctgaggcca gataccttta     120
tgatcagttg gctactatct gtccaattgt tgtaagtaga aattacctct tattttaaat     180
actacttcgt atgaaataag atagcatgtg cagaatttac tgacagtgtg ctatttaagt     240
ccagttaaga cctcagtcag agatggacta atataaatag tatgtaggtt taggtataat     300
gaactgagag tctacactgt agaagtttac tcttgctagt acaacattga tttgttaaat     360
gtgaagtttg aatgtggcca ttttccctcc cccatacttc atgtcctcac attagagaga     420
ggatgattta agtgaatcaa acccaaggaa ctggattctt cctggtatat ttcactgtaa     480
gataggcaca ggtacatgtg ctctgtatgg gttgcataaa catgcttttt gatcagaaat     540
ataactgcat ggagcttttt ttagcatgta agtgacactt tgaatttgca ggagctgact     600
tttgtttgtt tttagatggc tttgagtgct gcatctccct tttaccgagg ctatgtgtca     660
gacattgatt gtcgctgggg agtgatttct gcatctgtag atgatagaac tcgggaggag     720
cgaggactgg aggtgggaat tgtttttcct taatagccct tttaagtcaa gcaggtaaaa     780
tggatctttt gtaactactt gcaatttcag gatgtctccc tgcaattttt atctgaaatg     840
gggaaaaaga tttggtctag gtggggagtt aatttttatc gtatgttgat gtctgtattt     900
gttttagctt catttaaaat tagtagtccg atttttctat attttggaag tgctgatggc     960
tgtttttacc aaaaggcttt ttggtgccac atgagtgttt t                        1001
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<210> 455
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele

<222> 501
<223> 12-468-424 : insertion T

<220>
<221> misc_binding
<222> 481..500
<223> 12-468-424.mis1, potential

<220>
<221> primer_bind
<222> 76..95
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 583..603
<223> downstream amplification primer, complement

<220>
<221> misc_feature
<222> 13,23,255,639,967,971
<223> n=a, g, c or t

<400> 455
gtataagtgc tgnttaagag tanttgattg ccttttcttg gtttaatatt aaaccagggt 60
gttctgccaa agaccgcata gtttctctga tatggttcca aagggatatt ctttccactg 120
aaacactgta tgtataccag taaatgcttc ctaatggtag atgataaata tttttgttgc 180
ttgtagatag aatttttcca tctagtgtaa gcttaggatt gttttctttt tcccagtgac 240
atgtacagtt tcacntactc cacttaaaaa aaatcgttag ctcagataaa gtgtgtggca 300
catgaaatga attttgccaa ttcaccaccg aaatccctgc tttatatctc ttcagtggaa 360
cactaaacca acttctttcc caagtacact gatttgatct ttacaaatta tatgaatgta 420
ttaaattatc acatgtgccc tgaaactgtg tacatctatt atgtatcatt agagagatgg 480
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ggctaatgga agacttactg tataaaacaa aaaggatttt aaccacattc aaattattga 600
ctgttttggg gcttttcagg aatcacttaa aaagcaccna agttcacagc caggcacggt 660
ggctcatgcc tgtaatccca gcactttggg aggctgaggt gggcagatca cttgaggtca 720
ggagtttgag acaagcctgg tcatcatggc aaaatctcat ctctactaaa aatacaaaaa 780
ttagacctgg tggcatgtgc ctgtaatccc agctactgag gagtctgagg catgagaaac 840
gcttgaacct gggaggcgga ggttgcagtg agccaagatc gtgccactgc attccagcct 900
ggggaacaga gcaagtcttt gtctcaaaaa aaaaaaaaaa aaaagcacta agttcatgac 960
aggttanggt nagcccctcc caccccccc caaagtcatg t 1001

<210> 456
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-481-293 : insertion T

<220>
<221> misc_binding
<222> 481..500
<223> 12-481-293.mis1, potential

<220>
<221> primer_bind
<222> 774..793
<223> upstream amplification primer, complement

<220>

<221> primer_bind
<222> 333..353
<223> downstream amplification primer

<400> 456
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gcaggaatta agtttaaaca caactctata gaaagaaagg agattattac ccagaattca 120
catgtagtga ttattaagga caattttttt ttttaactaa aaaagttggc ggcaggggtg 180
gggggtggca atcatttttc ttcctataca tacaaaggat attgtcaaaa atggcgttct 240
tctcttgtgg cctgttattc tgattgctgc tgtatacagt tttgtcactc tttagttttt 300
agttaagcat actgatagac tttcctctaa aagccattca ctccagattt tacctgggga 360
atattctaca tactgcttac tttctctata aaactcatca ataaatcatg aaaggcactg 420
agttttgtaa atcaggaccc taaatgttta attgtaaata agtttcagat aattattata 480
gctttgcgtt gaagtttgtt gtttttttc tcaactagtt aagtcaactg cttctgaaat 540
aactctgtat tgtagattat gcagatcttt acaggcataa atatttaaac tgtaatatgc 600
taacttgaag agattgcaat aaagctgctt cagctaaccc tgtttatgtt taaatactag 660
ggtttgttct atattttata catgcatttt ggatgattaa agaatgcctg gttttcgttt 720
gcaatttgct tgtgtaaatc aggttgtaaa aaggcagata aattgaaatg tttgtggtat 780
gaggaaataa aagaatggaa ttagctttca ttcagaaacc tttgagtgtg tgtgagttcc 840
acagctaaac aaatagtaga agagtttggt ttttgtaatt aacccaaata ccatgaaatt 900
attttttcat cattgcgacc tcagatgttt ctagaaagaa gcatagtgat gaagacaaac 960
agatgccgta tctcccctag tagctatcaa ccccggtggg g 1001

<210> 457
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-499-86 : deletion GGG

<220>
<221> misc_binding
<222> 481..500
<223> 12-499-86.mis1, potential

<220>
<221> primer_bind
<222> 567..586
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 136..156
<223> downstream amplification primer

<220>
<221> misc_feature
<222> 77,302,451,665
<223> n=a, g, c or t

<400> 457
aaacttactg caacctttgc tttccagcct tccacacaca cacaagtctc catggaatca 60
cagggcagtt gcaactnccc ctttcaacag gaaaactgca acagcctccc ttctacccaa 120
aaggcatcac gtcatttaaa agaaggatga ggcagggcag tcagtaataa caatggcaac 180
cacaataggt gtcactccat tttgatgtta ggaaactcaa cagagaaaat cagagaggtt 240
gaatgagttg ctcaaggtca cagacctaag aaaaccatgc tcaggatttg aaccaaggac 300
tngcctctct ccaaacacac ctatgccatc tcccataaaa ggactggatt tttttctgtc 360
ccatggctgt ttttacctct tgctgagcct atcagctgag gtacgtaggg taaggtgtgg 420
ggaagcacaa actcctccat gtgcaatggg nttgaaacac ctattccaca ttactgctgt 480
tgttgcagca gggataaagg ggggggtcgt gacctaccaa aaggcccctg aatttatttt 540

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tcagctttta gcttatattt ttgtttctat tgtaccattt gatgcatgca cttaagtgcc    600
tttaaaaagg aaactccaaa cagctgagaa agaaacgtta taaaattgat gacatctttt    660
ttttnttttt tttttttttt tttttgagac agagtcttgc tctgtcgccc aggctggagt    720
gcagtggcat ggtcttgggc cactgcaatc tccctctcct ggcctcaagc aattctcctg    780
cctcagcctc ctgagtagct gggactacag ccacctgcca ccacacccag ctaagttttg    840
tatttttagt agagacgggg tttcaccatg ttggccaggc tggtctcaaa ctcctgaact    900
caggtaatct gcccgcctca gcctcccaaa gtgctgggat tacaggcatg agccaccgca    960
cccggcttga tgacatcttt tatgaaatcc tttttatgtt t                       1001
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<210> 458
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-500-217 : insertion CAATA

<220>
<221> misc_binding
<222> 481..500
<223> 12-500-217.mis1, potential

<220>
<221> primer_bind
<222> 286..306
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 714..734
<223> downstream amplification primer, complement

<400> 458

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agatcccatc tcttgaaaaa aaaaagcaac tggaaagaat tactattttt taaaaaatac     60
ttttaaacct tttttagaga cagggtctca ctatgttgct caggctggtc tcgaactcct    120
gggctgaaat gatcgtcctc ctgctgcctc agccttccag gtagctggaa ttacagacac    180
aaaccaccat gctcagcttt ggaaagagtt cttaaaggaa ttctaattag tggcctcaga    240
caaattctag agaggttcag tcacatccat aaaacaagta ttatagattg tgcttattta    300
atggtgagta ttctcaccag tagagcagat gttgaatatc caaggtagtg atttaaaaga    360
ccaaatgaag attaatccca gcaggatggt gaagaaatgg aaattatgga aatcctgaag    420
catggaaagc tctggaaaat tcaatgtttg tgtaataatt tagaagagga gaatagttta    480
tataggaaag atatacaata atcaaagaaa taatagaatt tttccttaat aagtcttcct    540
taaggatgag acaaatattt aactcaaatg taggcattta ttaatctcaa agagaaaatt    600
aactgtccgg acaggagaaa aaattaggag acatgaaaag gggggaaaat caactgatat    660
tacttttcat ttgcaacatt aaatgctaga tggaaagaag ttttcagaat ctcgagaggt    720
aaagaattaa caaccacaga attatcttct cagccaaatt attctttaaa tttcaggtga    780
ttctaacaaa actgaatgga tcaagttagg gctaaaagta tgccagaagt cttatctagt    840
gtcttggttt gtttgggctg ctgtaacaaa aataccttac agtgggtggc ttataaacaa    900
caggaatgta ttgctcacag ttctggaggc tgggaagttc acgatcaagt caccggcagt    960
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<210> 459
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-511-101 : deletion A

<220>
<221> misc_binding
<222> 481..500
<223> 12-511-101.mis1, potential

<220>
<221> primer_bind
<222> 585..602
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 152..172
<223> downstream amplification primer

<220>
<221> misc_feature
<222> 129,588,664
<223> n=a, g, c or t

<400> 459
ggcttgtgta gttttgccct gcacatgtgc agccctgccc tcagccaagg atctgtaggg 60
aactcccact tagacttcta ggaactcatc tttgcagctc cctccttact ggtaccatgc 120
cctgcaaant tccaaacttt ttgcatccct gaacttcagt ctctgcctct tcagctcagg 180
gagactgctg tgctctgttt gggctccact tcatggcctc tgttgttcaa aaagttgccc 240
ccaaacctgg ggcaaatgtg ctgctcactt cataggcttc ctttctctga aggagcacag 300
ttctatgctg ccttgcttcc aacgtccgaa aatagctgtc atttattttg tcatttaaaa 360
accttgaatt acagtaaggg aaagcatatt cataaatgaa atgatgtaaa gactttaagt 420
ctacctaaca tctagttttt ttcttttttg ctaattggac tattcctctt ttcattcatg 480
tcctttaagt ttgtttatgg aaaaaaatta tgacgaccac actcttctgt ggttatagga 540
actttcacac ccattacaac attatgcatt tatattctga cgaccttnga tgggacacac 600
aaaacctgat tcttgcaact ttgccatgaa ctttgtgatt tccagagact ggtaaccact 660
tagnccccac aaacttctaa ttctctacac agattatctc tctttccttg actcttatgg 720
tttgtaaata aatgtctttt acacacaact ctgaagcgcg tcagatttta tggtacccca 780
tagggctata atgcctatag aaatgggacc aaattgaaat tttggaaatc tctcttggct 840
ttgtagacta gttggtcgta acttcccaag tcacacttct gatacacctg tgagggatta 900
ctgctttgtg ccacactaga tgacctgcaa ggttttctaa ccatagataa agccagtctg 960
tgattctcat ggacaaattt tatgtgtttg ttggaaccag g 1001

<210> 460
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-586-443 : deletion C

<220>
<221> misc_binding
<222> 481..500
<223> 12-586-443.mis1, potential

<220>
<221> primer_bind
<222> 59..78
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 523..543
<223> downstream amplification primer, complement

<400> 460
ttgacatttt atgttcagct tgcacttctc tttctcttct ttagtgcctg caacttctca 60
cccacacttt caacagagaa ttcagccagg tgcacggcag cgtcagtgac tgtaaggtga 120
gcacattgac tgtaattttt agccagtatg ttgataactg atttctccac agcagcccag 180
attacctatt cctggttttt gctgctttta agcaacttgt catgggcata gcattgtatt 240
tgaaaattta tgacatactg ctctggtatt cattctaatt tttcagagtc cgaacactga 300
cttctgaaga taaaagtact cctttgtgtc tcttagagtg attatcagat gggaaacatt 360
ttggcttttt catgactcct ttggaggaga atattctatg gggaggtggt atgttattct 420
ttgccagggt acaaggaaac cctgaggttc ctggtggcat aaagttttat tgacttcaac 480
aaagagtgaa gtaaacactt cagagaattt ctgtgttatt cactcaattc tagtcagctt 540
gaccttaaac cctcccggct cattcctgcc ttggggtctt tgcacaccta ctatttcttt 600
gcctggaatt gcctttctcc aggtattgcc atggttggct cccttacctc tttcattttt 660
ctactccatt atcacctcct gtgagtcgac tctgttaaca cctgataata aatctgacag 720
ctgtctgaaa ctttctacct acccctcttt cctgctttat tttttgctat agcactaatt 780
actacctgat gctttttaaa gtgtttgttg agtggtttat tgtctgtctt aagctccagg 840
gaggcagatc ctctgccata ttattagaac aatgcctagt acatggaagg tgcaccactg 900
taataccact tatattaatt caggggctgg gtgtggtggt gcatacctgt aatcccagca 960
ctttgggagg ccaagatgag ggatcgcttt gaggccaata g 1001

<210> 461
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-593-287 : insertion TAAAT

<220>
<221> misc_binding
<222> 481..500
<223> 12-593-287.mis1, potential

<220>
<221> primer_bind
<222> 771..788
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 251..271
<223> downstream amplification primer

<220>
<221> misc_feature
<222> 135,300,327,765,797
<223> n=a, g, c or t

<400> 461
ttatctttat gttgaccagt ttgttccact ttttgaagta acttcattga actttctgct 60
aacgtatcct ttccatattc ccctctctca tccctgttct ccttcagtct gctaggtcaa 120
agtataagga ttctncaaaa atgcagagta attatgaaaa ttctgtttaa aaagcttcag 180
aatagaatgt ttatatagca ttgatttgga gctaagggct atattctggt aacataacaa 240
ggtgctatct agtgaatgtg tgattgtgta gtcatggagc tgatgtccct gccatagaan 300
ttacagaatt atctaaaaag ggaaatncta taataatggc cttcaatgct cccacacttg 360
gactagccat tgccataggc agaaaggcaa tctcatcttt actgtgtgtg caaacagtac 420
tttaatgtaa tgtgtgctta atataagctt tctttaaaaa aaaaaaaggt ggctcctgtt 480
tttgaatagc tatttttaag atagatatag ttaggaatct aaatgtgttc tatatagtta 540
atatccatta tgaggtggct ctgaaaaatc aacctagtat aagttggatg gctttgcttt 600
tctgcttctg ttataaccca tttttctaga aaagcttcca cttctactta aagataagag 660
gcaaatcatt ttcctgttcc cttatgcaca tagatgttca cttaccaaat atttatagag 720

tggcccagcc ctctgcagac agtggtgagc aaaaccagac atggnttcct gccctcatag 780
acttatagtc tgatggnatg acacagacat aaattaaata attgcacaaa taaatgtaaa 840
ttatagcagt gatgaaatag ttgtgtgtgt tgtcggagat cacataacgt tgggggacct 900
gttatgagaa agtggtgttt gaaataagac ctgaagatgt gaaatcaaag gcgtgaggct 960
gggtgtggta gctcacgcct gtaatcccag cactttggga g 1001

<210> 462
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-795-383 : insertion CA

<220>
<221> misc_binding
<222> 481..500
<223> 12-795-383.mis1, potential

<220>
<221> primer_bind
<222> 119..136
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 679..696
<223> downstream amplification primer, complement

<220>
<221> misc_feature
<222> 408,416..417
<223> n=a, g, c or t

<400> 462
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ctagggctgc tctttttagt aaagctaaac aaaacctggc gtcctacagc cttactaacc 120
tttgttaatc cgcctgctcg tcacatcttt gtatggcatc tgtgctcact catgggggaa 180
agagattctg gaagaagcaa cagcaataac caaggcaaat gtggggaagt gtctgcatgg 240
gttgttagca tgatgtgtgg ggcctaggtt ttacttcatt ttcttcgaat agtgaggtcg 300
ttaagtcacg ccatttgaat aattttgtat gaccataggg tgacatactc atccctgttg 360
tcaattctcc taagaaattt ggtggcaaat ttcatcactt aagccagnaa agtggnnaaa 420
tttggattag ggatgccaaa taagcaaatc tttatattga tagaaatgta cataggcgta 480
tgtcttaata gacttccaca ttattgaggg gttttttttg gttttgtttt gtttttagt 540
ttttttggtc ttatttttaa atttggttaa ggcttttttg cttgcttttt cttcgattta 600
attttccttt tttacatttt aattttggtt attttggggc catttttga ttttgttttt 660
ccaaaggacg cggattctga tagcggggac gattctgaca agaggtcgtg tgaagagagc 720
tggaaactga ttacttctct gagagaaaag ctacctccca gcaagttgca aaccattgtt 780
aaaaaatgtg gcctcccaag cagtgggaag aaacgtgaac caattaaaat gtatcagata 840
ccccaaagaa ggcgcttgag taaagattcc aagtgggtca caatctcaga tcttaaaatt 900
caggctgtca aagagatttg ctatgaggtt gctctcaatg acttcaggca cagtcggcag 960
gagattgaag ccctggccat tgtcaagatg aaggagcttt g 1001

<210> 463
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501

<223> 10-494-332 : insertion ATAAAA

<220>
<221> misc_binding
<222> 481..500
<223> 10-494-332.mis1, potential

<220>
<221> primer_bind
<222> 170..188
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 574..591
<223> downstream amplification primer, complement

<400> 463
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tttttcatat agtggtttgc cacatatagt ttctttttga aaagtgtaac aactttttaa     60
atacttgaac ttttcattga ttatcttatt tgtctaagct actattttga aaaatcatga    120
tttccttata tacctaatta tgaaattaag gaaatgaaat atgagtattc tatttacatc    180
agtctgagta gttcttgtta cttaacatcc cttgttcttc tcattgttaa tctctttaga    240
tttctaacat tctatgactt ttgagttcca ctcatggaat aagatatttt cttcactgta    300
acaggttctg tggagatttg atgggaataa accagatact ttaggactca atactcggct    360
gtacaagtgg ataccccaga atgatcttct tggtaagtct ctgaagaaca aatactgaat    420
atattagtaa cagattatta aagtgttaat agttatcatg aaacaagctt actgaacatt    480
tgttatggaa aaacttaaaa tgaaacttct ttatatttat tttccagtcc cgggggaaaa    540
gaataaatga taattgttgg cattttatga tatgcaccca cattctttac aatcagagtc    600
agagtatctt tatttcaggt gttattacct cccacagaat ttttctggca cttcctgggt    660
tgtcttcctt tctcatattt ctacaacttt acacctgttc tttcctcctc tgtagggtta    720
tttcaaatgt cactaaaagt aacagctctt ctgctatcac cagggatgct gcattttctg    780
taggattaaa tccctaatct taatcaaaaa gtgatgacac atttcataat gaaatgtgac    840
ctgtctttcc tcaattctag caccaccacc acctcactgc ctgctgcctt gcacacccta    900
catatcacac tccgtgactg tacttaagag aacacattct ggctgggcac ggtggctcac    960
gcctgcaatc ctagcacttt gggaggctga tgcaggtgga t                       1001
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<210> 464
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-494-380 : deletion GATAAT

<220>
<221> misc_binding
<222> 481..500
<223> 10-494-380.mis1, potential

<220>
<221> primer_bind
<222> 122..140
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 526..543
<223> downstream amplification primer, complement

<400> 464
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acaacttttt aaatacttga acttttcatt gattatctta tttgtctaag ctactatttt     60
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gaaaaatcat gatttcctta tatacctaat tatgaaatta aggaaatgaa atatgagtat 120
tctatttaca tcagtctgag tagttcttgt tacttaacat cccttgttct tctcattgtt 180
aatctcttta gatttctaac attctatgac ttttgagttc cactcatgga ataagatatt 240
ttcttcactg taacaggttc tgtggagatt tgatgggaat aaaccagata ctttaggact 300
caatactcgg ctgtacaagt ggatacccca gaatgatctt cttggtaagt ctctgaagaa 360
caaatactga atatattagt aacagattat taaagtgtta atagttatca tgaaacaagc 420
ttactgaaca tttgttatgg aaaaacttaa aatgaaactt ctttatattt attttccagt 480
cccgggggaa aagaataaat gataattgtt ggcattttat gatatgcacc cacattcttt 540
acaatcagag tcagagtatc tttatttcag gtgttattac ctcccacaga atttttctgg 600
cacttcctgg gttgtcttcc tttctcatat ttctacaact ttacacctgt tctttcctcc 660
tctgtagggt tatttcaaat gtcactaaaa gtaacagctc ttctgctatc accagggatg 720
ctgcattttc tgtaggatta aatccctaat cttaatcaaa aagtgatgac acatttcata 780
atgaaatgtg acctgtcttt cctcaattct agcaccacca ccacctcact gcctgctgcc 840
ttgcacaccc tacatatcac actccgtgac tgtacttaag agaacacatt ctggctgggc 900
acggtggctc acgcctgcaa tcctagcact ttgggaggct gatgcaggtg gattgactga 960
gctcaggagt tcaagaccat cctgggcaac atggtgaaac t 1001

<210> 465
<211> 929
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 429
<223> 12-659-251 : deletion TT

<220>
<221> misc_binding
<222> 409..428
<223> 12-659-251.mis1, potential

<220>
<221> primer_bind
<222> 179..198
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 611..631
<223> downstream amplification primer, complement

<220>
<221> misc_feature
<222> 80,605
<223> n=a, g, c or t

<400> 465
ttgattttat attaaatcag attaaataaa atcatgatgt tttatacaaa gtgacttaga 60
tattgagata ataaatgaan cattcaaata tttaagtaat cattaggcag acataattcc 120
agtgtaaaga tgagtaaaaa attactaatg gtccccaccc tttttattaa tgtatttact 180
acattcactt tcaacttcca aataatgtta agcttttcat ttctaaagca atgaaaaggg 240
agtgagttta cttatattca cttgtttcat aagttatatt cccatatctg atgatttaca 300
aagaaagcaa atctatcaat catctatgtc tgagaaatac attaatctgc ttaaaaggca 360
catataattt gtttccgatt acaaattatt aagcactttt tccaagaaaa aaattcaagt 420
gacttttttt cccatatgtg cagaataata tcgcatgtgc tacaattgga aattatttaa 480
aggtggaaaa gactgattgg cagttcttta ataataggtc tgtttaaaat atcccaaatt 540
tgtggtgatg ctaaatttca ttctgctggc tcttaactct tcagtggcac aatccaaagc 600
gttgncagca gtggtttata tggtctgcta tagctaagcc atgtagtaca tgcctagtac 660
caacatgtgg tactgatttt ggaattacca agcaatcttc ataaactagt gtataatcta 720
caagttttta acgtgtactt gctatctgag ttttaaaagt aactacacat ttgcatcaaa 780
aaattagtat aggtgattac aagaatgtta tacaggatat aaaactaaaa actgctttat 840
aaatattcaa atatcaaagt tgctgcatca gctcagagac gctgaagctg tgctggaggc 900

agcagagtta atggcggcaa gtccctgtg 929

<210> 466
<211> 987
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-912-419 : deletion A

<220>
<221> misc_binding
<222> 481..500
<223> 12-912-419.mis1, potential

<220>
<221> primer_bind
<222> 83..103
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 554..574
<223> downstream amplification primer, complement

<220>
<221> misc_feature
<222> 86
<223> n=a, g, c or t

<400> 466
aagtttactt attatcctgt gaagtatatt ttcatacctg aattttacct agcttcagcc 60
ttccattaac gttgcattca ttcttnaaca tttgtaaacc accatatttt ctagaaattg 120
gtgactatat tctaaaatca ttgtagtcac gaaatcatat gaatacctgc ttggcctctc 180
cggatagggt caagtttctc acataagcaa aatttactta tttggcatat acaatgtgaa 240
cataatctta aaacctgact ttggcttttg gtgttattaa taaggttctt aatccaattt 300
ttgttttttt tttacagaag tgatacagct atactgtaat cctagcattc ctgagttttg 360
tatatagctt ggaaataata tttattgtca aatattttta aatacttcac tttcttctaa 420
tatatttatt aaccttagca tctttttttg catttttcc ctgtgaagtg tcattcactc 480
tatcaattac tatcagaaaa atctgttatc atcttgccta tttatgcaaa gcaaatgatt 540
ctccaactgt tgactctaat ccttcctctc aaataggttc tgctaaataa atgaccctga 600
gtctctgaga catttgttgt atcaaagcac aacaacatta acagtaaaac aaaaaatatt 660
gtgaaatatg aaatatctga tcctttctcc ctctctcaaa aattctgtct gccaggtgtg 720
gtggctcacg cctgtaatcc cagcactttg ggatgacaag atgtttggat cacctgaggt 780
caggagtttg agaccagact ggacaatgcg gtaaaactcc gtccctgcta aaaatacaaa 840
aattaaccag gcatggtagc acatgcctgc aatcccagct actcaggaga ctaaggcaca 900
agaattgcat gaaccaagaa ggcagaagtt gcagtgagct gagatcgcag cactgcactc 960
tggcctgggc aacagagcaa gactccg 987

<210> 467
<211> 806
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 306
<223> 12-914-28 : deletion T

<220>
<221> misc_binding

<222> 286..305
<223> 12-914-28.mis1, potential

<220>
<221> primer_bind
<222> 279..298
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 773..793
<223> downstream amplification primer, complement

<220>
<221> misc_feature
<222> 536
<223> n=a, g, c or t

<400> 467
aactcctatt atatggaggt agttttctta ataatgtttg atactttcca tatgcctact 60
tcactaattt taattatttc tcttttttg ctcttctgat tgggtaatta catatgtttt 120
atctttagga ttgctgattc cttactctgt ttgaccaagt ctgctgttga agttttctac 180
tgagtttttc aattcacttc acatattttt tattaattgg atttcttttt atttttaaaa 240
catttccact tctttgcaaa atttatcatc attttcctgg attattctct aaagtgtgtt 300
ttttttcaac tctctattca tatgtgctgt gatttctgaa cttttaaaat aggtgtgcac 360
tgaatttctt gtcaaaaatt ttatggagca tctgaacctt aattctgcac tgtaacttaa 420
aactagactt gcagtgattt ctaggtctgt gagatactta agcaataact ggagcttaat 480
ctcaaatgtt atacttgttt gcaggtcata gaaaagctcc gtatgagtaa ctgggnatta 540
taaaaatacc tgccaaagat tcaggccttc ctttggattt tggcccctgc agtgttatgg 600
aactggtcag actcctcagc gtggcattcc tgctaatagg aacaccaagc agttgctgag 660
atgtgtgtgc ctgtcactgt gattagtact tccactcttg tttccaattc accccaggtc 720
attcaactct atagccactc ctaatgcctc tcctgaggta ggacaaaagt gggcttccca 780
aaccaaaaag attcacagat ccatga 806

<210> 468
<211> 1001
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-624-307 : deletion T

<220>
<221> misc_binding
<222> 481..500
<223> 12-624-307.mis1, potential

<220>
<221> primer_bind
<222> 788..808
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 340..360
<223> downstream amplification primer

<220>
<221> misc_feature
<222> 132,690,865
<223> n=a, g, c or t

<400> 468
tgagatagca tgttcttggg ttttaatata atattatcaa tccattagtg ccatttagaa 60
aacttaaatt gaccagcaat ccggtgctct ctatctgata aatttacagc ctgtttttgg 120
acacctactt gnatatttta aatatttatt aataaatata ttagaatgtt aattaaaatt 180
tttaattatg gctaaaattt tagtaaacaa atttttaaaa ttttaatgtc ttatgtcaac 240
attttatgaa ttctacagta gtttagtgat ttcttctaat ttttaaggtt atatttgcag 300
taattttgag atgtgattac aaatgcattg gcaatcctct catcaagtca tataccсttc 360
ctgtgaaatt tagcaaattt tgtggctgtc tcaaaaaaga gaatatagtg gaagtgagga 420
gcttaacttc caaagctcaa aaaaattgtt aatacatttt ctctgtctgt ccttctgtcc 480
ttttctctgt gtttctgtca ttcttttttc ctttttctct gtctctccac tcgctttgga 540
gccctgtgct atatccacag tccccaggag aaatatacca tttggtgtag aaatacatat 600
gtatgcctaa taagtcacaa ttggcccagc actgcagtag cttgagactt ttaatactaa 660
tcaccagata tgtgagtgat taaccttcan gatgattagc ccaagctacc ttaggacagt 720
aaccaactga gaaatgctgt gccataaaca cctaattgag cctggccaac aacctagaat 780
taaaacagat gatgataaaa tgttgctgtt ctaagcacct tcatttcaga gcagttggtt 840
aagcagtgat agacaaccag aaaanatatt tttacatatt tgagttatac tcctgtaata 900
atattaaaat taatatatac ctacaaaaaa agtgaatcta tattacattt tgtaactacc 960
tgtaacccag aaagagtagt cagcatagga tggtgggtaa g 1001

<210> 469
<211> 1000
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-290-326 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 10-290-326.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-290-326.mis2, potential complement

<220>
<221> primer_bind
<222> 177..196
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 576..595
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-290-326 potential probe

<400> 469
atgctttgaa tgttcaaaga aaccaagtga tctctatggc taggcattcc ctttaactta 60
tgtgatgagc taaaattttc aaattgcaaa aatatagaag ttctggacag tgttaacgat 120
aggacagcct acctcaggac tctcagcttc cttattacag tccagtttgt cacttttctc 180
cctcatgtcc actctgcagg atcaccggtt tccgactgag tctggggatt ttggccttgt 240
tgaccctcct aggtgccctg ggaattgcaa acagctttct ggatgaatat ctggacctca 300
atattgccaa gaaactgagg cggcaattct aacttttct cttcccttta atgcttgcag 360
aagctgttcc caccatgaag gtaatatggt atcatttgtt aaataaaaat aaagtcttta 420

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ttctgttttt cttgaaatgg ctttgtagaa acacacactt tagagaatac atttcctgtt     480
taagaactga aatttgcttg rggtaggtac atccatatca tcagtggaag tgtgttgtgc     540
cctagtttta gaaatgcatg ctgaagtcat gaccggttgt gtagggacac agcagcctga     600
cccgtgtgct ggccgttccg aggactactg acatatcctg ccactctgac tgcttctctc     660
ttgatggaaa gtttcagaca gaagctgata aagcagctga gccctttcat tggttatagg     720
aaaacaacag ataggaaggc atgtggggga catcaggcaa acacatagag tagccagaga     780
agggagtcat caactgatag cacaaaacaa aacaggttat agaaggctgg gcgtggtggc     840
tcatgcctgt aatcccagca ctttgagaag ccgaggcggg cagatcacaa ggtcaggaga     900
tcgagaccat cctggctaac acagtgaaac cctgtctcta ctaaagatac aaaaaattag     960
ccgggcatgg tggcgggtgc ctgtagtcct agctactcgg                          1000
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<210> 470
<211> 1000
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-290-37 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 10-290-37.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-290-37.mis2, potential complement

<220>
<221> primer_bind
<222> 465..484
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 864..883
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-290-37 potential probe

<400> 470

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aaaaaacggt aaggagaacc cagtaatttt gtatttatgc aaaaagtagc aggataaggt      60
ctgggtcagt ttccttctcc tgagagatat taacagcact gtgagttgtg gtggcaaaag     120
taatccatac tgtctgaggt caagtcttgc cagttcatac acaattaggc atgagatggg     180
aaaatgcaag tataaaactg tgcactgaat gtggactcta gttccttgca aaaattttgc     240
attgtctcca gaaagttacc gaggaaataa tcctgcctag ccttgataat gctttgaatg     300
ttcaaagaaa ccaagtgatc tctatggcta ggcattccct ttaacttatg tgatgagcta     360
aaattttcaa attgcaaaaa tatagaagtt ctggacagtg ttaacgatag gacagcctac     420
ctcaggactc tcagcttcct tattacagtc cagtttgtca cttttctccc tcatgtccac     480
tctgcaggat caccggtttc ygactgagtc tggggatttt ggccttgttg accctcctag     540
gtgccctggg aattgcaaac agctttctgg atgaatatct ggacctcaat attgccaaga     600
aactgaggcg gcaattctaa ctttttctct tccctttaat gcttgcagaa gctgttccca     660
ccatgaaggt aatatggtat catttgttaa ataaaaataa agtctttatt ctgtttttct     720
tgaaatggct ttgtagaaac acacacttta gagaatacat ttcctgttta agaactgaaa     780
tttgcttggg gtaggtacat ccatatcatc agtggaagtg tgttgtgccc tagttttaga     840
aatgcatgct gaagtcatga ccggttgtgt agggacacag cagcctgacc cgtgtgctgg     900
ccgttccgag gactactgac atatcctgcc actctgactg cttctctctt gatggaaagt     960
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ttcagacaga agctgataaa gcagctgagc cctttcattg 1000

<210> 471
<211> 1000
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-523-232 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 10-523-232.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-523-232.mis2, potential complement

<220>
<221> primer_bind
<222> 270..288
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 527..545
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-523-232 potential probe

<400> 471
acttcaggag attttaaggg aattatttaa agaccatttt gtaatgttct gggtaactca 60
agtggaaggc aatggatgtg agggaatttt taaaataaga aatctcttga atatgaattg 120
agtaatctct taagttcttt agataagata tggagtgatc tttaggctca ggaggcctgt 180
cttttgggaa agtgctataa ctcacttcta ctaccggcaa cttaatacgt aagagaatat 240
tcttggccct gctctgaggt ttaaacaatg ttcaaccttg aaagattgat tttaaatgta 300
aaggtcattt aaactctttt gtaagttctt atattttgtt aaaataggct gaacatttac 360
ctctagatga aaaatcaatg cttcagtgta tacttttctc ataaaataac ctatgtcttt 420
atttttttct gcagacaaaa ctgtgtggag ttttatccta tattcataat tacattgtgg 480
atggctgggt ggtatttcaa ycaaggtaat gttaaaatac agtcaactgt gttctaatga 540
tgactatgat gcttaaacga ttaaggagta gatatatggc caggcacggt ggctcacacc 600
tatattccca gcactttggg aggcccaggt gggtggatca cctgaggtca ggagttcgag 660
accagcctgg ccaaaatggt gaaaccctgt ctctactaaa aatacaaaaa ttagctaagt 720
gtggtggcgc atgcctgtaa tcccagctac ttgggaggct gagacaggag aatcacttga 780
acccaggagg tggaggctgc agtgagctga gatcgtgcca ctacactcca gtctgggtga 840
cagagactcc atctcaaaaa aacaaacaaa aaaaggagca gatatgcaac tatatagcta 900
ccaatcctgg agactaaaca aaataaacag tgtgtgcatc agagtgctat gttgcaggta 960
tatgaacttt ggcttcattc taatttaatt caataatgaa 1000

<210> 472
<211> 1000
<212> DNA
<213> Homo Sapiens

<220>
<221> allele

<222> 501
<223> 12-449-300 : polymorphic base T or C

<220>
<221> misc_binding
<222> 481..500
<223> 12-449-300.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-449-300.mis2, potential complement

<220>
<221> primer_bind
<222> 783..800
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 325..345
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-449-300 potential probe

<400> 472
ccaccagagt tcataccagc atggaatctg tacacatctt taaatgatac ttagatttac 60
ttccaaataa agagctcttt catctcataa tgcaactgtc cattatataa ccaaacccat 120
actaactctt tctccaaaag aggatccaaa gtccctttat ccctctttgg gccatgatta 180
tttgtcttct aacagagtca cattgtctcc ttgagacgta aagatgcatt tagatgcagg 240
gggacggaag aaaggaaaag aaaaaatagt ttatatgtat atacatttgt atcaaaataa 300
gaaataaata ctcataatta ttacaatttt cctctgaaag tagtcacatg gttatacctg 360
gtatttattt atttttatt attattatta ttatttgaga cagggtctca ccctgtcaca 420
caggctggag tgcagtggtg caattatggc tcactgctac ctctgccacc tgggctcaag 480
ccatcctctc accttagcct yctgaacagc tgggatacat gtgcactaat tttttttttt 540
ttgaaacaaa aatatttgtg tagaaggcac aaaagctaca atcacagact ccactgtgca 600
aaggcgcaac ctgcctcatt gatctctagt gtacaccaac ccagcttccc tttccattca 660
gcctgtgaaa ggagatagtg cttgggccat ttggtaaaag aaggggatgg gagatgatca 720
aaaccccaag taaggttcat ccaatatggt gtctaagcag caaatgacta attgctgaag 780
aaggagacta gacagaggat tagaggcagc catggggcca gtgcagctgt ggagagctct 840
gagcaaagaa acaaggttgg caggtgagga ggcctaggat agaggccaga aggccaagcc 900
tggggctgca tgtgcactaa tttttgtatt tttttgcttt tttgatagag atgagatttc 960
atcatgttgc acaggtgggt cttgaagtcc tgggctcaag 1000

<210> 473
<211> 432
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 212
<223> 10-186-212 : polymorphic base G or C

<220>
<221> misc_binding
<222> 192..211
<223> 10-186-212.mis1, potential

<220>

<221> misc_binding
<222> 213..232
<223> 10-186-212.mis2, potential complement

<220>
<221> primer_bind
<222> 1..20
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 413..432
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 200..224
<223> 10-186-212 potential probe

<400> 473
agtatgacga taggcagatg ttgtcttgca aaacgagcaa acaggcatat gaaatcagat 60
acctagctgc caaactatat gtgaggcatt tccgaagaat ttaacgacct cgatagagcg 120
cagtcaagtt tggtgaacag aatatgtctc tgaactagag gagtcctcac acaaggagta 180
gggtcagacc ccgcagtgga ggaggaggga gsagtagaaa cagtccagct cgccgcccaa 240
gtaacctggg tcctgaatcg gcccgccttg gccagtgctc cagaagcgcg gagaggaacg 300
ggctggggcc caaaaaagag gggggagcct gaacgtccgg gggaagtttc ggaggcggcg 360
gaacccacgg atggaaccct gtctttgggg aaaaggacca cacctgtcag cagagtccgt 420
cagacgtgag aa 432

<210> 474
<211> 1000
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-286-289 : polymorphic base G or C

<220>
<221> misc_binding
<222> 481..500
<223> 10-286-289.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-286-289.mis2, potential complement

<220>
<221> primer_bind
<222> 213..231
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 613..631
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-286-289 potential probe

<400> 474
aaaaaaaaaa gtatgattat tatcagagtc tctaggtgac agtgagaggc agcctggtgc 60
aggggatagg gcacagttgt aatctgctag actgggttca aatcctaaat cggccattca 120
gagcgtgaat acattagaac tggcttaaat tagcatttaa aatgtcaaca ggattaagta 180
agtagttcct tctcactttt tccacaggag gtgagaaagg tctcagcaag gccctaggag 240
ggaagggcgt ggggatgaaa gggatccaga gagtctgtgc attggcagag aagatagtgt 300
aactggcact gcggctggag ggctggtccc acagtgagct acagccctgc ccgctggccg 360
tgggagaggc ttaaaacaaa cgccggaagc aactcccagc cccataaaga tctgtgaccg 420
gcagccccag acctgcctgc cttcctgact tctgttccag agcaaaggtc attcagccgc 480
ttgaatcagc cttttccccc sacccggtcc ccaactttgt ttacccgata aggaaggtca 540
gcattcaaag tcaagaagcg ccatttatct tcccgtgcgc tctacaaata gttccgtgag 600
aaagatggcc gggaactcga tcctgctggc tgctgtctct attctctcgg cctgtcagca 660
aagtaagagg catgggaagt tcgtgtgtgt gcgcgtgtgt gcgtgtgtgt gtgtgtgtga 720
caaggcttgc gggagagaga gggagggagg gagatgggtc cggtgttttg tttcctactt 780
gcccttgcag gtagctctgg gtcctcagag cacagtcgcc tcagggtcac ccatgccgcc 840
tgctaccctc cttcccaggg gcaagcagag actgagaaca ttccagagat tagttctccc 900
aactggaacg ctgtggggcc tcagagctca gcgattctgc atcatctgtg attacgaccc 960
acagcccgtt caaacgagcg ttagtagcct gctaacctgc 1000

<210> 475
<211> 1000
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-286-345 : polymorphic base A or T

<220>
<221> misc_binding
<222> 481..500
<223> 10-286-345.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-286-345.mis2, potential complement

<220>
<221> primer_bind
<222> 158..176
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 558..576
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-286-345 potential probe

<400> 475
ggtgcagggg atagggcaca gttgtaatct gctagactgg gttcaaatcc taaatcggcc 60
attcagagcg tgaatacatt agaactggct taaattagca tttaaaatgt caacaggatt 120
aagtaagtag ttccttctca ctttttccac aggaggtgag aaaggtctca gcaaggccct 180
aggagggaag ggcgtgggga tgaaagggat ccagagagtc tgtgcattgg cagagaagat 240
agtgtaactg gcactgcggc tggagggctg gtcccacagt gagctacagc cctgcccgct 300
ggccgtggga gaggcttaaa acaaacgccg gaagcaactc ccagccccat aaagatctgt 360
gaccggcagc cccagacctg cctgccttcc tgacttctgt tccagagcaa aggtcattca 420

gccgcttgaa tcagcctttt ccccccaccc ggtccccaac tttgtttacc cgataaggaa 480
ggtcagcatt caaagtcaag wagcgccatt tatcttcccg tgcgctctac aaatagttcc 540
gtgagaaaga tggccgggaa ctcgatcctg ctggctgctg tctctattct ctcggcctgt 600
cagcaaagta agaggcatgg gaagttcgtg tgtgtgcgcg tgtgtgcgtg tgtgtgtgtg 660
tgtgacaagg cttgcgggag agagagggag ggagggagat gggtccggtg ttttgtttcc 720
tacttgccct tgcaggtagc tctgggtcct cagagcacag tcgcctcagg gtcacccatg 780
ccgcctgcta ccctccttcc caggggcaag cagagactga gaacattcca gagattagtt 840
ctcccaactg gaacgctgtg ggcctcaga gctcagcgat tctgcatcat ctgtgattac 900
gacccacagc ccgttcaaac gagcgttagt agcctgctaa cctgcaggaa gtggtgtgaa 960
tattaattac aagtgttcca aaggaaacgt gcctgcttct 1000

<210> 476
<211> 1000
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-286-375 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 10-286-375.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-286-375.mis2, potential complement

<220>
<221> primer_bind
<222> 128..146
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 528..546
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-286-375 potential probe

<400> 476
gctagactgg gttcaaatcc taaatcggcc attcagagcg tgaatacatt agaactggct 60
taaattagca tttaaaatgt caacaggatt aagtaagtag ttccttctca ctttttccac 120
aggaggtgag aaaggtctca gcaaggccct aggagggaag ggcgtgggga tgaaagggat 180
ccagagagtc tgtgcattgg cagagaagat agtgtaactg gcactgcggc tggagggctg 240
gtcccacagt gagctacagc cctgcccgct ggccgtggga gaggcttaaa acaaacgccg 300
gaagcaactc ccagccccat aaagatctgt gaccggcagc cccagacctg cctgccttcc 360
tgacttctgt tccagagcaa aggtcattca gccgcttgaa tcagcctttt ccccccaccc 420
ggtccccaac tttgtttacc cgataaggaa ggtcagcatt caaagtcaag aagcgccatt 480
tatcttcccg tgcgctctac raatagttcc gtgagaaaga tggccgggaa ctcgatcctg 540
ctggctgctg tctctattct ctcggcctgt cagcaaagta agaggcatgg gaagttcgtg 600
tgtgtgcgcg tgtgtgcgtg tgtgtgtgtg tgtgacaagg cttgcgggag agagagggag 660
ggagggagat gggtccggtg ttttgtttcc tacttgccct tgcaggtagc tctgggtcct 720
cagagcacag tcgcctcagg gtcacccatg ccgcctgcta ccctccttcc caggggcaag 780
cagagactga gaacattcca gagattagtt ctcccaactg gaacgctgtg ggcctcaga 840
gctcagcgat tctgcatcat ctgtgattac gacccacagc ccgttcaaac gagcgttagt 900
agcctgctaa cctgcaggaa gtggtgtgaa tattaattac aagtgttcca aaggaaacgt 960

gcctgcttct aaacctggtt gtgatttctt gaacgttgat 1000

<210> 477
<211> 1000
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 10-289-201 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 10-289-201.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-289-201.mis2, potential complement

<220>
<221> primer_bind
<222> 307..324
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 700..719
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-289-201 potential probe

<400> 477
tgcaacctcc acctcctggg ttcaaacgat tctcctgcct cagcttcctg agtagctggg 60
actgcaggtg cccgccacca tgcccagcta atttttgtat ttttagtaga gacgaggttt 120
cacaatgttg gccaggctgg tcttgaactc ctgacctcaa gtgattcacc ccccctcggc 180
ctctcaaagt gttgggaata caggcctgag ctaccacgtc cagcctcatt atagatttaa 240
gtgggaattt gttgatgttg aatcatgttg aaacattttt cttgagatta ttggcacatt 300
tgtttccttc ctatgtggat tctctctata ttctgaatat aagtatcttg tccaatatat 360
gttttgtgaa tatttttctca gtcgtcgtac aacatcttaa gagactgctg ttgtattttg 420
tgccttttct tttttttttcc cacccccccta tagtttttgc tacttgtctg ggtctggtgt 480
acatatatgg ccgtcaccta yacttctggg gatattcaga agctgctaaa aaacggtaag 540
gagaacccag taattttgta tttatgcaaa aagtagcagg ataaggtctg ggtcagtttc 600
cttctcctga gagatattaa cagcactgtg agttgtggtg gcaaaagtaa tccatactgt 660
ctgaggtcaa gtcttgccag ttcatacaca attaggcatg agatgggaaa atgcaagtat 720
aaaactgtgc actgaatgtg gactctagtt ccttgcaaaa attttgcatt gtctccagaa 780
agttaccgag gaaataatcc tgcctagcct tgataatgct ttgaatgttc aaagaaacca 840
agtgatctct atggctaggc attcccttta acttatgtga tgagctaaaa ttttcaaatt 900
gcaaaaatat agaagttctg gacagtgtta acgataggac agcctacctc aggactctca 960
gcttccttat tacagtccag tttgtcactt ttctccctca 1000

<210> 478
<211> 1000
<212> DNA
<213> Homo Sapiens

<220>
<221> allele

<222> 501
<223> 10-321-28 : polymorphic base A or G

<220>
<221> misc_binding
<222> 481..500
<223> 10-321-28.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 10-321-28.mis2, potential complement

<220>
<221> primer_bind
<222> 474..491
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 890..909
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 10-321-28 potential probe

<400> 478
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tgcacacccc cagccccatg tcccctcact tgtccccacg gggcagcacc ttgcttttgc      60
ccttttctc ctcctctatt tcaaaagagg cccccacccc tgacatctct ggctggaaag      120
gctgctgctg gggtggcccc gacccaagat ttacctggga atgggtagcc tcactcagaa     180
gggtgccctg atgtgggggc acaggtgggt ctttggggac ccctcctggg tggtgccagg     240
gagagaatag cggcttcagc atgcttcggg gcagctgtaa aacgaggggg tcctgcaaag     300
cgtgcagggt aagtggtgtc tggtgggagc cccgggtcct agcccaggct cttctgcctc     360
cacggctgca gctttggagc gatggtgtat tcaccacgga caggcatcat cctcaacaac     420
gagctcctgg acttatgcga gcgatgcccc cggggttccg gcaccacccc ctcacctggt     480
gagaacaaag cttcccaccc rgggtccaca agggcccccc accaggggag aggagggagg     540
gggctgggct ggggttgcat gctaacccct ggatgggtca ctgcacttgc caagacgctg     600
tttgctcagc agtgagtgga gacagggtgg gtggagctcc cggaaggtgc tggcccccag     660
ttccaggcga gcgttcccca tcctccatgg tgccctccat cttgatcaac aaagcccagg     720
ggtcgaagct agtgattggc ggggctggcg gggagctcat catctctgct gtggcccagg     780
tgagtctggg gctcctggct cgagtgtctc ctctctgggc agcatactgt ctgactgtct     840
ctggagtggg gatgtgaggg ctgatgtagg gtagcagggt gccccctttc tccctgaaac     900
cctcatctct cccccaggcc atcatgagca agctgtggct tggctttgac ctgagagcgg     960
ccattgcagc ccccatcctg catgtcaaca gcaagggctg                           1000
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<210> 479
<211> 422
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 265
<223> 10-98-265 : polymorphic base A or G

<220>
<221> misc_binding
<222> 245..264
<223> 10-98-265.mis1, potential

<220>

<221> misc_binding
<222> 266..285
<223> 10-98-265.mis2, potential complement

<220>
<221> primer_bind
<222> 1..19
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 404..422
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 253..277
<223> 10-98-265 potential probe

<400> 479
ctgtcttcag gaaactcaca ggctagggcc agagaaagct aatgctggat acatacatag 60
cagatacttg ggaaatgatg gtttccttgt ttctgtcttc cttctttcct caccttacac 120
tacacggttc aggatttgac acagtcacca cagccatctc ctggagcctc atgtaccttg 180
tgaccaagcc tgagatacag aggaagatcc agaaggwgct gggtacatgg gggcccccaa 240
ccctatagcc aggagaagcc ttgaraccca ggttgtttgt tcagtctaca aacacctgtt 300
atgtgcctgc tgtgtgcaag ccctgggcac acagtagtgc ctgcccttgc ctagaagatg 360
tgggaggtta gtggggtcgc agacttgtga atagacagtc ttacatagag tgacatgggg 420
ta 422

<210> 480
<211> 1000
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-157-115 : polymorphic base C or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-157-115.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-157-115.mis2, potential complement

<220>
<221> primer_bind
<222> 387..407
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 833..853
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-157-115 potential probe

<400> 480
gggagtgctg ccgccatcat ggtcaccaaa agccaccacc ccctgcttgt gttggacagg 60
cggtcatcaa ggcagaaccg actgacaacc tggtttctcc agtgcgagcc ttggcgatgg 120
aggccctctc gcacctgagg tgagctgggt tcccaccctc accccatccc aaggggtagg 180
gaaaagttca agaccattcc tcggtgctcc ttcaggggtt gtgcctcctt tttcctctcc 240
tccctctgta gcaggggtct cacttggcgg ctccccaggg caatgggcca gcctagatga 300
tgggggtcgg cctcagccac tcttttctat aattctcagc cagatttcaa gttgggtgct 360
tctccttgga tttatggcac atgggtgggc tgctcttcca ttgattgggg atattttgag 420
caaaataaca gtgataacac tgaagagcat tgcaagcatc cttcaagatg agtcaggctc 480
agtgagtgag ttgaagggct yagtcaacta tttgttgata ccactggtac aaaatgatct 540
aaagcccaag acttaccttc ctggagatgc caatccattg gtggggaggg ggaaagggga 600
agaagttatg gatttataaa attagtattt aaagagtttg ggtcatctct aagaatacct 660
cccctatagg ggaagattca ttacttaggc gcatagcaga actatctgtt actttaagct 720
gcatcaaaca ggcagatttt aaaataaatg tcatgaacat caactaagca caatgatatg 780
ctgagtactg aagggacaca gagatacata agacctagtc ccagcctttt aaggacttag 840
agataagaca gacacataca aacaggatta taggtcaaag ctgactaaca ggactgtgtt 900
tacaggtaaa cccacacaca catcagcaaa aaaatatctg agaacaaaaa aaaaggggct 960
actaacaaaa gcaactcagt ttatacaaaa ggagctatca 1000

<210> 481
<211> 1000
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-472-48 : polymorphic base G or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-472-48.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-472-48.mis2, potential complement

<220>
<221> primer_bind
<222> 454..472
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 919..939
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-472-48 potential probe

<400> 481
atgaagcgtt gttaacttgc ccctctctgc ccagcacctt ccttctctga cttcactgct 60
tggggagcat gctaatgatt ccttggtgtt aataactttg caattcttaa acaggtgaca 120
ttccaagcct gcagtatatc tgaggccaga tacctttatg atcagttggc tactatctgt 180
ccaattgttg taagtagaaa ttacctctta ttttaaatac tacttcgtat gaaataagat 240
agcatgtgca gaatttactg acagtgtgct atttaagtcc agttaagacc tcagtcagag 300
atggactaat ataaatagta tgtaggttta ggtataatga actgagagtc tacactgtag 360
aagtttactc ttgctagtac aacattgatt tgttaaatgt gaagtttgaa tgtggccatt 420

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ttcccctcccc catacttcat gtcctcacat tagagagagg atgatttaag tgaatcaaac     480
ccaaggaact ggattcttcc kggtatattt cactgtaaga taggcacagg tacatgtgct     540
ctgtatgggt tgcataaaca tgctttttga tcagaaatat aactgcatgg agcttttttt     600
agcatgtaag tgacactttg aatttgcagg agctgacttt tgtttgtttt tagatggctt     660
tgagtgctgc atctcccttt taccgaggct atgtgtcaga cattgattgt cgctggggag     720
tgatttctgc atctgtagat gatagaactc gggaggagcg aggactggag gtgggaattg     780
tttttcctta atagcccttt taagtcaagc aggtaaaatg gatcttttgt aactacttgc     840
aatttcagga tgtctccctg caatttttat ctgaaatggg gaaaaagatt tggtctaggt     900
ggggagttaa tttttatcgt atgttgatgt ctgtatttgt tttagcttca tttaaaatta     960
gtagtccgat ttttctatat tttggaagtg ctgatggctg                           1000
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<210> 482
<211> 1000
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-477-151 : polymorphic base G or A

<220>
<221> misc_binding
<222> 481..500
<223> 12-477-151.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-477-151.mis2, potential complement

<220>
<221> primer_bind
<222> 631..651
<223> upstream amplification primer, complement

<220>
<221> primer_bind
<222> 113..133
<223> downstream amplification primer

<220>
<221> misc_binding
<222> 489..513
<223> 12-477-151 potential probe

<220>
<221> misc_feature
<222> 419
<223> n=a, g, c or t

<400> 482

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tgtattagtc ttctatacct atctcctaca gaaaaaatct tttaagactt atcagttact      60
gtgacctacc atatcatggt tgaattcctc catgttaaga ccctactgtc tagaagtatg     120
gtgttagcag atgtactcat tgattggtac tgtctgtagt ttcattttga agcataaacc     180
tgagtaacat tcagtaagac tctgtatgtt cagaaaagat gtcacaatat taattgagcc     240
tctaacatca ctatttatgt ttctgaacat ttttacatac tgtcaaggca tctgaatata     300
ttcttaaagt tagaaaactg tatatgaagc attactgata ttgctggtat tactggaaag     360
accatatcct aacgagcttg ctaattagta ctctgtttct acatttcatg atataatcna     420
ggtgttttta aaaaaacatt ttaacagctt tattgagtta taattaacat aaagttaact     480
gcacatattt aaaatgtaca rtttggtaag ttttgatata tgtatacatc ataaaatcac     540
ctctgataat aagtatattc attatctcca aaaatgtcat catgcccctt tggtaatttc     600
ttcctctggc catcccatgc agctgatttg ctttctgtag tttgcatttt ctagattttc     660
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atatttaaga aatcatagtt tgcatttgat atctagtttc atatacctag gaaatcatcc 720
agcatatcct cttttggtct gccttcttag agtctacata aatattttga gatccatcca 780
tgttgttaca tgtgtcagta gttcattcct tttcgtcgct gagtaatatt tcattccatg 840
gttataccag tttgtttata cattcaccat ttgtgttgca ttcagttttt cactattata 900
aaaaaattat atgaacatta acatacaagt ttgtatgtat ggactaatgc ttttcttcat 960
cttattaccc taggagtagc gtgttgttaa ctttttaagg 1000

<210> 483
<211> 1000
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 501
<223> 12-479-214 : polymorphic base G or T

<220>
<221> misc_binding
<222> 481..500
<223> 12-479-214.mis1, potential

<220>
<221> misc_binding
<222> 502..521
<223> 12-479-214.mis2, potential complement

<220>
<221> primer_bind
<222> 288..305
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 753..773
<223> downstream amplification primer, complement

<220>
<221> misc_binding
<222> 489..513
<223> 12-479-214 potential probe

<220>
<221> misc_feature
<222> 519
<223> n=a, g, c or t

<400> 483
gggggagaag gttacgatgg aataggagac agagagggaa tacatagaac ctcatgcaat 60
tcttagatct gcctcctctc ctgttactcc cccttctctc actccactcc agccatacta 120
gcctccttac tgttctttga ccactctagc ttccctccct gcctgaggcc tttgtatcag 180
ctgttccctc tgcctggaat ggctgaattt ccttacctcc ttcaaatcct tgcttaatcc 240
ctccttctca aagagaccta aacaccctgg ccaccttctt taatataata ttctgaccat 300
gcacctaacc tcacaccctg atcccctgct ctaatctgtc tttttcataa tgtttatcaa 360
cttctgactt tctatatagt tatttattgt gcatgttgtg tgcctcccct tgctaaaatg 420
taagctccac aagggcaggc atgcttgttt gttatagtca gtgatgtatc ctaagcacct 480
agaacagtac ttgcctgatg ktgagtgctc aatgaacant ttgcagaaaa atgaatgaat 540
gaatgccagg cattcataag cccacaaaaa aaatctatgt gtcattctac accttcactg 600
tagcctaatg cttcatgctc caaaaagaaa gaagaggcat cattttctct gtttcctgtg 660
ctccacctct cgcacattcc ccactctcct agctgctgtc tttcccctga ctttttttgtc 720
tagtaacaag aactccctgc ctggtgaaag tcggcatttt cttctcaatt tacttctaaa 780
tattagtgct tttgtttacc ctgtgaagca gatggtaaca gttaatgtaa taaccagact 840
gtctcctctc tcttgtttga cacagtagat gtcatgagcc atattttccc ttggttatat 900

ttgttaaata gaagacagga gatctgctat atggtcaaca ttaggtctgg tcactgcttt 960
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<210> 484
<211> 1000
<212> DNA
<213> Homo Sapiens

<220>
<221> allele
<222> 500
<223> 10-290-328 : deletion of G

<220>
<221> misc_binding
<222> 481..499
<223> 10-290-328.mis1, potential

<220>
<221> primer_bind
<222> 174..193
<223> upstream amplification primer

<220>
<221> primer_bind
<222> 573..592
<223> downstream amplification primer, complement

<400> 484
ctttgaatgt tcaaagaaac caagtgatct ctatggctag gcattcccttt taacttatgt 60
gatgagctaa aattttcaaa ttgcaaaaat atagaagttc tggacagtgt taacgatagg 120
acagcctacc tcaggactct cagcttcctt attacagtcc agtttgtcac ttttctccct 180
catgtccact ctgcaggatc accggtttcc gactgagtct ggggattttg gccttgttga 240
ccctcctagg tgccctggga attgcaaaca gctttctgga tgaatatctg gacctcaata 300
ttgccaagaa actgaggcgg caattctaac tttttctctt ccctttaatg cttgcagaag 360
ctgttcccac catgaaggta atatggtatc atttgttaaa taaaaataaa gtctttattc 420
tgtttttctt gaaatggctt tgtagaaaca cacactttag agaatacatt tcctgtttaa 480
gaactgaaat ttgcttgggg taggtacatc catatcatca gtggaagtgt gttgtgccct 540
agttttagaa atgcatgctg aagtcatgac cggttgtgta gggacacagc agcctgaccc 600
gtgtgctggc cgttccgagg actactgaca tatcctgcca ctctgactgc ttctctcttg 660
atggaaagtt tcagacagaa gctgataaag cagctgagcc ctttcattgg ttataggaaa 720
acaacagata ggaaggcatg tgggggacat caggcaaaca catagagtag ccagagaagg 780
gagtcatcaa ctgatagcac aaaacaaaac aggttataga aggctgggcg tggtggctca 840
tgcctgtaat cccagcactt tgagaagccg aggcgggcag atcacaaggt caggagatcg 900
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<210> 485
<211> 49312
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 5466..7466
<223> 5'regulatory region

<220>
<221> exon
<222> 7467..7725
<223> exon 1

<220>

<221> exon
<222> 20256..20355
<223> exon 2

<220>
<221> exon
<222> 36905..36975
<223> exon 3

<220>
<221> exon
<222> 45167..45248
<223> exon 4

<220>
<221> exon
<222> 45728..45965
<223> exon 5

<220>
<221> misc_feature
<222> 45966..49312
<223> 3'regulatory region

<220>
<221> allele
<222> 7564
<223> 10-286-289 : polymorphic base G or C

<220>
<221> allele
<222> 7619
<223> 10-286-345 : polymorphic base A or T

<220>
<221> allele
<222> 7649
<223> 10-286-375 : polymorphic base A or G

<220>
<221> allele
<222> 17258
<223> 12-425-57 : polymorphic base A or G

<220>
<221> allele
<222> 21590
<223> 12-421-135 : insertion of T

<220>
<221> allele
<222> 21595
<223> 12-421-140 : polymorphic base A or G

<220>
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cccgataagg aaggtcagca ttcaaagtca agwagcgcca tttatcttcc cgtgcgctct    180
acraatagtt ccgtgagaaa g atg gcc ggg aac tcg atc ctg ctg gct gct      231
                        Met Ala Gly Asn Ser Ile Leu Leu Ala Ala
                        1               5                   10
gtc tct att ctc tcg gcc tgt cag caa aac aaa act gtg tgg agt ttt      279
Val Ser Ile Leu Ser Ala Cys Gln Gln Asn Lys Thr Val Trp Ser Phe
                15                  20                  25
atc cta tat tca taa ttacattgtg gatggctggg tggtatttca aycaagtttt      334
Ile Leu Tyr Ser  *
            30
```

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tgctacttgt ctgggtctgg tgtacatata tggccgtcac ctayacttct ggggatattc     394
agaagctgct aaaaaacgga tcaccggttt cygactgagt ctggggattt tggccttgtt     454
gaccctccta ggtgccctgg gaattgcaaa cagctttctg gatgaatatc tggacctcaa     514
tattgccaag aaactgaggc ggcaattcta actttttctc ttccctttaa tgcttgcaga     574
agctgttccc accatgaagg taatatggta tcatttgtta aataaaaata aagtctttat     634
tctgtttttc ttgaaa                                                     650

<210> 488
<211> 147
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> 93
<223> Xaa=Tyr or His

<220>
<221> VARIANT
<222> 109
<223> Xaa=Arg or Stop

<400> 488
Met Ala Gly Asn Ser Ile Leu Leu Ala Ala Val Ser Ile Leu Ser Ala
1               5                   10                  15
Cys Gln Gln Ser Tyr Phe Ala Leu Gln Val Gly Lys Ala Arg Leu Lys
            20                  25                  30
Tyr Lys Val Thr Pro Pro Ala Val Thr Gly Ser Pro Glu Phe Glu Arg
        35                  40                  45
Val Phe Arg Ala Gln Gln Asn Cys Val Glu Phe Tyr Pro Ile Phe Ile
    50                  55                  60
Ile Thr Leu Trp Met Ala Gly Trp Tyr Phe Asn Gln Val Phe Ala Thr
65                  70                  75                  80
Cys Leu Gly Leu Val Tyr Ile Tyr Gly Arg His Leu Xaa Phe Trp Gly
                85                  90                  95
Tyr Ser Glu Ala Ala Lys Lys Arg Ile Thr Gly Phe Xaa Leu Ser Leu
            100                 105                 110
Gly Ile Leu Ala Leu Leu Thr Leu Leu Gly Ala Leu Gly Ile Ala Asn
        115                 120                 125
Ser Phe Leu Asp Glu Tyr Leu Asp Leu Asn Ile Ala Lys Lys Leu Arg
    130                 135                 140
Arg Gln Phe
145

<210> 489
<211> 30
<212> PRT
<213> Homo sapiens

<400> 489
Met Ala Gly Asn Ser Ile Leu Leu Ala Ala Val Ser Ile Leu Ser Ala
1               5                   10                  15
Cys Gln Gln Asn Lys Thr Val Trp Ser Phe Ile Leu Tyr Ser
            20                  25                  30

<210> 490
<211> 357
<212> DNA
<213> Homo sapiens

<400> 490
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aaaggtcatt cagccgcttg aatcagcctt ttccccccac ccggtcccca actttgttta     120
```

```
cccgataagg aaggtcagca ttcaaagtca agaagcgcca tttatcttcc cgtgcgctct    180
acaaatagtt ccgtgagaaa gatggccggg aactcgatcc tgctggctgc tgtctctatt    240
ctctcggcct gtcagcaaag ttattttgct ttgcaagttg gaaaggcaag attaaratac    300
aaagttacgc ccccagcagt cactgggtca ccagagtttg agagagtatt tcgggca       357
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<210> 491
<211> 274
<212> DNA
<213> Homo sapiens

<400> 491

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ccccaacttt gtttacccga taaggaaggt cagcattcaa agtcaagaag cgccatttat     60
cttcccgtgc gctctacaaa tagttccgtg agaaagatgg ccgggaactc gatcctgctg    120
gctgctgtct ctattctctc ggcctgtcag caaaacaaaa ctgtgtggag ttttatccta    180
tattcataat tacattgtgg atggctgggt ggtatttcaa ccaagttttt gctacttgtc    240
tgggtctggt gtacatatat ggccgtcact tggg                                274
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<210> 492
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> sequencing oligonucleotide PrimerPU

<400> 492
tgtaaaacga cggccagt 18

<210> 493
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> sequencing oligonucleotide PrimerRP

<400> 493
caggaaacag ctatgacc 18